Rafael Rivilla

List of Publications by Year
in descending order

63	2,694	126708	189595
papers	citations	33 h-index	50 g-index

66	66	66	2848
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Transcriptomic analysis of Pseudomonas ogarae F113 reveals the antagonistic roles of AmrZ and FleQ during rhizosphere adaption. Microbial Genomics, 2022, 8, .	1.0	6
2	Regulation of extracellular matrix components by AmrZ is mediated by c-di-GMP in Pseudomonas ogarae F113. Scientific Reports, 2022, 12, .	1.6	4
3	Soil Microbiome Structure and Function in Ecopiles Used to Remediate Petroleum-Contaminated Soil. Frontiers in Environmental Science, 2021, 9, .	1.5	11
4	Pseudomonas fluorescens F113 type VI secretion systems mediate bacterial killing and adaption to the rhizosphere microbiome. Scientific Reports, 2021, 11, 5772.	1.6	31
5	Comparative genomics of the Pseudomonas corrugata subgroup reveals high species diversity and allows the description of Pseudomonas ogarae sp. nov.. Microbial Genomics, 2021, 7, .	1.0	19
6	Effectiveness of biochar application and bioaugmentation techniques for the remediation of freshly and aged diesel-polluted soils. International Biodeterioration and Biodegradation, 2021, 163, 105259.	1.9	10
7	In Silico Characterization and Phylogenetic Distribution of Extracellular Matrix Components in the Model Rhizobacteria Pseudomonas fluorescens F113 and Other Pseudomonads. Microorganisms, 2020, 8, 1740.	1.6	20
8	Comparative Genomics of the Rhodococcus Genus Shows Wide Distribution of Biodegradation Traits. Microorganisms, 2020, 8, 774.	1.6	25
9	Analysis of the biodegradative and adaptive potential of the novel polychlorinated biphenyl degrader Rhodococcus sp. WAY2 revealed by its complete genome sequence. Microbial Genomics, 2020, 6, .	1.0	20
10	Metagenomic Insights into the Bacterial Functions of a Diesel-Degrading Consortium for the Rhizoremediation of Diesel-Polluted Soil. Genes, 2019, 10, 456.	1.0	79
11	The diguanylate cyclase AdrA regulates flagellar biosynthesis in Pseudomonas fluorescens F113 through SadB. Scientific Reports, 2019, 9, 8096.	1.6	12
12	A partnerâ€switching system controls activation of mixedâ€linkage Î²â€glucan synthesis by câ€diâ€GMP inSinorhizobium meliloti. Environmental Microbiology, 2019, 21, 3379-3391.	1.8	11
13	Phylogenomic Analyses of Bradyrhizobium Reveal Uneven Distribution of the Lateral and Subpolar Flagellar Systems, Which Extends to Rhizobiales. Microorganisms, 2019, 7, 50.	1.6	16
14	AmrZ is a major determinant of c-di-GMP levels in Pseudomonas fluorescens F113. Scientific Reports, 2018, 8, 1979.	1.6	27
15	Genome-wide analysis of the FleQ direct regulon in Pseudomonas fluorescens F113 and Pseudomonas putida KT2440. Scientific Reports, 2018, 8, 13145.	1.6	44
16	Metagenomic Analysis of a Biphenyl-Degrading Soil Bacterial Consortium Reveals the Metabolic Roles of Specific Populations. Frontiers in Microbiology, 2018, 9, 232.	1.5	58
17	What makes rhizobia rhizosphere colonizers?. Environmental Microbiology, 2017, 19, 4379-4381.	1.8	1
18	Classification of Isolates from the Pseudomonas fluorescens Complex into Phylogenomic Groups Based in Group-Specific Markers. Frontiers in Microbiology, 2017, 8, 413.	1.5	51

