Silvia Restrepo

List of Publications by Year
in descending order

129	4,927	126907	106344
papers	citations	33 h-index	65 g-index

138	138	138	6324
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genotypic and phenotypic characterization of Streptomyces species associated with potato crops in the central part of Colombia. Plant Pathology, 2022, 71, 750-761.	2.4	2
2	Searching for the Mechanism that Mediates Mefenoxam-Acquired Resistance in Phytophthora infestans and How It Is Regulated. Phytopathology, 2022, 112, 1118-1133.	2.2	3
3	Phenotypic and Genotypic Characterization of Phytophthora infestans Isolates Associated with Tomato and Potato Crops in Colombia. Phytopathology, 2022, 112, 1783-1794.	2.2	2
4	Colletotrichum Species Complexes Associated with Crops in Northern South America: A Review. Agronomy, 2022, 12, 548.	3.0	6
5	The type VI secretion system of Xanthomonas phaseoli pv. manihotis is involved in virulence and in vitro motility. BMC Microbiology, 2021, 21, 14.	3.3	16
6	TAL Effector Repertoires of Strains of Xanthomonas phaseoli pv. manihotis in Commercial Cassava Crops Reveal High Diversity at the Country Scale. Microorganisms, 2021, 9, 315.	3.6	7
7	COVID-19 spread, detection, and dynamics in Bogota, Colombia. Nature Communications, 2021, 12, 4726.	12.8	18
8	Comprehensive Time-Series Analysis of the Gene Expression Profile in a Susceptible Cultivar of Tree Tomato (Solanum betaceum) During the Infection of Phytophthora betacei. Frontiers in Plant Science, 2021, 12, 730251.	3.6	4
9	A whole genome duplication drives the genome evolution of Phytophthora betacei, a closely related species to Phytophthora infestans. BMC Genomics, 2021, 22, 795.	2.8	6
10	Is the Phenomenon of Mefenoxam-Acquired Resistance in Phytophthora infestans Universal?. Plant Disease, 2020, 104, 211-221.	1.4	10
11	Differential Susceptibility of Tree Tomato (Solanum betaceum) Cultivars to Late Blight Caused by Phytophthora betacei. Plant Disease, 2020, 104, 1113-1117.	1.4	2
12	Genome-Wide Association Study Identifies Single Nucleotide Polymorphism Markers Associated with Mycelial Growth (at 15, 20, and 25Â°C), Mefenoxam Resistance, and Mating Type in Phytophthora infestans. Phytopathology, 2020, 110, 822-833.	2.2	8
13	Analysis of Malassezia Lipidome Disclosed Differences Among the Species and Reveals Presence of Unusual Yeast Lipids. Frontiers in Cellular and Infection Microbiology, 2020, 10, 338.	3.9	22
14	Genome-Scale Metabolic Model of Xanthomonas phaseoli pv. manihotis: An Approach to Elucidate Pathogenicity at the Metabolic Level. Frontiers in Genetics, 2020, 11, 837.	2.3	5
15	A One Health Perspective to Recognize Fusarium as Important in Clinical Practice. Journal of Fungi (Basel, Switzerland), 2020, 6, 235.	3.5	29
16	Genomic Variability ofPhytophthora palmivoraIsolates from Different Oil Palm Cultivation Regions in Colombia. Phytopathology, 2020, 110, 1553-1564.	2.2	4
17	Two Clonal Species of Phytophthora Associated to Solanaceous Crops Coexist in Central and Southern Colombia. Phytopathology, 2020, 110, 1342-1351.	2.2	2
18	Effector Repertoire of Phytophthora betacei: In Search of Possible Virulence Factors Responsible for Its Host Specificity. Frontiers in Genetics, 2020, 11, 579.	2.3	4

