Hiromasa Saitoh

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A genetically linked pair of NLR immune receptors shows contrasting patterns of evolution. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	19
2	Multiple variants of the fungal effector AVR-Pik bind the HMA domain of the rice protein OsHIPP19, providing a foundation to engineer plant defense. Journal of Biological Chemistry, 2021, 296, 100371.	3.4	57
3	Using genomics tools to understand plant resistance against pathogens: A case study of Magnaporthe-rice interactions. , 2020, , 181-188.		2
4	The rice NLR pair Pikp-1/Pikp-2 initiates cell death through receptor cooperation rather than negative regulation. PLoS ONE, 2020, 15, e0238616.	2.5	31
5	Comparative Analysis of Bacterial Diversity and Community Structure in the Rhizosphere and Root Endosphere of Two Halophytes, <i>Salicornia europaea</i> and <i>Glaux maritima</i> , Collected from Two Brackish Lakes in Japan. Microbes and Environments, 2020, 35, n/2	1.6	11
6	Cross-reactivity of a rice NLR immune receptor to distinct effectors from the rice blast pathogen Magnaporthe oryzae provides partial disease resistance. Journal of Biological Chemistry, 2019, 294, 13006-13016.	3.4	29
7	RNAâ€Seq of <i>in planta</i> â€expressed <i>Magnaporthe oryzae</i> genes identifies <i>MoSVP</i> as a highly expressed gene required for pathogenicity at the initial stage of infection. Molecular Plant Pathology, 2019, 20, 1682-1695.	4.2	20
8	Conserved fungal effector suppresses PAMP-triggered immunity by targeting plant immune kinases. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 496-505.	7.1	155
9	Bacterial Diversity Associated With the Rhizosphere and Endosphere of Two Halophytes: Glaux maritima and Salicornia europaea. Frontiers in Microbiology, 2018, 9, 2878.	3.5	73
10	Polymorphic residues in rice NLRs expand binding and response to effectors of the blast pathogen. Nature Plants, 2018, 4, 576-585.	9.3	127
11	Lessons in Effector and NLR Biology of Plant-Microbe Systems. Molecular Plant-Microbe Interactions, 2018, 31, 34-45.	2.6	109
12	Genome analysis of the foxtail millet pathogen Sclerospora graminicola reveals the complex effector repertoire of graminicolous downy mildews. BMC Genomics, 2017, 18, 897.	2.8	27
13	Host specialization of the blast fungus Magnaporthe oryzae is associated with dynamic gain and loss of genes linked to transposable elements. BMC Genomics, 2016, 17, 370.	2.8	157
14	Rice Exo70 interacts with a fungal effector <i>, </i> <scp>AVR</scp> â€Pii, and is required for <scp>AVR</scp> â€Piiâ€ŧriggered immunity. Plant Journal, 2015, 83, 875-887.	5.7	128
15	<pre><scp>M</scp>ut<scp>M</scp>apâ€<scp>G</scp>ap: wholeâ€genome resequencing of mutant <scp>F</scp>2 progeny bulk combined with <i>de novo</i>assembly of gap regions identifies the rice blast resistance gene <scp><i>Pii</i></scp>. New Phytologist, 2013, 200, 276-283.</pre>	7.3	196
16	Large-Scale Gene Disruption in Magnaporthe oryzae Identifies MC69, a Secreted Protein Required for Infection by Monocot and Dicot Fungal Pathogens. PLoS Pathogens, 2012, 8, e1002711.	4.7	150
17	Effector-Mediated Suppression of Chitin-Triggered Immunity by <i>Magnaporthe oryzae</i> Is Necessary for Rice Blast Disease Â. Plant Cell, 2012, 24, 322-335.	6.6	493
18	Arms race coâ€evolution of <i>Magnaporthe oryzae AVRâ€Pik</i> and rice <i>Pik</i> genes driven by their physical interactions. Plant Journal, 2012, 72, 894-907.	5.7	249

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19	A multifaceted genomics approach allows the isolation of the rice <i>Pia</i> â€blast resistance gene consisting of two adjacent NBSâ€LRR protein genes. Plant Journal, 2011, 66, 467-479.	5.7	287
20	Characterization of endo-1,3–1,4-β-glucanases in GH family 12 from Magnaporthe oryzae. Applied Microbiology and Biotechnology, 2010, 88, 1113-1123.	3.6	29
21	Association Genetics Reveals Three Novel Avirulence Genes from the Rice Blast Fungal Pathogen <i>Magnaporthe oryzae</i> Â Â. Plant Cell, 2009, 21, 1573-1591.	6.6	410
22	Gene expression analysis of plant host-pathogen interactions by SuperSAGE. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 15718-15723.	7.1	273