

GaÃ«tan Ja Thilliez

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1749167/publications.pdf>

Version: 2024-02-01

17
papers

1,156
citations

759055

12
h-index

887953

17
g-index

23
all docs

23
docs citations

23
times ranked

2019
citing authors

#	ARTICLE	IF	CITATIONS
1	The Rice Resistance Protein Pair RGA4/RGA5 Recognizes the <i>Magnaporthe oryzae</i> Effectors AVR-Pia and AVR1-CO39 by Direct Binding. <i>Plant Cell</i> , 2013, 25, 1463-1481.	3.1	466
2	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021, 374, 423-431.	6.0	144
3	Utilizing Omicron-Technologies to Identify and Prioritize Novel Sources of Resistance to the Oomycete Pathogen <i>Phytophthora infestans</i> in Potato Germplasm Collections. <i>Frontiers in Plant Science</i> , 2016, 7, 672.	1.7	69
4	A Perspective on CRN Proteins in the Genomics Age: Evolution, Classification, Delivery and Function Revisited. <i>Frontiers in Plant Science</i> , 2017, 8, 99.	1.7	66
5	<i>Phytophthora infestans</i> RXLR effectors act in concert at diverse subcellular locations to enhance host colonization. <i>Journal of Experimental Botany</i> , 2019, 70, 343-356.	2.4	66
6	The role of effectors in nonhost resistance to filamentous plant pathogens. <i>Frontiers in Plant Science</i> , 2014, 5, 582.	1.7	59
7	SGI-4 in Monophasic <i>Salmonella Typhimurium</i> ST34 Is a Novel ICE That Enhances Resistance to Copper. <i>Frontiers in Microbiology</i> , 2019, 10, 1118.	1.5	53
8	Evolution of <i>Salmonella enterica</i> serotype Typhimurium driven by anthropogenic selection and niche adaptation. <i>PLoS Genetics</i> , 2020, 16, e1008850.	1.5	48
9	Pathogen enrichment sequencing (PenSeq) enables population genomic studies in oomycetes. <i>New Phytologist</i> , 2019, 221, 1634-1648.	3.5	43
10	<i>Albugo candida</i> race diversity, ploidy and host-associated microbes revealed using DNA sequence capture on diseased plants in the field. <i>New Phytologist</i> , 2019, 221, 1529-1543.	3.5	41
11	Genomic epidemiology and the role of international and regional travel in the SARS-CoV-2 epidemic in Zimbabwe: a retrospective study of routinely collected surveillance data. <i>The Lancet Global Health</i> , 2021, 9, e1658-e1666.	2.9	19
12	Ecological niche adaptation of <i>Salmonella Typhimurium</i> U288 is associated with altered pathogenicity and reduced zoonotic potential. <i>Communications Biology</i> , 2021, 4, 498.	2.0	17
13	Whole-genome epidemiology links phage-mediated acquisition of a virulence gene to the clonal expansion of a pandemic <i>Salmonella enterica</i> serovar Typhimurium clone. <i>Microbial Genomics</i> , 2020, 6, .	1.0	15
14	Random mutagenesis screen shows that <i>Phytophthora capsici</i> CRN83_152-mediated cell death is not required for its virulence function(s). <i>Molecular Plant Pathology</i> , 2018, 19, 1114-1126.	2.0	14
15	Genomic diversity of <i>Escherichia coli</i> isolates from non-human primates in the Gambia. <i>Microbial Genomics</i> , 2020, 6, .	1.0	12
16	Enhanced biofilm and extracellular matrix production by chronic carriage versus acute isolates of <i>Salmonella Typhi</i> . <i>PLoS Pathogens</i> , 2021, 17, e1009209.	2.1	9
17	Molecular epidemiology of extended-spectrum beta-lactamase-producing extra-intestinal pathogenic <i>Escherichia coli</i> strains over a 2-year period (2017-2019) from Zimbabwe. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2021, , 1.	1.3	5