Manuel Fernandez-Lopez

List of Publications by Year
in descending order

59 papers	1,839 citations	257450 24 h-index	276875 41 g-index
59 all docs	59 docs citations	59 times ranked	2120 citing authors

#	Article	IF	Citations
1	Impacts of the Biocontrol Strain Pseudomonas simiae PICF7 on the Banana Holobiont: Alteration of Root Microbial Co-occurrence Networks and Effect on Host Defense Responses. Frontiers in Microbiology, 2022, 13, 809126.	3.5	5
2	Correlating the above- and belowground genotype of Pinus pinaster trees and rhizosphere bacterial communities under drought conditions. Science of the Total Environment, 2022, 832, 155007.	8.0	6
3	Coupling the endophytic microbiome with the host transcriptome in olive roots. Computational and Structural Biotechnology Journal, 2021, 19, 4777-4789.	4.1	8
4	The Banana Root Endophytome: Differences between Mother Plants and Suckers and Evaluation of Selected Bacteria to Control Fusarium oxysporum f.sp. cubense. Journal of Fungi (Basel, Switzerland), 2021, 7, 194.	3.5	26
5	Involvement of the metabolically active bacteria in the organic matter degradation during olive mill waste composting. Science of the Total Environment, 2021, 789, 147975.	8.0	18
6	Exploring the effect of composting technologies on the recovery of hydrocarbon contaminated soil post chemical oxidative treatment. Applied Soil Ecology, 2020, 150, 103459.	4.3	8
7	Holm oak decline and mortality exacerbates drought effects on soil biogeochemical cycling and soil microbial communities across a climatic gradient. Soil Biology and Biochemistry, 2020, 149, 107921.	8.8	16
8	The endosphere bacteriome of diseased and healthy tomato plants. Archives of Microbiology, 2020, 202, 2629-2642.	2.2	10
9	Characterization of the Belowground Microbial Community in a Poplar-Phytoremediation Strategy of a Multi-Contaminated Soil. Frontiers in Microbiology, 2020, 11, 2073.	3.5	19
10	Comparative study of neighboring Holm oak and olive trees-belowground microbial communities subjected to different soil management. PLoS ONE, 2020, 15, e0236796.	2.5	10
11	Complete Genome Sequence of Sinorhizobium meliloti Strain AK21, a Salt-Tolerant Isolate from the Aral Sea Region. Microbiology Resource Announcements, 2020, 9, .	0.6	1
12	Linking belowground microbial network changes to different tolerance level towards Verticillium wilt of olive. Microbiome, 2020, 8, 11.	11.1	78
13	Title is missing!. , 2020, 15, e0236796.		0
14	Title is missing!. , 2020, 15, e0236796.		0
15	Title is missing!. , 2020, 15, e0236796.		0
16	Title is missing!. , 2020, 15, e0236796.		0
17	Bacteria from the endosphere and rhizosphere of Quercus spp. use mainly cell wall-associated enzymes to decompose organic matter. PLoS ONE, 2019, 14, e0214422.	2.5	31
18	Metabarcoding reveals that rhizospheric microbiota of Quercus pyrenaica is composed by a relatively small number of bacterial taxa highly abundant. Scientific Reports, 2019, 9, 1695.	3.3	23

