

Silvia Restrepo

List of Publications by Year in descending order

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129
papers

4,927
citations

126907

33
h-index

106344

65
g-index

138
all docs

138
docs citations

138
times ranked

6324
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequence and analysis of the Irish potato famine pathogen <i>Phytophthora infestans</i> . <i>Nature</i> , 2009, 461, 393-398.	27.8	1,405
2	Complex history of the amphibian-killing chytrid fungus revealed with genome resequencing data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 9385-9390.	7.1	238
3	The Irish potato famine pathogen <i>Phytophthora infestans</i> originated in central Mexico rather than the Andes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 8791-8796.	7.1	186
4	Comparative Analyses of Potato Expressed Sequence Tag Libraries. <i>Plant Physiology</i> , 2003, 131, 419-429.	4.8	174
5	Surviving Chytridiomycosis: Differential Anti-Batrachochytrium dendrobatidis Activity in Bacterial Isolates from Three Lowland Species of <i>Atelopus</i> . <i>PLoS ONE</i> , 2012, 7, e44832.	2.5	100
6	Evaluation of Adult Chronic Chagas' Heart Disease Diagnosis by Molecular and Serological Methods. <i>Journal of Clinical Microbiology</i> , 2009, 47, 3945-3951.	3.9	89
7	The Plant Pathogen <i>Phytophthora andina</i> Emerged via Hybridization of an Unknown <i>Phytophthora</i> Species and the Irish Potato Famine Pathogen, <i>P. infestans</i> . <i>PLoS ONE</i> , 2011, 6, e24543.	2.5	88
8	Gene expression profile in response to <i>Xanthomonas axonopodis</i> pv. <i>manihotis</i> infection in cassava using a cDNA microarray. <i>Plant Molecular Biology</i> , 2005, 57, 393-410.	3.9	86
9	Effects of dark septate endophytes on tomato plant performance. <i>Mycorrhiza</i> , 2011, 21, 413-422.	2.8	77
10	Genomes-based phylogeny of the genus <i>Xanthomonas</i> . <i>BMC Microbiology</i> , 2012, 12, 43.	3.3	71
11	Production of Polyunsaturated Fatty Acids and Lipids from Autotrophic, Mixotrophic and Heterotrophic cultivation of <i>Galdieria</i> sp. strain USBA-GBX-832. <i>Scientific Reports</i> , 2019, 9, 10791.	3.3	69
12	Five new species of entomopathogenic fungi from the Amazon and evolution of neotropical <i>Ophiocordyceps</i> . <i>Fungal Biology</i> , 2015, 119, 901-916.	2.5	68
13	Phylogeography and molecular epidemiology of Papaya ringspot virus. <i>Virus Research</i> , 2011, 159, 132-140.	2.2	63
14	Genetic diversity of <i>Phytophthora infestans</i> in the Northern Andean region. <i>BMC Genetics</i> , 2011, 12, 23.	2.7	58
15	Characterization of <i>Phytophthora infestans</i> Populations in Colombia: First Report of the A2 Mating Type. <i>Phytopathology</i> , 2009, 99, 82-88.	2.2	56
16	Microbial and Functional Diversity within the Phyllosphere of Espeletia Species in an Andean High-Mountain Ecosystem. <i>Applied and Environmental Microbiology</i> , 2016, 82, 1807-1817.	3.1	55
17	A unigene catalogue of 5700 expressed genes in cassava. <i>Plant Molecular Biology</i> , 2004, 56, 541-554.	3.9	53
18	Exploring the biocontrol potential of fungal endophytes from an Andean Colombian Paramo ecosystem. <i>BioControl</i> , 2012, 57, 697-710.	2.0	53

