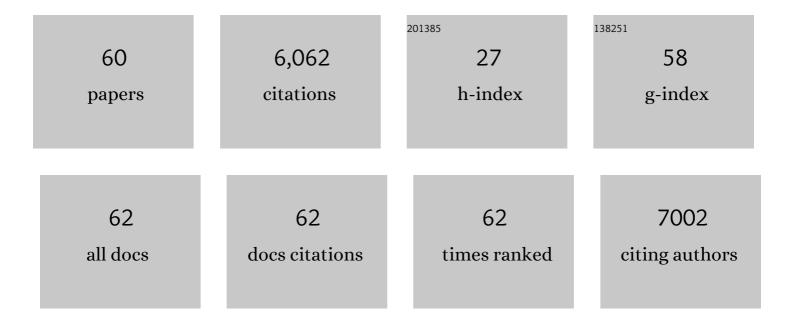
Claudia Barros Monteiro-Vitorello

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A bacterial type three secretion-based delivery system for functional characterization ofÂSporisorium scitamineumÂplant immune suppressing effector proteins. Phytopathology, 2022, , .	1.1	2
2	Revealing the high variability on nonconserved core and mobile elements of Austropuccinia psidii and other rust mitochondrial genomes. PLoS ONE, 2021, 16, e0248054.	1.1	5
3	Complete Chromosome-Scale Genome Sequence Resource for <i>Sporisorium panici-leucophaei</i> , the Causal Agent of Sourgrass Smut Disease. Molecular Plant-Microbe Interactions, 2021, 34, 448-452.	1.4	3
4	A genome sequence resource for the genus <i>Passiflora</i> , the genome of the wild diploid species <i>Passiflora organensis</i> . Plant Genome, 2021, 14, e20117.	1.6	8
5	Arabidopsis-Based Dual-Layered Biological Network Analysis Elucidates Fully Modulated Pathways Related to Sugarcane Resistance on Biotrophic Pathogen Infection. Frontiers in Plant Science, 2021, 12, 707904.	1.7	0
6	Characterization of genes responsive to osmotic and oxidative stresses of the sugarcane bacterial pathogen Leifsonia xyli subsp. xyli. Brazilian Journal of Microbiology, 2020, 51, 77-86.	0.8	7
7	Differential responses of genes and enzymes associated with ROS protective responses in the sugarcane smut fungus. Fungal Biology, 2020, 124, 1039-1051.	1.1	8
8	Multiple resistance of <i>Plasmopara viticola</i> to QoI and CAA fungicides in Brazil. Plant Pathology, 2020, 69, 1708-1720.	1.2	13
9	Leaping into the Unknown World of Sporisorium scitamineum Candidate Effectors. Journal of Fungi (Basel, Switzerland), 2020, 6, 339.	1.5	7
10	Time-series expression profiling of sugarcane leaves infected with Puccinia kuehnii reveals an ineffective defense system leading to susceptibility. Plant Cell Reports, 2020, 39, 873-889.	2.8	25
11	Genome survey of resistance gene analogs in sugarcane: genomic features and differential expression of the innate immune system from a smut-resistant genotype. BMC Genomics, 2019, 20, 809.	1.2	22
12	Didelphis albiventris: an overview of unprecedented transcriptome sequencing of the white-eared opossum. BMC Genomics, 2019, 20, 866.	1.2	0
13	Genome-wide alternative splicing landscapes modulated by biotrophic sugarcane smut pathogen. Scientific Reports, 2019, 9, 8876.	1.6	24
14	Aulas Práticas de Laboratório como Método de Ensino de Genética Molecular. Revista De Graduação USP, 2018, 3, 81-85.	0.2	2
15	Revisiting Meiosis in Sugarcane: Chromosomal Irregularities and the Prevalence of Bivalent Configurations. Frontiers in Genetics, 2018, 9, 213.	1.1	31
16	Comparative Genomics of Smut Pathogens: Insights From Orphans and Positively Selected Genes Into Host Specialization. Frontiers in Microbiology, 2018, 9, 660.	1.5	33
17	Novel Insights Into the Early Stages of Ratoon Stunting Disease of Sugarcane Inferred from Transcript and Protein Analysis. Phytopathology, 2018, 108, 1455-1466.	1.1	25
18	Progress in understanding fungal diseases affecting sugarcane: smut. Burleigh Dodds Series in Agricultural Science, 2018, , 221-243.	0.1	2

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19	Sugarcane smut: shedding light on the development of the whip-shaped sorus. Annals of Botany, 2017, 119, mcw169.	1.4	25