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19	The Soil Microbiome of the Laurel Forest in Garajonay National Park (La Gomera, Canary Islands): Comparing Unburned and Burned Habitats after a Wildfire. Forests, 2019, 10, 1051.	2.1	14
20	Defining the root endosphere and rhizosphere microbiomes from the World Olive Germplasm Collection. Scientific Reports, 2019, 9, 20423.	3.3	65
21	Whole-Genome Sequences of Two Arthrobacter Strains Isolated from a Holm Oak Rhizosphere Affected by Wildfire. Genome Announcements, 2018, 6, .	0.8	4
22	Analysis of rhizobial endosymbionts of Vicia, Lathyrus and Trifolium species used to maintain mountain firewalls in Sierra Nevada National Park (South Spain). Systematic and Applied Microbiology, 2017, 40, 92-101.	2.8	10
23	Arbuscular mycorrhizal fungi inoculation mediated changes in rhizosphere bacterial community structure while promoting revegetation in a semiarid ecosystem. Science of the Total Environment, 2017, 584-585, 838-848.	8.0	65
24	Striking alterations in the soil bacterial community structure and functioning of the biological N cycle induced by Pennisetum setaceum invasion in a semiarid environment. Soil Biology and Biochemistry, 2017, 109, 176-187.	8.8	50
25	The rhizosphere microbiome of burned holm-oak: potential role of the genus Arthrobacter in the recovery of burned soils. Scientific Reports, 2017, 7, 6008.	3.3	88
26	Rational application of treated sewage sludge with urea increases GHG mitigation opportunities in Mediterranean soils. Agriculture, Ecosystems and Environment, 2017, 238, 114-127.	5.3	15
27	Taxonomic and Functional Diversity of a Quercus pyrenaica Willd. Rhizospheric Microbiome in the Mediterranean Mountains. Forests, 2017, 8, 390.	2.1	8
28	The early events underlying genome evolution in a localized Sinorhizobium meliloti population. BMC Genomics, 2016, 17, 556.	2.8	5
29	Bacterial Communities in the Rhizosphere of Amilaceous Maize (Zea mays L.) as Assessed by Pyrosequencing. Frontiers in Plant Science, 2016, 7, 1016.	3.6	58
30	Changes in soil nutrient content and bacterial community after 12â€‰years of organic amendment application to a vineyard. European Journal of Soil Science, 2015, 66, 802-812.	3.9	49
31	Genomic characterization of Sinorhizobium meliloti AK21, a wild isolate from the Aral Sea Region. SpringerPlus, 2015, 4, 259.	1.2	5
32	Metagenomic Assessment of the Potential Microbial Nitrogen Pathways in the Rhizosphere of a Mediterranean Forest After a Wildfire. Microbial Ecology, 2015, 69, 895-904.	2.8	68
33	Thirteen years of continued application of composted organic wastes in a vineyard modify soil quality characteristics. Soil Biology and Biochemistry, 2015, 90, 241-254.	8.8	86
34	The endemic Genista versicolor from Sierra Nevada National Park in Spain is nodulated by putative new Bradyrhizobium species and a novel symbiovar (sierranevadense). Systematic and Applied Microbiology, 2014, 37, 177-185.	2.8	45
35	Functional diversification within bacterial lineages promotes wide functional overlapping between taxonomic groups in a Mediterranean forest soil. FEMS Microbiology Ecology, 2014, 90, 54-67.	2.7	18
36	Strong functional stability of soil microbial communities under semiarid Mediterranean conditions and subjected to long-term shifts in baseline precipitation. Soil Biology and Biochemistry, 2014, 69, 223-233.	8.8	121