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19	AFLP fingerprinting: an efficient technique for detecting genetic variation of <i>Xanthomonas axonopodis</i> pv. <i>manihotis</i> . <i>Microbiology</i> (United Kingdom), 1999, 145, 107-114.	1.8	52
20	Evolutionary Origins of Rhizarian Parasites. <i>Molecular Biology and Evolution</i> , 2016, 33, 980-983.	8.9	47
21	Speciation Associated with Shifts in Migratory Behavior in an Avian Radiation. <i>Current Biology</i> , 2020, 30, 1312-1321.e6.	3.9	45
22	Survey and analysis of microsatellites from transcript sequences in <i>Phytophthora</i> species: frequency, distribution, and potential as markers for the genus. <i>BMC Genomics</i> , 2006, 7, 245.	2.8	43
23	Colonization of roots of cultivated <i>Solanum lycopersicum</i> by dark septate and other ascomycetous endophytes. <i>Mycologia</i> , 2011, 103, 710-721.	1.9	43
24	Entomopathogens of Amazonian stick insects and locusts are members of the <i>Beauveria</i> species complex (<i>Cordyceps</i> sensu stricto). <i>Mycologia</i> , 2014, 106, 260-275.	1.9	43
25	Species from the <i>Colletotrichum acutatum</i> , <i>Colletotrichum boninense</i> and <i>Colletotrichum gloeosporioides</i> species complexes associated with tree tomato and mango crops in Colombia. <i>Plant Pathology</i> , 2016, 65, 227-237.	2.4	42
26	Genomic Survey of Pathogenicity Determinants and VNTR Markers in the Cassava Bacterial Pathogen <i>Xanthomonas axonopodis</i> pv. <i>Manihotis</i> Strain CIO151. <i>PLoS ONE</i> , 2013, 8, e79704.	2.5	42
27	Novel Protocol for Persister Cells Isolation. <i>PLoS ONE</i> , 2014, 9, e88660.	2.5	42
28	AFLP assessment of genetic variability in cassava accessions (<i>Manihot esculenta</i>) resistant and susceptible to the cassava bacterial blight (CBB). <i>Genome</i> , 1999, 42, 163-172.	2.0	40
29	Biological and molecular characterization of the response of tomato plants treated with <i>Trichoderma koningiopsis</i> . <i>Physiological and Molecular Plant Pathology</i> , 2009, 74, 111-120.	2.5	40
30	Detection and functional characterization of a large genomic deletion resulting in decreased pathogenicity in <i>Ralstonia solanacearum</i> race 3 biovar 2 strains. <i>Environmental Microbiology</i> , 2011, 13, 3172-3185.	3.8	39
31	An EST resource for cassava and other species of Euphorbiaceae. <i>Plant Molecular Biology</i> , 2004, 56, 527-539.	3.9	38
32	An Ephemeral Sexual Population of <i>Phytophthora infestans</i> in the Northeastern United States and Canada. <i>PLoS ONE</i> , 2014, 9, e116354.	2.5	38
33	TALE1 from <i>Xanthomonas axonopodis</i> pv. <i>manihotis</i> acts as a transcriptional activator in plant cells and is important for pathogenicity in cassava plants. <i>Molecular Plant Pathology</i> , 2013, 14, 84-95.	4.2	37
34	Speciation in Fungal and Oomycete Plant Pathogens. <i>Annual Review of Phytopathology</i> , 2014, 52, 289-316.	7.8	36
35	Annotation of a hybrid partial genome of the coffee rust (<i>Hemileia vastatrix</i>) contributes to the gene repertoire catalog of the Pucciniales. <i>Frontiers in Plant Science</i> , 2014, 5, 594.	3.6	34
36	Physiological and Molecular Characterization of Atypical Isolates of <i>Malassezia furfur</i> . <i>Journal of Clinical Microbiology</i> , 2009, 47, 48-53.	3.9	33