20	Functional analysis of oxidative burst in sugarcane smut-resistant and -susceptible genotypes. Planta, 2017, 245, 749-764.	1.6	43
21	Metabolome Dynamics of Smutted Sugarcane Reveals Mechanisms Involved in Disease Progression and Whip Emission. Frontiers in Plant Science, 2017, 8, 882.	1.7	40
22	Molecular variability and genetic relationship among Brazilian strains of the sugarcane smut fungus. FEMS Microbiology Letters, 2016, 363, fnw277.	0.7	6
23	Draft Genome Sequence of <i>Burkholderia ambifaria</i> RZ2MS16, a Plant Growth-Promoting Rhizobacterium Isolated from Guarana, a Tropical Plant. Genome Announcements, 2016, 4, .	0.8	6
24	A stable <i>Leifsonia xyli</i> subsp. <i>xyli </i> <scp>GFP</scp> â€ŧagged strain reveals a new colonization niche in sugarcane tissues. Plant Pathology, 2016, 65, 154-162.	1.2	19
25	<i>Sporisorium scitamineum</i> colonisation of sugarcane genotypes susceptible and resistant to smut revealed by <scp>GFP</scp> â€tagged strains. Annals of Applied Biology, 2016, 169, 329-341.	1.3	16
26	Development of a qPCR for Leifsonia xyli subsp. xyli and quantification of the effects of heat treatment of sugarcane cuttings on Lxx. Crop Protection, 2016, 80, 51-55.	1.0	22
27	RNAseq Transcriptional Profiling following Whip Development in Sugarcane Smut Disease. PLoS ONE, 2016, 11, e0162237.	1.1	56
28	Analysis of plant gene expression during passion fruit– <i>Xanthomonas axonopodis</i> interaction implicates lipoxygenase 2 in host defence. Annals of Applied Biology, 2015, 167, 135-155.	1.3	33
29	Complete Genome Sequence of Sporisorium scitamineum and Biotrophic Interaction Transcriptome with Sugarcane. PLoS ONE, 2015, 10, e0129318.	1.1	93
30	Building the sugarcane genome for biotechnology and identifying evolutionary trends. BMC Genomics, 2014, 15, 540.	1.2	136
31	The Role of Prophage in Plant-Pathogenic Bacteria. Annual Review of Phytopathology, 2013, 51, 429-451.	3.5	76
32	Complete Genome Sequence of Leifsonia xyli subsp. <i>cynodontis</i> Strain DSM46306, a Gram-Positive Bacterial Pathogen of Grasses. Genome Announcements, 2013, 1, .	0.8	9
33	Leptospira interrogans serovar Copenhageni Harbors Two lexA Genes Involved in SOS Response. PLoS ONE, 2013, 8, e76419.	1.1	13
34	Strain-specific polyketide synthase genes of Aspergillus niger. International Journal of Food Microbiology, 2012, 155, 137-145.	2.1	32
35	Xylella fastidiosa comparative genomic database is an information resource to explore the annotation, genomic features, and biology of different strains. Genetics and Molecular Biology, 2012, 35, 149-152.	0.6	15
36	Genetic Diversity and a PCR-Based Method for <i>Xanthomonas axonopodis</i> Detection in Passion Fruit. Phytopathology, 2011, 101, 416-424.	1.1	15

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37	An EST-based analysis identifies new genes and reveals distinctive gene expression features of Coffea arabica and Coffea canephora. BMC Plant Biology, 2011, 11, 30.	1.6	67
38	The Cryphonectria parasitica mitochondrial rns gene: Plasmid-like elements, introns and homing endonucleases. Fungal Genetics and Biology, 2009, 46, 837-848.	0.9	41