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37	Changes in soil bacterial community triggered by droughtâ€induced gap succession preceded changes in soil C stocks and quality. Ecology and Evolution, 2012, 2, 3016-3031.	1.9	39
38	Bacterial community in the rhizosphere of the cactus species Mammillaria carnea during dry and rainy seasons assessed by deep sequencing. Plant and Soil, 2012, 357, 275-288.	3.7	38
39	Use of RmInt1, a Group IIB Intron Lacking the Intron-Encoded Protein Endonuclease Domain, in Gene Targeting. Applied and Environmental Microbiology, 2011, 77, 854-861.	3.1	20
40	Rhizosphere-Bacterial Community in Eperua falcata (Caesalpiniaceae) a Putative Nitrogen-Fixing Tree from French Guiana Rainforest. Microbial Ecology, 2007, 53, 317-327.	2.8	20
41	Dispersal and Evolution of the Sinorhizobium meliloti Group II RmInt1 Intron in Bacteria that Interact with Plants. Molecular Biology and Evolution, 2005, 22, 1518-1528.	8.9	27
42	The RmInt1 group II intron has two different retrohoming pathways for mobility using predominantly the nascent lagging strand at DNA replication forks for priming. Nucleic Acids Research, 2004, 32, 2880-2888.	14.5	54
43	Diversity of group II introns in the genome of Sinorhizobium meliloti strain 1021: splicing and mobility of RmInt1. Molecular Genetics and Genomics, 2003, 268, 628-636.	2.1	14
44	Description of new Ensifer strains from nodules and proposal to transfer Ensifer adhaerens Casida 1982 to Sinorhizobium as Sinorhizobium adhaerens comb. nov. Request for an Opinion. International Journal of Systematic and Evolutionary Microbiology, 2003, 53, 1207-1217.	1.7	110
45	Sinorhizobium morelense sp. nov., a Leucaena leucocephala-associated bacterium that is highly resistant to multiple antibiotics. International Journal of Systematic and Evolutionary Microbiology, 2002, 52, 1687-1693.	1.7	58
46	Identification and characterization of bacterial class E group II introns. Gene, 2002, 299, 245-250.	2.2	30
47	Sinorhizobium morelense sp. nov., a Leucaena leucocephala-associated bacterium that is highly resistant to multiple antibiotics.. International Journal of Systematic and Evolutionary Microbiology, 2002, 52, 1687-1693.	1.7	42
48	Characterisation of symbiotically efficient alfalfa-nodulating rhizobia isolated from acid soils of Argentina and Uruguay. FEMS Microbiology Ecology, 1999, 28, 169-176.	2.7	22
49	Characterisation of symbiotically efficient alfalfa-nodulating rhizobia isolated from acid soils of Argentina and Uruguay. FEMS Microbiology Ecology, 1999, 28, 169-176.	2.7	3
50	Changes in the glycosylation pattern at the reducing end of azorhizobial Nod factors affect nodulation efficiency. FEMS Microbiology Letters, 1998, 158, 237-242.	1.8	9
51	Soluble and membrane-bound nitrate reductase from Bradyrhizobium japonicum bacteroids. Plant Physiology and Biochemistry, 1998, 36, 279-283.	5.8	9
52	Changes in the glycosylation pattern at the reducing end of azorhizobial Nod factors affect nodulation efficiency. FEMS Microbiology Letters, 1998, 158, 237-242.	1.8	6
53	Ethylene-mediated phenotypic plasticity in root nodule development on Sesbania rostrata. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 12724-12728.	7.1	105
54	Structureâ€"Function Relationship of Nod Factors Synthesized by Azorhizobium caulinodans. Current Plant Science and Biotechnology in Agriculture, 1998, , 250-250.	0.0	0

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55	Purification and characterization of the membrane-bound nitrate reductase isoenzymes ofBradyrhizobium japonicum. FEBS Letters, 1996, 392, 1-5.	2.8	12
56	Fucosylation and arabinosylation of Nod factors in Azorhizobium caulinodans : involvement of nolK nodZ as well as noeC and/or downstream genes. Molecular Microbiology, 1996, 21, 409-419.	2.5	66
57	Role of nodl and nodj in lipo-chitooligosaccharide secretion in Azorhizobium caulinodans and Escherichia coli. Molecular Microbiology, 1996, 20, 993-1000.	2.5	38
58	Two differentially regulated nitrate reductases required for nitrate-dependent, microaerobic growth of Bradyrhizobium japonicum. Archives of Microbiology, 1994, 162, 310-315.	2.2	10
59	Melanin production by Rhizobium meliloti GR4 is linked to nonsymbiotic plasmid pRmeGR4b: cloning, sequencing, and expression of the tyrosinase gene mepA. Journal of Bacteriology, 1993, 175, 5403-5410.	2.2	74