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37	The role of type III effectors from <i>Xanthomonas axonopodis</i> pv. <i>manihotis</i> in virulence and suppression of plant immunity. <i>Molecular Plant Pathology</i> , 2018, 19, 593-606.	4.2	33
38	Antibacterial Activities of Azole Complexes Combined with Silver Nanoparticles. <i>Molecules</i> , 2018, 23, 361.	3.8	33
39	Genetic Structure and Population Dynamics of <i>Xanthomonas axonopodis</i> pv. <i>manihotis</i> in Colombia from 1995 to 1999. <i>Applied and Environmental Microbiology</i> , 2004, 70, 255-261.	3.1	32
40	A Complex Population Structure of the Cassava Pathogen <i>Xanthomonas axonopodis</i> pv. <i>manihotis</i> in Recent Years in the Caribbean Region of Colombia. <i>Microbial Ecology</i> , 2014, 68, 155-167.	2.8	32
41	Genotyping of <i>Fusarium</i> Isolates from Onychomycoses in Colombia: Detection of Two New Species Within the <i>Fusarium solani</i> Species Complex and In Vitro Antifungal Susceptibility Testing. <i>Mycopathologia</i> , 2016, 181, 165-174.	3.1	32
42	Lipid Metabolic Versatility in <i>Malassezia</i> spp. Yeasts Studied through Metabolic Modeling. <i>Frontiers in Microbiology</i> , 2017, 8, 1772.	3.5	31
43	Recent progress in the characterization of molecular determinants in the <i>Xanthomonas axonopodis</i> pv. <i>manihotis</i> –cassava interaction. <i>Plant Molecular Biology</i> , 2004, 56, 573-584.	3.9	30
44	<i>Lecanicillium sabanense</i> sp. nov. (Cordycipitaceae) a new fungal entomopathogen of coccids. <i>Phytotaxa</i> , 2015, 234, 63.	0.3	30
45	Draft Genome Sequence of the Animal and Human Pathogen <i>Malassezia pachydermatis</i> Strain CBS 1879. <i>Genome Announcements</i> , 2015, 3, .	0.8	30
46	<i>Fusarium</i> species detected in onychomycosis in Colombia. <i>Mycoses</i> , 2009, 52, 350-356.	4.0	29
47	Amatoxin and phallotoxin composition in species of the genus <i>Amanita</i> in Colombia: A taxonomic perspective. <i>Toxicon</i> , 2011, 58, 583-590.	1.6	29
48	A One Health Perspective to Recognize <i>Fusarium</i> as Important in Clinical Practice. <i>Journal of Fungi</i> (Basel, Switzerland), 2020, 6, 235.	3.5	29
49	Virulence Gene Expression in <i>Malassezia</i> spp from Individuals with Seborrheic Dermatitis. <i>Journal of Investigative Dermatology</i> , 2011, 131, 2134-2136.	0.7	28
50	Selection of antagonistic bacteria isolated from the <i>Physalis peruviana</i> rhizosphere against <i>Fusarium oxysporum</i> . <i>Journal of Applied Microbiology</i> , 2011, 111, 707-716.	3.1	26
51	The genomic study of an environmental isolate of <i>Scedosporium apiospermum</i> shows its metabolic potential to degrade hydrocarbons. <i>Standards in Genomic Sciences</i> , 2017, 12, 71.	1.5	25
52	Contrasting Symbiotic Patterns in Two Closely Related Lineages of Trimembered Lichens of the Genus <i>Peltigera</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2770.	3.5	25
53	Entomopathogens of Amazonian stick insects and locusts are members of the <i>Beauveria</i> species complex (<i>Cordyceps</i> sensu stricto). <i>Mycologia</i> , 2014, 106, 260-275.	1.9	25
54	De novo pyrimidine biosynthesis in the oomycete plant pathogen <i>Phytophthora infestans</i> . <i>Gene</i> , 2014, 537, 312-321.	2.2	24