39	Characterization of new IS elements and studies of their dispersion in two subspecies of Leifsonia xyli. BMC Microbiology, 2008, 8, 127.	1.3	12
40	The Universal Protein Resource (UniProt). Nucleic Acids Research, 2007, 35, D193-D197.	6.5	488
41	The Universal Protein Resource (UniProt). Nucleic Acids Research, 2007, 36, D190-D195.	6.5	852
42	Brazilian coffee genome project: an EST-based genomic resource. Brazilian Journal of Plant Physiology, 2006, 18, 95-108.	0.5	112
43	XylellaandXanthomonasMobil'omics. OMICS A Journal of Integrative Biology, 2005, 9, 146-159.	1.0	46
44	Comparative bioinformatic analysis of genes expressed in common bean (Phaseolus vulgaris L.) seedlings. Genome, 2005, 48, 562-570.	0.9	50
45	Genome features of Leptospira interrogans serovar Copenhageni. Brazilian Journal of Medical and Biological Research, 2004, 37, 459-477.	0.7	175
46	Comparative Genomics of Two Leptospira interrogans Serovars Reveals Novel Insights into Physiology and Pathogenesis. Journal of Bacteriology, 2004, 186, 2164-2172.	1.0	406
47	The Genome Sequence of the Gram-Positive Sugarcane Pathogen Leifsonia xyli subsp. xyli. Molecular Plant-Microbe Interactions, 2004, 17, 827-836.	1.4	119
48	EST analysis of mRNAs expressed during embryogenesis in Gallus gallus. International Journal of Developmental Biology, 2004, 48, 333-337.	0.3	10
49	Analysis and Functional Annotation of an Expressed Sequence Tag Collection for Tropical Crop Sugarcane. Genome Research, 2003, 13, 2725-2735.	2.4	254
50	Comparative Analyses of the Complete Genome Sequences of Pierce's Disease and Citrus Variegated Chlorosis Strains of Xylella fastidiosa. Journal of Bacteriology, 2003, 185, 1018-1026.	1.0	307
51	COMPARATIVEGENOMICANALYSIS OFPLANT-ASSOCIATEDBACTERIA. Annual Review of Phytopathology, 2002, 40, 169-189.	3.5	171
52	Comparison of the genomes of two Xanthomonas pathogens with differing host specificities. Nature, 2002, 417, 459-463.	13.7	1,074
53	A new member of the chalcone synthase (CHS) family in sugarcane. Genetics and Molecular Biology, 2001, 24, 257-261.	0.6	4
54	Screening and genetic improvement of pectinolytic fungi for degumming of textile fibers. Brazilian Journal of Microbiology, 2001, 32, 320.	0.8	29

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#	Article	IF	CITATIONS
55	The genome sequence of the plant pathogen Xylella fastidiosa. Nature, 2000, 406, 151-157.	13.7	827
56	A circular mitochondrial plasmid incites hypovirulence in some strains of Cryphonectria parasitica. Current Genetics, 2000, 37, 242-256.	0.8	30
57	A long open reading frame in the mitochondrial LSU rRNA group-l intron of Cryphonectria parasitica encodes a putative S5 ribosomal protein fused to a maturase. Current Genetics, 1999, 35, 109-117.	0.8	13
58	Physical and genetic map of the mitochondrial genome of Cryphonectria parasitica Ep155. Current Genetics, 1996, 30, 34-43.	0.8	23
59	A cytoplasmically transmissible hypovirulence phenotype associated with mitochondrial DNA mutations in the chestnut blight fungus Cryphonectria parasitica Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 5935-5939.	3.3	48
60	Elevated mitochondrial alternative oxidase activity in dsRNA-free, hypovirulent isolates of Cryphonectria parasitica. Physiological and Molecular Plant Pathology, 1993, 42, 455-463.	1.3	32