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19	New Therapeutic Candidates for the Treatment of Malassezia pachydermatis -Associated Infections. Scientific Reports, 2020, 10, 4860.	3.3	7
20	Design and validation of a transposon that promotes expression of genes in episomal DNA. Journal of Biotechnology, 2020, 310, 1-5.	3.8	1
21	Speciation Associated with Shifts in Migratory Behavior in an Avian Radiation. Current Biology, 2020, 30, 1312-1321.e6.	3.9	45
22	A Checklist of Ectomycorrhizal Mushrooms Associated with Quercus humboldtii in Colombia. , 2020, , 425-450.		6
23	Salifodinibacter halophilus 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
24	In Colombia the Eurasian fungusAmanita muscariais expanding its range into native, tropicalQuercus humboldtiiforests. Mycologia, 2019, 111, 758-771.	1.9	10
25	Phytophthora infestans Dihydroorotate Dehydrogenase Is a Potential Target for Chemical Control â€“ A Comparison With the Enzyme From Solanum tuberosum. Frontiers in Microbiology, 2019, 10, 1479.	3.5	12
26	Production of Polyunsaturated Fatty Acids and Lipids from Autotrophic, Mixotrophic and Heterotrophic cultivation of Galdieria sp. strain USBA-GBX-832. Scientific Reports, 2019, 9, 10791.	3.3	69
27	Multivariate Method for Inferential Identification of Differentially Expressed Genes in Gene Expression Experiments. Journal of Computational Biology, 2019, 26, 866-874.	1.6	1
28	Gene regulatory networks on transfer entropy (GRNTE): a novel approach to reconstruct gene regulatory interactions applied to a case study for the plant pathogen Phytophthora infestans. Theoretical Biology and Medical Modelling, 2019, 16, 7.	2.1	20
29	An Optimized Microsatellite Scheme for Assessing Populations of Xanthomonas phaseoli pv. manihotis. Phytopathology, 2019, 109, 859-869.	2.2	9
30	Determining Whether Geographic Origin and Potato Genotypes Shape the Population Structure of Phytophthora infestans in the Central Region of Colombia. Phytopathology, 2019, 109, 145-154.	2.2	2
31	Gene co-expression network for Xanthomonas-challenged cassava reveals key regulatory elements of immunity processes. European Journal of Plant Pathology, 2019, 153, 1083-1104.	1.7	6
32	The role of type III effectors from Xanthomonas axonopodis pv. manihotis in virulence and suppression of plant immunity. Molecular Plant Pathology, 2018, 19, 593-606.	4.2	33
33	A genome-scale metabolic model of potato late blight suggests a photosynthesis suppression mechanism. BMC Genomics, 2018, 19, 863.	2.8	24
34	Contrasting Symbiotic Patterns in Two Closely Related Lineages of Trimembered Lichens of the Genus Peltigera. Frontiers in Microbiology, 2018, 9, 2770.	3.5	25
35	Antibacterial Activities of Azole Complexes Combined with Silver Nanoparticles. Molecules, 2018, 23, 361.	3.8	33
36	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

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37	Network Analyses in Plant Pathogens. Frontiers in Microbiology, 2018, 9, 35.	3.5	18
38	First Report ofColletotrichum kahawaesubsp.ciggaroCausing Anthracnose Disease on Tree Tomato in Cundinamarca, Colombia. Plant Disease, 2018, 102, 2031-2031.	1.4	9
39	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
40	Defining the phylogenetic position of Amanita species from Andean Colombia. Mycologia, 2017, 109, 261-276.	1.9	7
41	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
42	Lipid Metabolic Versatility in Malassezia spp. Yeasts Studied through Metabolic Modeling. Frontiers in Microbiology, 2017, 8, 1772.	3.5	31
43	Compartmentalized metabolic network reconstruction of microbial communities to determine the effect of agricultural intervention on soils. PLoS ONE, 2017, 12, e0181826.	2.5	6
44	The genomic study of an environmental isolate of Scedosporium apiospermum shows its metabolic potential to degrade hydrocarbons. Standards in Genomic Sciences, 2017, 12, 71.	1.5	25
45	Draft genome sequence of Pseudomonas extremaustralis strain USBA-GBX 515 isolated from Superparamo soil samples in Colombian Andes. Standards in Genomic Sciences, 2017, 12, 78.	1.5	7
46	Draft genome sequence of Dethiosulfovibrio salsuginis DSM 21565T an anaerobic, slightly halophilic bacterium isolated from a Colombian saline spring. Standards in Genomic Sciences, 2017, 12, 86.	1.5	0
47	Draft genome and description of Consotaella salsifontis 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
48	Metabolomic profile and nucleoside composition of Cordyceps nidus sp. nov. (Cordycipitaceae): A new source of active compounds. PLoS ONE, 2017, 12, e0179428.	2.5	21
49	Mycofier: a new machine learning-based classifier for fungal ITS sequences. BMC Research Notes, 2016, 9, 402.	1.4	15
50	Species from the Colletotrichum acutatum, Colletotrichum boninense and Colletotrichum gloeosporioides species complexes associated with tree tomato and mango crops in Colombia. Plant Pathology, 2016, 65, 227-237.	2.4	42
51	Genotyping of Fusarium Isolates from Onychomycoses in Colombia: Detection of Two New Species Within the Fusarium solani Species Complex and In Vitro Antifungal Susceptibility Testing. Mycopathologia, 2016, 181, 165-174.	3.1	32
52	Evolutionary Origins of Rhizarian Parasites. Molecular Biology and Evolution, 2016, 33, 980-983.	8.9	47
53	Microbial and Functional Diversity within the Phyllosphere of Espeletia Species in an Andean High-Mountain Ecosystem. Applied and Environmental Microbiology, 2016, 82, 1807-1817.	3.1	55
54	Development of a genetic tool for functional screening of anti-malarial bioactive extracts in metagenomic libraries. Malaria Journal, 2015, 14, 233.	2.3	5