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55	A genome-scale metabolic model of potato late blight suggests a photosynthesis suppression mechanism. <i>BMC Genomics</i> , 2018, 19, 863.	2.8	24
56	Analysis of <i>Malassezia</i> Lipidome Disclosed Differences Among the Species and Reveals Presence of Unusual Yeast Lipids. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 338.	3.9	22
57	Isoenzyme characterization of proteases and amylases and partial purification of proteases from filamentous fungi causing biodeterioration of industrial paper. <i>International Biodeterioration and Biodegradation</i> , 2009, 63, 169-175.	3.9	21
58	Metabolomic profile and nucleoside composition of <i>Cordyceps nidus</i> sp. nov. (Cordycipitaceae): A new source of active compounds. <i>PLoS ONE</i> , 2017, 12, e0179428.	2.5	21
59	Characterization of pathogenic and nonpathogenic strains of <i>Xanthomonas axonopodis</i> pv. <i>manihotis</i> by PCR-based DNA fingerprinting techniques. <i>FEMS Microbiology Letters</i> , 2002, 215, 23-31.	1.8	20
60	Characterization of cellulases of fungal endophytes isolated from <i>Espeletia</i> spp.. <i>Journal of Microbiology</i> , 2012, 50, 1009-1013.	2.8	20
61	Gene regulatory networks on transfer entropy (GRNTE): a novel approach to reconstruct gene regulatory interactions applied to a case study for the plant pathogen <i>Phytophthora infestans</i> . <i>Theoretical Biology and Medical Modelling</i> , 2019, 16, 7.	2.1	20
62	Assembly and Analysis of Differential Transcriptome Responses of <i>Hevea brasiliensis</i> on Interaction with <i>Microcyclus ulei</i> . <i>PLoS ONE</i> , 2015, 10, e0134837.	2.5	18
63	Network Analyses in Plant Pathogens. <i>Frontiers in Microbiology</i> , 2018, 9, 35.	3.5	18
64	COVID-19 spread, detection, and dynamics in Bogota, Colombia. <i>Nature Communications</i> , 2021, 12, 4726.	12.8	18
65	Targeted metabolic reconstruction: a novel approach for the characterization of plant-pathogen interactions. <i>Briefings in Bioinformatics</i> , 2011, 12, 151-162.	6.5	16
66	Population typing of the causal agent of cassava bacterial blight in the Eastern Plains of Colombia using two types of molecular markers. <i>BMC Microbiology</i> , 2014, 14, 161.	3.3	16
67	The type VI secretion system of <i>Xanthomonas phaseoli</i> pv. <i>manihotis</i> is involved in virulence and in vitro motility. <i>BMC Microbiology</i> , 2021, 21, 14.	3.3	16
68	Seborrheic dermatitis: predisposing factors and ITS2 secondary structure for <i>Malassezia</i> phylogenetic analysis. <i>Medical Mycology</i> , 2013, 51, 868-875.	0.7	15
69	Mycofier: a new machine learning-based classifier for fungal ITS sequences. <i>BMC Research Notes</i> , 2016, 9, 402.	1.4	15
70	Identification of genes in cassava that are differentially expressed during infection with <i>Xanthomonas axonopodis</i> pv. <i>manihotis</i> . <i>Molecular Plant Pathology</i> , 2004, 5, 549-558.	4.2	14
71	Gene profiling in partially resistant and susceptible near-isogenic tomatoes in response to late blight in the field. <i>Molecular Plant Pathology</i> , 2013, 14, 171-184.	4.2	14
72	Resistance spectrum of selected <i>Manihot esculenta</i> genotypes under field conditions. <i>Field Crops Research</i> , 2000, 65, 69-77.	5.1	13

