

# Raksha Singh

## List of Publications by Year in descending order

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Version: 2024-02-01

20  
papers

624  
citations

759233

12  
h-index

752698

20  
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23  
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23  
docs citations

23  
times ranked

944  
citing authors

#	ARTICLE	IF	CITATIONS
1	Rice Mitogen-Activated Protein Kinase Interactome Analysis Using the Yeast Two-Hybrid System. <i>Plant Physiology</i> , 2012, 160, 477-487.	4.8	81
2	The rice MAPK interactome: the biological significance of MAPK components in hormone signal transduction. <i>Plant Cell Reports</i> , 2013, 32, 923-931.	5.6	68
3	Rice OsACDR1 ( <i>Oryza sativa</i> Accelerated Cell Death and Resistance 1) Is a Potential Positive Regulator of Fungal Disease Resistance. <i>Molecules and Cells</i> , 2009, 28, 431-440.	2.6	67
4	Magnaporthe oryzae Effector AVR-Pii Helps to Establish Compatibility by Inhibition of the Rice NADP-Malic Enzyme Resulting in Disruption of Oxidative Burst and Host Innate Immunity. <i>Molecules and Cells</i> , 2016, 39, 426-438.	2.6	67
5	Understanding the Responses of Rice to Environmental Stress Using Proteomics. <i>Journal of Proteome Research</i> , 2013, 12, 4652-4669.	3.7	63
6	Systematic Secretome Analyses of Rice Leaf and Seed Callus Suspension-Cultured Cells: Workflow Development and Establishment of High-Density Two-Dimensional Gel Reference Maps. <i>Journal of Proteome Research</i> , 2008, 7, 5187-5210.	3.7	58
7	Exploring DNA variant segregation types in pooled genome sequencing enables effective mapping of weeping trait in <i>Malus</i> . <i>Journal of Experimental Botany</i> , 2018, 69, 1499-1516.	4.8	33
8	Secretome analysis of <i>Magnaporthe oryzae</i> using in vitro systems. <i>Proteomics</i> , 2012, 12, 878-900.	2.2	30
9	Visualization of Multicolored in vivo Organelle Markers for Co-Localization Studies in <i>Oryza sativa</i> . <i>Molecules and Cells</i> , 2017, 40, 828-836.	2.6	26
10	Two Chloroplast-Localized Proteins: AtNHR2A and AtNHR2B, Contribute to Callose Deposition During Nonhost Disease Resistance in <i>Arabidopsis</i> . <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 1280-1290.	2.6	22
11	Recovery Plan for Tar Spot of Corn, Caused by <i>Phyllachora maydis</i> . <i>Plant Health Progress</i> , 2021, 22, 596-616.	1.4	22
12	Protein interactome analysis of 12 mitogen-activated protein kinase kinase kinase in rice using a yeast two-hybrid system. <i>Proteomics</i> , 2014, 14, 105-115.	2.2	14
13	Mitogen-Activated Protein Kinase OsMEK2 and OsMPK1 Signaling Is Required for Ferroptotic Cell Death in Rice-Magnaporthe oryzae Interactions. <i>Frontiers in Plant Science</i> , 2021, 12, 710794.	3.6	14
14	Draft Genome Sequence Resource for <i>Phyllachora maydis</i> —An Obligate Pathogen That Causes Tar Spot of Corn with Recent Economic Impacts in the United States. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 884-887.	2.6	11
15	Exploring the Corn Microbiome: A Detailed Review on Current Knowledge, Techniques, and Future Directions. <i>PhytoFrontiers</i> , 2022, 2, 158-175.	1.6	11
16	The Arabidopsis Proteins AtNHR2A and AtNHR2B Are Multi-Functional Proteins Integrating Plant Immunity With Other Biological Processes. <i>Frontiers in Plant Science</i> , 2020, 11, 232.	3.6	9
17	Dissecting the functional domains of the Arabidopsis thaliana nonhost resistance 2B (AtNHR2B) protein. <i>Plant Signaling and Behavior</i> , 2018, 13, e1530024.	2.4	8
18	Plant proteomics in India and Nepal: current status and challenges ahead. <i>Physiology and Molecular Biology of Plants</i> , 2013, 19, 461-477.	3.1	7

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19	The <i>Pseudomonas syringae</i> type III effector HopG1 triggers necrotic cell death that is attenuated by AtNHR2B. <i>Scientific Reports</i> , 2022, 12, 5388.	3.3	7
20	Yeast Two-Hybrid System for Dissecting the Rice MAPK Interactome. <i>Methods in Molecular Biology</i> , 2014, 1171, 195-216.	0.9	5