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55	Lecanicillium sabanense sp. nov. (Cordycipitaceae) a new fungal entomopathogen of coccids. Phytotaxa, 2015, 234, 63.	0.3	30
56	Draft Genome Sequence of the Animal and Human Pathogen Malassezia pachydermatis Strain CBS 1879. Genome Announcements, 2015, 3, .	0.8	30
57	Assembly and Analysis of Differential Transcriptome Responses of Hevea brasiliensis on Interaction with Microcyclus ulei. PLoS ONE, 2015, 10, e0134837.	2.5	18
58	Five new species of entomopathogenic fungi from the Amazon and evolution of neotropical Ophiocordyceps. Fungal Biology, 2015, 119, 901-916.	2.5	68
59	A comparison between functional frequency and metabolic flows framed by biogeochemical cycles in metagenomes: The case of â€œEl Coquitoâ€•hot spring located at Colombia's national Nevados park. Ecological Modelling, 2015, 313, 259-265.	2.5	3
60	Physalis peruvianaresponses toPhytophthora infestansare typical of an incompatible interaction. Canadian Journal of Plant Pathology, 2015, 37, 106-117.	1.4	3
61	An Ephemeral Sexual Population of Phytophthora infestans in the Northeastern United States and Canada. PLoS ONE, 2014, 9, e116354.	2.5	38
62	Identification of Transcription Factor Genes and Their Correlation with the High Diversity of Stramenopiles. PLoS ONE, 2014, 9, e111841.	2.5	12
63	Entomopathogens of Amazonian stick insects and locusts are members of theBeauveriaspecies complex (Cordycepssensu stricto). Mycologia, 2014, 106, 260-275.	1.9	43
64	Annotation of a hybrid partial genome of the coffee rust (Hemileia vastatrix) contributes to the gene repertoire catalog of the Pucciniales. Frontiers in Plant Science, 2014, 5, 594.	3.6	34
65	De novo pyrimidine biosynthesis in the oomycete plant pathogen Phytophthora infestans. Gene, 2014, 537, 312-321.	2.2	24
66	Population typing of the causal agent of cassava bacterial blight in the Eastern Plains of Colombia using two types of molecular markers. BMC Microbiology, 2014, 14, 161.	3.3	16
67	A Complex Population Structure of the Cassava Pathogen Xanthomonas axonopodis pv. manihotis in Recent Years in the Caribbean Region of Colombia. Microbial Ecology, 2014, 68, 155-167.	2.8	32
68	Speciation in Fungal and Oomycete Plant Pathogens. Annual Review of Phytopathology, 2014, 52, 289-316.	7.8	36
69	The Irish potato famine pathogen Phytophthora infestans originated in central Mexico rather than the Andes. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 8791-8796.	7.1	186
70	Novel Protocol for Persister Cells Isolation. PLoS ONE, 2014, 9, e88660.	2.5	42
71	Entomopathogens of Amazonian stick insects and locusts are members of the Beauveria species complex (Cordyceps sensu stricto). Mycologia, 2014, 106, 260-275.	1.9	25
72	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

