

# Hiromasa Saitoh

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2454290/publications.pdf>

Version: 2024-02-01

22  
papers

3,110  
citations

430874

18  
h-index

677142

22  
g-index

31  
all docs

31  
docs citations

31  
times ranked

3019  
citing authors

#	ARTICLE	IF	CITATIONS
1	Effector-Mediated Suppression of Chitin-Triggered Immunity by <i>Magnaporthe oryzae</i> Is Necessary for Rice Blast Disease. <i>Plant Cell</i> , 2012, 24, 322-335.	6.6	493
2	Association Genetics Reveals Three Novel Avirulence Genes from the Rice Blast Fungal Pathogen <i>Magnaporthe oryzae</i> . <i>Plant Cell</i> , 2009, 21, 1573-1591.	6.6	410
3	A multifaceted genomics approach allows the isolation of the rice blast resistance gene consisting of two adjacent NBS-LRR protein genes. <i>Plant Journal</i> , 2011, 66, 467-479.	5.7	287
4	Gene expression analysis of plant host-pathogen interactions by SuperSAGE. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 15718-15723.	7.1	273
5	Arms race co-evolution of <i>Magnaporthe oryzae</i> AVR-Pik and rice Pik genes driven by their physical interactions. <i>Plant Journal</i> , 2012, 72, 894-907.	5.7	249
6	Whole-genome resequencing of mutant progeny bulk combined with <i>de novo</i> assembly of gap regions identifies the rice blast resistance gene <i>Pii</i> . <i>New Phytologist</i> , 2013, 200, 276-283.	7.3	196
7	Host specialization of the blast fungus <i>Magnaporthe oryzae</i> is associated with dynamic gain and loss of genes linked to transposable elements. <i>BMC Genomics</i> , 2016, 17, 370.	2.8	157
8	Conserved fungal effector suppresses PAMP-triggered immunity by targeting plant immune kinases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 496-505.	7.1	155
9	Large-Scale Gene Disruption in <i>Magnaporthe oryzae</i> Identifies MC69, a Secreted Protein Required for Infection by Monocot and Dicot Fungal Pathogens. <i>PLoS Pathogens</i> , 2012, 8, e1002711.	4.7	150
10	Rice Exo70 interacts with a fungal effector, AVR-Pii, and is required for AVR-Pii-triggered immunity. <i>Plant Journal</i> , 2015, 83, 875-887.	5.7	128
11	Polymorphic residues in rice NLRs expand binding and response to effectors of the blast pathogen. <i>Nature Plants</i> , 2018, 4, 576-585.	9.3	127
12	Lessons in Effector and NLR Biology of Plant-Microbe Systems. <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 34-45.	2.6	109
13	Bacterial Diversity Associated With the Rhizosphere and Endosphere of Two Halophytes: <i>Glaux maritima</i> and <i>Salicornia europaea</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2878.	3.5	73
14	Multiple variants of the fungal effector AVR-Pik bind the HMA domain of the rice protein OsHIPP19, providing a foundation to engineer plant defense. <i>Journal of Biological Chemistry</i> , 2021, 296, 100371.	3.4	57
15	The rice NLR pair <i>Pikp-1/Pikp-2</i> initiates cell death through receptor cooperation rather than negative regulation. <i>PLoS ONE</i> , 2020, 15, e0238616.	2.5	31
16	Characterization of endo-1,4- $\beta$ -glucanases in GH family 12 from <i>Magnaporthe oryzae</i> . <i>Applied Microbiology and Biotechnology</i> , 2010, 88, 1113-1123.	3.6	29
17	Cross-reactivity of a rice NLR immune receptor to distinct effectors from the rice blast pathogen <i>Magnaporthe oryzae</i> provides partial disease resistance. <i>Journal of Biological Chemistry</i> , 2019, 294, 13006-13016.	3.4	29
18	Genome analysis of the foxtail millet pathogen <i>Sclerospora graminicola</i> reveals the complex effector repertoire of gramminicolous downy mildews. <i>BMC Genomics</i> , 2017, 18, 897.	2.8	27

#	ARTICLE	IF	CITATIONS
19	RNA-Seq of <i>in planta</i> -expressed <i>Magnaporthe oryzae</i> genes identifies <i>MoSVP</i> as a highly expressed gene required for pathogenicity at the initial stage of infection. <i>Molecular Plant Pathology</i> , 2019, 20, 1682-1695.	4.2	20
20	A genetically linked pair of NLR immune receptors shows contrasting patterns of evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	19
21	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. <i>Microbes and Environments</i> , 2020, 35, n/a.	1.6	11
22	Using genomics tools to understand plant resistance against pathogens: A case study of <i>Magnaporthe</i> -rice interactions. , 2020, , 181-188.		2