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73	Characterization of the First Batrachochytrium dendrobatidis Isolate from the Colombian Andes, an Amphibian Biodiversity Hotspot. EcoHealth, 2013, 10, 72-76.	2.0	13
74	Identification of Transcription Factor Genes and Their Correlation with the High Diversity of Stramenopiles. PLoS ONE, 2014, 9, e111841.	2.5	12
75	Phytophthora infestans Dihydroorotate Dehydrogenase Is a Potential Target for Chemical Control “A Comparison With the Enzyme From Solanum tuberosum. Frontiers in Microbiology, 2019, 10, 1479.	3.5	12
76	Isolation and characterization of two strains of Fusarium oxysporum causing potato dry rot in Solanum tuberosum in Colombia. Revista Iberoamericana De Micologia, 2011, 28, 166-172.	0.9	11
77	Physiological and molecular characterization of Phytophthora infestans isolates from the Central Colombian Andean Region. Revista Iberoamericana De Micologia, 2013, 30, 81-87.	0.9	11
78	Influence of agricultural activities in the structure and metabolic functionality of paramo soil samples in Colombia studied using a metagenomics analysis in dynamic state. Ecological Modelling, 2017, 351, 63-76.	2.5	11
79	A Genome-Scale Metabolic Reconstruction of Phytophthora infestans With the Integration of Transcriptional Data Reveals the Key Metabolic Patterns Involved in the Interaction of Its Host. Frontiers in Genetics, 2018, 9, 244.	2.3	11
80	Computational models in plant-pathogen interactions: the case of Phytophthora infestans. Theoretical Biology and Medical Modelling, 2009, 6, 24.	2.1	10
81	In Colombia the Eurasian fungus <i>Amanita muscaria</i> is expanding its range into native, tropical <i>Quercus humboldtii</i> forests. Mycologia, 2019, 111, 758-771.	1.9	10
82	Is the Phenomenon of Mefenoxam-Acquired Resistance in <i>Phytophthora infestans</i> Universal?. Plant Disease, 2020, 104, 211-221.	1.4	10
83	Draft genome and description of <i>Consotaella salsifontis</i> gen. nov. sp. nov., a halophilic, free-living, nitrogen-fixing alphaproteobacterium isolated from an ancient terrestrial saline spring. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 3744-3751.	1.7	10
84	<i>Salifodinibacter halophilus</i> gen. nov., sp. nov., a halophilic gammaproteobacterium in the family Salinisphaeraceae isolated from a salt mine in the Colombian Andes. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5888-5898.	1.7	10
85	Computational Biology in Colombia. PLoS Computational Biology, 2009, 5, e1000535.	3.2	9
86	An Optimized Microsatellite Scheme for Assessing Populations of <i>Xanthomonas phaseoli</i> pv. <i>manihotis</i> . Phytopathology, 2019, 109, 859-869.	2.2	9
87	First Report of <i>Colletotrichum kahawae</i> subsp. <i>ciggaro</i> Causing Anthracnose Disease on Tree Tomato in Cundinamarca, Colombia. Plant Disease, 2018, 102, 2031-2031.	1.4	9
88	Discovery of <i>Phytophthora infestans</i> Genes Expressed in Planta through Mining of cDNA Libraries. PLoS ONE, 2010, 5, e9847.	2.5	8
89	Recovery of mitosporic fungi actively growing in soils after bacterial bioremediation of oily sludge and their potential for removing recalcitrant hydrocarbons. International Biodeterioration and Biodegradation, 2011, 65, 649-655.	3.9	8
90	In vitro and in silico characterization of metagenomic soil-derived cellulases capable of hydrolyzing oil palm empty fruit bunch. Biotechnology Reports (Amsterdam, Netherlands), 2017, 15, 55-62.	4.4	8