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73	Application of Genome Studies of Coffee Rust. Advances in Intelligent Systems and Computing, 2014, , 133-139.	0.6	1
74	Seborrheic dermatitis: predisposing factors and ITS2 secondary structure forMalasseziaphylogenic analysis. Medical Mycology, 2013, 51, 868-875.	0.7	15
75	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
76	Complex history of the amphibian-killing chytrid fungus revealed with genome resequencing data. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 9385-9390.	7.1	238
77	<scp>TALE</scp>1 from <scp>X</scp>anthomonas axonopodis pv. manihotis acts as a transcriptional activator in plant cells and is important for pathogenicity in cassava plants. Molecular Plant Pathology, 2013, 14, 84-95.	4.2	37
78	Developing a taxonomic identification system of Phytophthora species based on microsatellites. Revista Iberoamericana De Micologia, 2013, 30, 88-95.	0.9	7
79	Gene profiling in partially resistant and susceptible nearâ€isogenic tomatoes in response to late blight in the field. Molecular Plant Pathology, 2013, 14, 171-184.	4.2	14
80	Chromosome 10 in the tomato plant carries clusters of genes responsible for field resistance/defence to Phytophthora infestans. Genomics, 2013, 101, 249-255.	2.9	7
81	Characterization of the First Batrachochytrium dendrobatidis Isolate from the Colombian Andes, an Amphibian Biodiversity Hotspot. EcoHealth, 2013, 10, 72-76.	2.0	13
82	Genomic Survey of Pathogenicity Determinants and VNTR Markers in the Cassava Bacterial Pathogen Xanthomonas axonopodis pv. Manihotis Strain CIO151. PLoS ONE, 2013, 8, e79704.	2.5	42
83	FBA Analysis, Plant-Pathogen Interactions. , 2013, , 733-736.		0
84	Metagenome, Metabolic Reconstruction and Analysis. , 2013, , 1283-1287.		0
85	Exploring the biocontrol potential of fungal endophytes from an Andean Colombian Paramo ecosystem. BioControl, 2012, 57, 697-710.	2.0	53
86	Genomes-based phylogeny of the genus Xanthomonas. BMC Microbiology, 2012, 12, 43.	3.3	71
87	Characterization of cellulases of fungal endophytes isolated from Espeletia spp.. Journal of Microbiology, 2012, 50, 1009-1013.	2.8	20
88	Surviving Chytridiomycosis: Differential Anti-Batrachochytrium dendrobatidis Activity in Bacterial Isolates from Three Lowland Species of Atelopus. PLoS ONE, 2012, 7, e44832.	2.5	100
89	Data Mining of the Coffee Rust Genome. Nature Precedings, 2012, , .	0.1	0
90	Defining species boundaries in the genus Phytophthora: the case of Phytophthora andina A response to â€˜Phytophthora andina sp. nov., a newly identified heterothallic pathogen of solanaceous hosts in the Andean highlandsâ€™ (Oliva etÂal., 2010). Plant Pathology, 2012, 61, 215-220.	2.4	6

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91	Targeted metabolic reconstruction: a novel approach for the characterization of plant-pathogen interactions. Briefings in Bioinformatics, 2011, 12, 151-162.	6.5	16
92	Amatoxin and phallotoxin composition in species of the genus Amanita in Colombia: A taxonomic perspective. Toxicon, 2011, 58, 583-590.	1.6	29
93	Colonization of roots of cultivatedSolanum lycopersicumby dark septate and other ascomycetous endophytes. Mycologia, 2011, 103, 710-721.	1.9	43
94	Differential PbP27 expression in the yeast and mycelial forms of the Paracoccidioides brasiliensis species complex. Fungal Genetics and Biology, 2011, 48, 1087-1095.	2.1	6
95	Phylogeography and molecular epidemiology of Papaya ringspot virus. Virus Research, 2011, 159, 132-140.	2.2	63
96	The Plant Pathogen Phytophthora andina Emerged via Hybridization of an Unknown Phytophthora Species and the Irish Potato Famine Pathogen, P. infestans. PLoS ONE, 2011, 6, e24543.	2.5	88
97	Detection and functional characterization of a large genomic deletion resulting in decreased pathogenicity in Ralstonia solanacearum race 3 biovar 2 strains. Environmental Microbiology, 2011, 13, 3172-3185.	3.8	39
98	Selection of antagonistic bacteria isolated from the Physalis peruviana rhizosphere against Fusarium oxysporum. Journal of Applied Microbiology, 2011, 111, 707-716.	3.1	26
99	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
100	Genetic diversity of Phytophthora infestans in the Northern Andean region. BMC Genetics, 2011, 12, 23.	2.7	58
101	Effects of dark septate endophytes on tomato plant performance. Mycorrhiza, 2011, 21, 413-422.	2.8	77
102	A network model for biofilm development in Escherichia coli K-12. Theoretical Biology and Medical Modelling, 2011, 8, 34.	2.1	4
103	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
104	Virulence Gene Expression in Malassezia spp from Individuals with Seborrheic Dermatitis. Journal of Investigative Dermatology, 2011, 131, 2134-2136.	0.7	28
105	Discovery of Phytophthora infestans Genes Expressed in Planta through Mining of cDNA Libraries. PLoS ONE, 2010, 5, e9847.	2.5	8
106	A new method for designing degenerate primers and its use in the identification of sequences in Brachiaria showing similarity to apomixis-associated genes. Bioinformatics, 2010, 26, 2053-2054.	4.1	6
107	An RNAi in silico approach to find an optimal shRNA cocktail against HIV-1. Virology Journal, 2010, 7, 369.	3.4	6
108	Evaluation of Adult Chronic Chagas' Heart Disease Diagnosis by Molecular and Serological Methods. Journal of Clinical Microbiology, 2009, 47, 3945-3951.	3.9	89

