

# Liliana M Cano

## List of Publications by Year in descending order

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56  
papers

9,925  
citations

109321

35  
h-index

182427

51  
g-index

64  
all docs

64  
docs citations

64  
times ranked

7736  
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	Genome sequencing reveals agronomically important loci in rice using MutMap. <i>Nature Biotechnology</i> , 2012, 30, 174-178.	17.5	1,087
3	QTL-seq: rapid mapping of quantitative trait loci in rice by whole genome resequencing of DNA from two bulked populations. <i>Plant Journal</i> , 2013, 74, 174-183.	5.7	1,065
4	Genome Evolution Following Host Jumps in the Irish Potato Famine Pathogen Lineage. <i>Science</i> , 2010, 330, 1540-1543.	12.6	440
5	Genome sequence of the necrotrophic plant pathogen <i>Pythium ultimum</i> reveals original pathogenicity mechanisms and effector repertoire. <i>Genome Biology</i> , 2010, 11, R73.	9.6	391
6	In Planta Expression Screens of <i>Phytophthora infestans</i> RXLR Effectors Reveal Diverse Phenotypes, Including Activation of the <i>Solanum tuberosum</i> Disease Resistance Protein Rpi-blb2. <i>Plant Cell</i> , 2009, 21, 2928-2947.	6.6	376
7	Understanding and Exploiting Late Blight Resistance in the Age of Effectors. <i>Annual Review of Phytopathology</i> , 2011, 49, 507-531.	7.8	369
8	The rise and fall of the <i>Phytophthora infestans</i> lineage that triggered the Irish potato famine. <i>ELife</i> , 2013, 2, e00731.	6.0	339
9	Ancient class of translocated oomycete effectors targets the host nucleus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 17421-17426.	7.1	326
10	Genome Analyses of an Aggressive and Invasive Lineage of the Irish Potato Famine Pathogen. <i>PLoS Pathogens</i> , 2012, 8, e1002940.	4.7	321
11	Adaptive Evolution Has Targeted the C-Terminal Domain of the RXLR Effectors of Plant Pathogenic Oomycetes. <i>Plant Cell</i> , 2007, 19, 2349-2369.	6.6	315
12	<i>Phytophthora infestans</i> effector AVRblb2 prevents secretion of a plant immune protease at the haustorial interface. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 20832-20837.	7.1	285
13	MutMap+: Genetic Mapping and Mutant Identification without Crossing in Rice. <i>PLoS ONE</i> , 2013, 8, e68529.	2.5	267
14	Genome Sequencing and Mapping Reveal Loss of Heterozygosity as a Mechanism for Rapid Adaptation in the Vegetable Pathogen <i>Phytophthora capsici</i> . <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 1350-1360.	2.6	264
15	Using Hierarchical Clustering of Secreted Protein Families to Classify and Rank Candidate Effectors of Rust Fungi. <i>PLoS ONE</i> , 2012, 7, e29847.	2.5	235
16	MutMap: whole genome resequencing of mutant F2 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
17	Analyses of genome architecture and gene expression reveal novel candidate virulence factors in the secretome of <i>Phytophthora infestans</i> . <i>BMC Genomics</i> , 2010, 11, 637.	2.8	188
18	Ten things to know about oomycete effectors. <i>Molecular Plant Pathology</i> , 2009, 10, 795-803.	4.2	185

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19	Effector Specialization in a Lineage of the Irish Potato Famine Pathogen. <i>Science</i> , 2014, 343, 552-555.	12.6	179
20	Qualitative and Quantitative Late Blight Resistance in the Potato Cultivar Sarpo Mira Is Determined by the Perception of Five Distinct RXLR Effectors. <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 910-919.	2.6	162
21	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
22	Presence/absence, differential expression and sequence polymorphisms between <i>PiAVR2</i> and <i>PiAVR2a-like</i> in <i>Phytophthora infestans</i> determine virulence on <i>R2</i> plants. <i>New Phytologist</i> , 2011, 191, 763-776.	7.3	142
23	Genome analyses of the sunflower pathogen <i>Plasmopara halstedii</i> provide insights into effector evolution in downy mildews and <i>Phytophthora</i> . <i>BMC Genomics</i> , 2015, 16, 741.	2.8	135
24	nQuire: a statistical framework for ploidy estimation using next generation sequencing. <i>BMC Bioinformatics</i> , 2018, 19, 122.	2.6	128
25	Recent developments in effector biology of filamentous plant pathogens. <i>Cellular Microbiology</i> , 2010, 12, 705-715.	2.1	108
26	Rerouting of Plant Late Endocytic Trafficking Toward a Pathogen Interface. <i>Traffic</i> , 2015, 16, 204-226.	2.7	103
27	Transient Expression of <i>Candidatus Liberibacter Asiaticus</i> Effector Induces Cell Death in <i>Nicotiana benthamiana</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 982.	3.6	93
28	From pathogen genomes to host plant processes: the power of plant parasitic oomycetes. <i>Genome Biology</i> , 2013, 14, 211.	8.8	64
29	Improved annotation of the insect vector of citrus greening disease: biocuration by a diverse genomics community. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	3.0	62
30	Genomics analysis of <i>Aphanomyces</i> spp. identifies a new class of oomycete effector associated with host adaptation. <i>BMC Biology</i> , 2018, 16, 43.	3.8	62
31	Coval: Improving Alignment Quality and Variant Calling Accuracy for Next-Generation Sequencing Data. <i>PLoS ONE</i> , 2013, 8, e75402.	2.5	58
32	Host-induced aneuploidy and phenotypic diversification in the Sudden Oak Death pathogen <i>Phytophthora ramorum</i> . <i>BMC Genomics</i> , 2016, 17, 385.	2.8	55
33	A Recent Expansion of the RXLR Effector Gene <i>Avrblb2</i> Is Maintained in Global Populations of <i>Phytophthora infestans</i> Indicating Different Contributions to Virulence. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 901-912.	2.6	44
34	Arabidopsis late blight: infection of a nonhost plant by <i>Albugo laibachii</i> enables full colonization by <i>Phytophthora infestans</i> . <i>Cellular Microbiology</i> , 2017, 19, e12628.	2.1	44
35	Gene expression polymorphism underpins evasion of host immunity in an asexual lineage of the Irish potato famine pathogen. <i>BMC Evolutionary Biology</i> , 2018, 18, 93.	3.2	41
36	Bioinformatic characterisation of the effector repertoire of the strawberry pathogen <i>Phytophthora cactorum</i> . <i>PLoS ONE</i> , 2018, 13, e0202305.	2.5	40

