Nam-Soo Jwa

List of Publications by Year in descending order

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NAM-SOO LWA

#	Article	IF	CITATIONS
1	Plant secretome: Unlocking secrets of the secreted proteins. Proteomics, 2010, 10, 799-827.	2.2	255
2	Integrated Transcriptomics, Proteomics, and Metabolomics Analyses To Survey Ozone Responses in the Leaves of Rice Seedling. Journal of Proteome Research, 2008, 7, 2980-2998.	3.7	159
3	Signalling molecules and blast pathogen attack activates rice OsPR1a and OsPR1b genes: A model illustrating components participating during defence/stress response. Plant Physiology and Biochemistry, 2001, 39, 1095-1103.	5.8	126
4	Convergent Evolution of Pathogen Effectors toward Reactive Oxygen Species Signaling Networks in Plants. Frontiers in Plant Science, 2017, 8, 1687.	3.6	126
5	Iron- and Reactive Oxygen Species-Dependent Ferroptotic Cell Death in Rice- <i>Magnaporthe oryzae</i> Interactions. Plant Cell, 2019, 31, 189-209.	6.6	123
6	Role ofÂdefense/stress-related marker genes, proteins andÂsecondary metabolites inÂdefining rice self-defense mechanisms. Plant Physiology and Biochemistry, 2006, 44, 261-273.	5.8	122
7	Molecular cloning and mRNA expression analysis of a novel rice (Oryzasativa L.) MAPK kinase kinase, OsEDR1, an ortholog of ArabidopsisAtEDR1, reveal its role in defense/stress signalling pathways and development. Biochemical and Biophysical Research Communications, 2003, 300, 868-876.	2.1	94
8	Importance of ascorbate peroxidases OsAPX1 and OsAPX2 in the rice pathogen response pathways and growth and reproduction revealed by their transcriptional profiling. Gene, 2003, 322, 93-103.	2.2	84
9	Rice Mitogen-Activated Protein Kinase Interactome Analysis Using the Yeast Two-Hybrid System Â. Plant Physiology, 2012, 160, 477-487.	4.8	81
10	Using metabolic profiling to assess plant-pathogen interactions: an example using rice (Oryza sativa) and the blast pathogen Magnaporthe grisea. European Journal of Plant Pathology, 2011, 129, 539-554.	1.7	68
11	The rice MAPKK–MAPK interactome: the biological significance of MAPK components in hormone signal transduction. Plant Cell Reports, 2013, 32, 923-931.	5.6	68
12	Rice OsACDR1 (Oryza sativa Accelerated Cell Death and Resistance 1) Is a Potential Positive Regulator of Fungal Disease Resistance. Molecules and Cells, 2009, 28, 431-440.	2.6	67
13	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. Molecules and Cells, 2016, 39, 426-438.	2.6	67
14	Understanding the Responses of Rice to Environmental Stress Using Proteomics. Journal of Proteome Research, 2013, 12, 4652-4669.	3.7	63
15	Effects of signaling molecules, protein phosphatase inhibitors and blast pathogen (Magnaporthe) Tj ETQq1 1 (peroxidase (OsPHGPX) gene in seedling leaves. Gene, 2002, 283, 227-236.	0.784314 rg 2.2	gBT /Overloc 60
16	The rice (Oryza sativa) Blast Lesion Mimic Mutant, blm, may confer resistance to blast pathogens by triggering multiple defense-associated signaling pathways. Plant Physiology and Biochemistry, 2005, 43, 397-406.	5.8	60
17	Rejuvenating rice proteomics: Facts, challenges, and visions. Proteomics, 2006, 6, 5549-5576.	2.2	58
18	Systematic Secretome Analyses of Rice Leaf and Seed Callus Suspension-Cultured Cells: Workflow Development and Establishment of High-Density Two-Dimensional Gel Reference Maps. Journal of Proteome Research, 2008, 7, 5187-5210.	3.7	58

NAM-SOO JWA

#	Article	IF	CITATIONS
19	Novel rice OsSIPK is a multiple stress responsive MAPK family member showing rhythmic expression at mRNA level. Planta, 2008, 227, 981-990.	3.2	57
20	Functional characterization ofÂOsRacB GTPase – aÂpotentially negative regulator ofÂbasal disease resistance inÂrice. Plant Physiology and Biochemistry, 2006, 44, 68-77.	5.8	43
21	Differential Expression of Defense/Stress-Related Marker Proteins in Leaves of a Unique Rice Blast Lesion Mimic Mutant (blm). Journal of Proteome Research, 2006, 5, 2586-2598.	3.7	37
22	Secretome analysis of <i>Magnaporthe oryzae</i> using in vitro systems. Proteomics, 2012, 12, 878-900.	2.2	30
23	Visualization of Multicolored in vivo Organelle Markers for Co-Localization Studies in Oryza sativa. Molecules and Cells, 2017, 40, 828-836.	2.6	26
24	RSL Class II Transcription Factors Guide the Nuclear Localization of RHL1 to Regulate Root Hair Development. Plant Physiology, 2019, 179, 558-568.	4.8	23
25	Rice OsSIPK and its orthologs: A "central master switch―for stress responses. Biochemical and Biophysical Research Communications, 2009, 379, 649-653.	2.1	21
26	Molecular Cloning and Functional Analysis of Rice (Oryza sativa L.) OsNDR1 on Defense Signaling Pathway. Plant Pathology Journal, 2005, 21, 149-157.	1.7	21
27	Two novel protein kinase genes,OsMSRPK1 andOsMSURPK2, are regulated by diverse environmental stresses in rice. Journal of Plant Biology, 2006, 49, 247-256.	2.1	16
28	Protein interactome analysis of 12 mitogenâ€activated protein kinase kinase kinase in rice using a yeast twoâ€hybrid system. Proteomics, 2014, 14, 105-115.	2.2	14
29	Mitogen-Activated Protein Kinase OsMEK2 and OsMPK1 Signaling Is Required for Ferroptotic Cell Death in Rice–Magnaporthe oryzae Interactions. Frontiers in Plant Science, 2021, 12, 710794.	3.6	14
30	Focal Accumulation of ROS Can Block Pyricularia oryzae Effector BAS4-Expression and Prevent Infection in Rice. International Journal of Molecular Sciences, 2020, 21, 6196.	4.1	13
31	Growth retardation and death of rice plants irradiated with carbon ion beams is preceded by very early dose- and time-dependent gene expression changes. Molecules and Cells, 2008, 25, 272-8.	2.6	13
32	Yeast Two-Hybrid System for Dissecting the Rice MAPK Interactome. Methods in Molecular Biology, 2014, 1171, 195-216.	0.9	5
33	Secretome: Toward Deciphering the Secretory Pathways and Beyond. , 0, , 83-90.		3
34	Rice <i>OsSIPK</i> . Plant Signaling and Behavior, 2009, 4, 448-450.	2.4	1