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109	Computational Biology in Colombia. PLoS Computational Biology, 2009, 5, e1000535.	3.2	9
110	Physiological and Molecular Characterization of Atypical Isolates of Malassezia furfur. Journal of Clinical Microbiology, 2009, 47, 48-53.	3.9	33
111	Computational models in plant-pathogen interactions: the case of Phytophthora infestans. Theoretical Biology and Medical Modelling, 2009, 6, 24.	2.1	10
112	Genome sequence and analysis of the Irish potato famine pathogen Phytophthora infestans. Nature, 2009, 461, 393-398.	27.8	1,405
113	Fusarium species detected in onychomycosis in Colombia. Mycoses, 2009, 52, 350-356.	4.0	29
114	Isoenzyme characterization of proteases and amylases and partial purification of proteases from filamentous fungi causing biodeterioration of industrial paper. International Biodeterioration and Biodegradation, 2009, 63, 169-175.	3.9	21
115	Characterization of Phytophthora infestans Populations in Colombia: First Report of the A2 Mating Type. Phytopathology, 2009, 99, 82-88.	2.2	56
116	Biological and molecular characterization of the response of tomato plants treated with Trichoderma koningiopsis. Physiological and Molecular Plant Pathology, 2009, 74, 111-120.	2.5	40
117	Mesoscale Modeling of the Bacillus Thuringiensis Sporulation Network Based on Stochastic Kinetics and Its Application for in Silico Scale-Down. , 2009, , .		6
118	Survey and analysis of microsatellites from transcript sequences in Phytophthora species: frequency, distribution, and potential as markers for the genus. BMC Genomics, 2006, 7, 245.	2.8	43
119	Gene expression profile in response to Xanthomonas axonopodis pv. manihotis infection in cassava using a cDNA microarray. Plant Molecular Biology, 2005, 57, 393-410.	3.9	86
120	Genetic Structure and Population Dynamics of Xanthomonas axonopodis pv. manihotis in Colombia from 1995 to 1999. Applied and Environmental Microbiology, 2004, 70, 255-261.	3.1	32
121	Identification of genes in cassava that are differentially expressed during infection with Xanthomonas axonopodis pv. manihotis. Molecular Plant Pathology, 2004, 5, 549-558.	4.2	14
122	A unigene catalogue of 5700 expressed genes in cassava. Plant Molecular Biology, 2004, 56, 541-554.	3.9	53
123	Recent progress in the characterization of molecular determinants in the Xanthomonas axonopodis pv. manihotisâ€“cassava interaction. Plant Molecular Biology, 2004, 56, 573-584.	3.9	30
124	An EST resource for cassava and other species of Euphorbiaceae. Plant Molecular Biology, 2004, 56, 527-539.	3.9	38
125	Comparative Analyses of Potato Expressed Sequence Tag Libraries. Plant Physiology, 2003, 131, 419-429.	4.8	174
126	Characterization of pathogenic and nonpathogenic strains ofXanthomonas axonopodispv.manihotisby PCR-based DNA fingerprinting techniques. FEMS Microbiology Letters, 2002, 215, 23-31.	1.8	20

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127	Resistance spectrum of selected Manihot esculenta genotypes under field conditions. Field Crops Research, 2000, 65, 69-77.	5.1	13
128	AFLP fingerprinting: an efficient technique for detecting genetic variation of Xanthomonas axonopodis pv. manihotis. Microbiology (United Kingdom), 1999, 145, 107-114.	1.8	52
129	AFLP assessment of genetic variability in cassava accessions (Manihot esculenta) resistant and susceptible to the cassava bacterial blight (CBB). Genome, 1999, 42, 163-172.	2.0	40