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37	Temporal and spatial detection of <i>Candidatus Liberibacter asiaticus</i> putative effector transcripts during interaction with Huanglongbing-susceptible, -tolerant, and -resistant citrus hosts. <i>BMC Plant Biology</i> , 2019, 19, 122.	3.6	38
38	Major Transcriptome Reprogramming Underlies Floral Mimicry Induced by the Rust Fungus <i>Puccinia monoica</i> in <i>Boechera stricta</i> . <i>PLoS ONE</i> , 2013, 8, e75293.	2.5	25
39	Diversity and evolutionary relationships of entomopathogenic nematodes (Steinernematidae and) <i>Tj ETQq1 1 0.784314 rgBT /Overlo</i>	0.6	17
40	<i>Quercus</i> leaf extracts display curative effects against <i>Candidatus Liberibacter asiaticus</i> that restore leaf physiological parameters in HLB-affected citrus trees. <i>Plant Physiology and Biochemistry</i> , 2020, 148, 70-79.	5.8	16
41	Recent developments in effector biology of filamentous plant pathogens. <i>Cellular Microbiology</i> , 2010, 12, 1015-1015.	2.1	11
42	The Effector Repertoire of the Hop Downy Mildew Pathogen <i>Pseudoperonospora humuli</i> . <i>Frontiers in Genetics</i> , 2020, 11, 910.	2.3	9
43	Draft Genome Sequence Resource of the Citrus Stem-End Rot Fungal Pathogen <i>Lasiodiplodia theobromae</i> CITRA15. <i>Phytopathology</i> , 2021, 111, 761-764.	2.2	9
44	Evaluation of High-Resolution Melting for Rapid Differentiation of <i>Phytophthora</i> Hybrids and Their Parental Species. <i>Plant Disease</i> , 2019, 103, 2295-2304.	1.4	6
45	Asian citrus psyllid stylet morphology and applicability to the model for inter-instar stylet replacement in the potato psyllid. <i>Arthropod Structure and Development</i> , 2018, 47, 542-551.	1.4	5
46	In Planta Localization of Endophytic <i>Cordyceps fumosorosea</i> in Carrizo Citrus. <i>Microorganisms</i> , 2021, 9, 219.	3.6	5
47	Lessons learned about the biology and genomics of <i>Diaphorina citri</i> infection with <i>Candidatus Liberibacter asiaticus</i> by integrating new and archived organ-specific transcriptome data. <i>GigaScience</i> , 2022, 11, .	6.4	5
48	First Report of <i>Gilbertella persicaria</i> Causing Postharvest Soft Rot of Strawberry Fruit in Florida. <i>Plant Disease</i> , 2020, 104, 2736.	1.4	4
49	Effect of Propagation Systems and Indole-3-Butyric Acid Potassium Salt (K-IBA) Concentrations on the Propagation of Peach Rootstocks by Stem Cuttings. <i>Plants</i> , 2021, 10, 1151.	3.5	4
50	Evolution of <i>Hyaloperonospora</i> effectors: ATR1 effector homologs from sister species of the downy mildew pathogen <i>H. arabidopsidis</i> are not recognised by RPP1WsB. <i>Mycological Progress</i> , 2015, 14, 1.	1.4	3
51	In Vitro Effects of Leaf Extracts from <i>Brassica rapa</i> on the Growth of Two Entomopathogenic Fungi. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 779.	3.5	2
52	Draft genome sequence resource for the orange rust pathogen of sugarcane <i>Puccinia kuehnii</i> . <i>Phytopathology</i> , 2021, , PHYTO01210008A.	2.2	1
53	Interactions between <i>Phytophthora infestans</i> and <i>Solanum</i> . , 0, , 287-302.		1
54	Reinterpretation of sperm pump or sperm syringe function with notes on other male internal reproductive organs in the Asian citrus psyllid, <i>Diaphorina citri</i> (Hemiptera: Liviidae). <i>Arthropod Structure and Development</i> , 2020, 54, 100915.	1.4	0

#	ARTICLE	IF	CITATIONS
55	2021â€“2022 Florida Citrus Production Guide: Decay Control of Florida Fresh Citrus. Edis, 0, , .	0.1	0
56	2020â€“2021 Florida Citrus Production Guide: Decay Control of Florida Fresh Citrus. Edis, 0, , .	0.1	0