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91	Genome-Wide Association Study Identifies Single Nucleotide Polymorphism Markers Associated with Mycelial Growth (at 15, 20, and 25°C), Mefenoxam Resistance, and Mating Type in <i>Phytophthora infestans</i> . <i>Phytopathology</i> , 2020, 110, 822-833.	2.2	8
92	Developing a taxonomic identification system of <i>Phytophthora</i> species based on microsatellites. <i>Revista Iberoamericana De Micologia</i> , 2013, 30, 88-95.	0.9	7
93	Chromosome 10 in the tomato plant carries clusters of genes responsible for field resistance/defence to <i>Phytophthora infestans</i> . <i>Genomics</i> , 2013, 101, 249-255.	2.9	7
94	Defining the phylogenetic position of <i>Amanita</i> species from Andean Colombia. <i>Mycologia</i> , 2017, 109, 261-276.	1.9	7
95	Draft genome sequence of <i>Pseudomonas extremaustralis</i> strain USBA-GBX 515 isolated from Superparamo soil samples in Colombian Andes. <i>Standards in Genomic Sciences</i> , 2017, 12, 78.	1.5	7
96	New Therapeutic Candidates for the Treatment of <i>Malassezia pachydermatis</i> -Associated Infections. <i>Scientific Reports</i> , 2020, 10, 4860.	3.3	7
97	TAL Effector Repertoires of Strains of <i>Xanthomonas phaseoli</i> pv. <i>manihotis</i> in Commercial Cassava Crops Reveal High Diversity at the Country Scale. <i>Microorganisms</i> , 2021, 9, 315.	3.6	7
98	Mesoscale Modeling of the <i>Bacillus Thuringiensis</i> Sporulation Network Based on Stochastic Kinetics and Its Application for in Silico Scale-Down. , 2009, , .		6
99	A new method for designing degenerate primers and its use in the identification of sequences in <i>Brachiaria</i> showing similarity to apomixis-associated genes. <i>Bioinformatics</i> , 2010, 26, 2053-2054.	4.1	6
100	An RNAi in silico approach to find an optimal shRNA cocktail against HIV-1. <i>Virology Journal</i> , 2010, 7, 369.	3.4	6
101	Differential PbP27 expression in the yeast and mycelial forms of the <i>Paracoccidioides brasiliensis</i> species complex. <i>Fungal Genetics and Biology</i> , 2011, 48, 1087-1095.	2.1	6
102	Defining species boundaries in the genus <i>Phytophthora</i> : the case of <i>Phytophthora andina</i> A response to <i>Phytophthora andina</i> sp. nov., a newly identified heterothallic pathogen of solanaceous hosts in the Andean highlands™ (Oliva et al., 2010). <i>Plant Pathology</i> , 2012, 61, 215-220.	2.4	6
103	Compartmentalized metabolic network reconstruction of microbial communities to determine the effect of agricultural intervention on soils. <i>PLoS ONE</i> , 2017, 12, e0181826.	2.5	6
104	Gene co-expression network for <i>Xanthomonas</i> -challenged cassava reveals key regulatory elements of immunity processes. <i>European Journal of Plant Pathology</i> , 2019, 153, 1083-1104.	1.7	6
105	A Checklist of Ectomycorrhizal Mushrooms Associated with <i>Quercus humboldtii</i> in Colombia. , 2020, , 425-450.		6
106	A whole genome duplication drives the genome evolution of <i>Phytophthora betacei</i> , a closely related species to <i>Phytophthora infestans</i> . <i>BMC Genomics</i> , 2021, 22, 795.	2.8	6
107	<i>Colletotrichum</i> Species Complexes Associated with Crops in Northern South America: A Review. <i>Agronomy</i> , 2022, 12, 548.	3.0	6
108	Development of a genetic tool for functional screening of anti-malarial bioactive extracts in metagenomic libraries. <i>Malaria Journal</i> , 2015, 14, 233.	2.3	5

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109	Genome-Scale Metabolic Model of <i>Xanthomonas phaseoli</i> pv. <i>manihotis</i> : An Approach to Elucidate Pathogenicity at the Metabolic Level. <i>Frontiers in Genetics</i> , 2020, 11, 837.	2.3	5
110	A network model for biofilm development in <i>Escherichia coli</i> K-12. <i>Theoretical Biology and Medical Modelling</i> , 2011, 8, 34.	2.1	4
111	Genomic Variability of <i>Phytophthora palmivora</i> Isolates from Different Oil Palm Cultivation Regions in Colombia. <i>Phytopathology</i> , 2020, 110, 1553-1564.	2.2	4
112	Effector Repertoire of <i>Phytophthora betacei</i> : In Search of Possible Virulence Factors Responsible for Its Host Specificity. <i>Frontiers in Genetics</i> , 2020, 11, 579.	2.3	4
113	Comprehensive Time-Series Analysis of the Gene Expression Profile in a Susceptible Cultivar of Tree Tomato (<i>Solanum betaceum</i>) During the Infection of <i>Phytophthora betacei</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 730251.	3.6	4
114	A comparison between functional frequency and metabolic flows framed by biogeochemical cycles in metagenomes: The case of "El Coquito" hot spring located at Colombia's national Nevados park. <i>Ecological Modelling</i> , 2015, 313, 259-265.	2.5	3
115	<i>Physalis peruviana</i> responses to <i>Phytophthora infestans</i> are typical of an incompatible interaction. <i>Canadian Journal of Plant Pathology</i> , 2015, 37, 106-117.	1.4	3
116	Searching for the Mechanism that Mediates Mefenoxam-Acquired Resistance in <i>Phytophthora infestans</i> and How It Is Regulated. <i>Phytopathology</i> , 2022, 112, 1118-1133.	2.2	3
117	Determining Whether Geographic Origin and Potato Genotypes Shape the Population Structure of <i>Phytophthora infestans</i> in the Central Region of Colombia. <i>Phytopathology</i> , 2019, 109, 145-154.	2.2	2
118	Differential Susceptibility of Tree Tomato (<i>Solanum betaceum</i>) Cultivars to Late Blight Caused by <i>Phytophthora betacei</i> . <i>Plant Disease</i> , 2020, 104, 1113-1117.	1.4	2
119	Two Clonal Species of <i>Phytophthora</i> Associated to Solanaceous Crops Coexist in Central and Southern Colombia. <i>Phytopathology</i> , 2020, 110, 1342-1351.	2.2	2
120	Genotypic and phenotypic characterization of <i>Streptomyces</i> species associated with potato crops in the central part of Colombia. <i>Plant Pathology</i> , 2022, 71, 750-761.	2.4	2
121	Phenotypic and Genotypic Characterization of <i>Phytophthora infestans</i> Isolates Associated with Tomato and Potato Crops in Colombia. <i>Phytopathology</i> , 2022, 112, 1783-1794.	2.2	2
122	Multivariate Method for Inferential Identification of Differentially Expressed Genes in Gene Expression Experiments. <i>Journal of Computational Biology</i> , 2019, 26, 866-874.	1.6	1
123	Design and validation of a transposon that promotes expression of genes in episomal DNA. <i>Journal of Biotechnology</i> , 2020, 310, 1-5.	3.8	1
124	Application of Genome Studies of Coffee Rust. <i>Advances in Intelligent Systems and Computing</i> , 2014, , 133-139.	0.6	1
125	Data Mining of the Coffee Rust Genome. <i>Nature Precedings</i> , 2012, , .	0.1	0
126	Draft genome sequence of <i>Dethiosulfovibrio salsuginis</i> DSM 21565T an anaerobic, slightly halophilic bacterium isolated from a Colombian saline spring. <i>Standards in Genomic Sciences</i> , 2017, 12, 86.	1.5	0

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127	FBA Analysis, Plant-Pathogen Interactions. , 2013, , 733-736.		0
128	Metagenome, Metabolic Reconstruction and Analysis. , 2013, , 1283-1287.		0
129	Analysis of Metabolic Functionality and Thermodynamic Feasibility of a Metagenomic Sample from â€œEl Coquitoâ€•Hot Spring. Advances in Intelligent Systems and Computing, 2014, , 287-293.	0.6	0