#	Article	IF	Citations
19	Pseudomonas fluorescens F113 Can Produce a Second Flagellar Apparatus, Which Is Important for Plant Root Colonization. Frontiers in Microbiology, 2016, 7, 1471.	1.5	18
20	<scp>AmrZ</scp> regulates cellulose production in <scp>P</scp>seudomonas syringae pv. tomato <scp>DC</scp>3000. Molecular Microbiology, 2016, 99, 960-977.	1.2	41
21	Genomic and Genetic Diversity within the Pseudomonas fluorescens Complex. PLoS ONE, 2016, 11, e0150183.	1.1	171
22	Chemotactic Motility of Pseudomonas fluorescens F113 under Aerobic and Denitrification Conditions. PLoS ONE, 2015, 10, e0132242.	1.1	23
23	AmrZ is a global transcriptional regulator implicated in iron uptake and environmental adaption in P. fluorescensF113. BMC Genomics, 2014, 15, 237.	1.2	41
24	Phase Variation in Plant-Associated Pseudomonads. , 2014, , 55-79.		1
25	Identification of flgZ as a Flagellar Gene Encoding a PilZ Domain Protein That Regulates Swimming Motility and Biofilm Formation in Pseudomonas. PLoS ONE, 2014, 9, e87608.	1.1	61
26	Genome sequence reveals that Pseudomonas fluorescens F113 possesses a large and diverse array of systems for rhizosphere function and host interaction. BMC Genomics, 2013, 14, 54.	1.2	78
27	Plant flavonoids target <scp>P</scp>seudomonas syringae pv. tomato <scp>DC</scp>3000 flagella and type <scp>III</scp> secretion system. Environmental Microbiology Reports, 2013, 5, 841-850.	1.0	71
28	Genome Sequence of the Biocontrol Strain Pseudomonas fluorescens F113. Journal of Bacteriology, 2012, 194, 1273-1274.	1.0	69
29	The Gac-Rsm and SadB Signal Transduction Pathways Converge on AlgU to Downregulate Motility in Pseudomonas fluorescens. PLoS ONE, 2012, 7, e31765.	1.1	63
30	Pseudomonas fluorescens F113 Mutant with Enhanced Competitive Colonization Ability and Improved Biocontrol Activity against Fungal Root Pathogens. Applied and Environmental Microbiology, 2011, 77, 5412-5419.	1.4	113
31	The Sinorhizobium meliloti RNA chaperone Hfq influences central carbon metabolism and the symbiotic interaction with alfalfa. BMC Microbiology, 2010, 10, 71.	1.3	58
32	Efficient rhizosphere colonization by Pseudomonas fluorescens f113 mutants unable to form biofilms on abiotic surfaces. Environmental Microbiology, 2010, 12, 3185-3195.	1.8	74
33	Three independent signalling pathways repress motility in Pseudomonas fluorescens F113. Microbial Biotechnology, 2009, 2, 489-498.	2.0	44
34	GeneSMb21071of plasmid pSymB is required for osmoadaptation ofSinorhizobium meliloti1021 and is implicated in modifications of cell surface polysaccharides structure in response to hyperosmotic stress. Canadian Journal of Microbiology, 2009, 55, 1145-1152.	0.8	2
35	Transcriptional Organization of the Region Encoding the Synthesis of the Flagellar Filament in Pseudomonas fluorescens. Journal of Bacteriology, 2008, 190, 4106-4109.	1.0	14
36	The introduction of genetically modified microorganisms designed for rhizoremediation induces changes on native bacteria in the rhizosphere but not in the surrounding soil. ISME Journal, 2007, 1, 215-223.	4.4	38

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37	The introduction of genetically modified microorganisms designed for rhizoremediation induces changes on native bacteria in the rhizosphere but not in the surrounding soil. ISME Journal, 2007, 1, 215-223.	4.4	53
38	Changes in Bacterial Populations and in Biphenyl Dioxygenase Gene Diversity in a Polychlorinated Biphenyl-Polluted Soil after Introduction of Willow Trees for Rhizoremediation. Applied and Environmental Microbiology, 2007, 73, 6224-6232.	1.4	63
39	Rhizosphere Selection of Highly Motile Phenotypic Variants of Pseudomonas fluorescens with Enhanced Competitive Colonization Ability. Applied and Environmental Microbiology, 2006, 72, 3429-3434.	1.4	78
40	Nitrogenase Inhibition in Nodules from Pea Plants Grown Under Salt Stress Occurs at the Physiological Level and can be Alleviated by B and Ca. Plant and Soil, 2006, 280, 135-142.	1.8	36
41	Polychlorinated Biphenyl Rhizoremediation by Pseudomonas fluorescens F113 Derivatives, Using a Sinorhizobium meliloti nod System To Drive bph Gene Expression. Applied and Environmental Microbiology, 2005, 71, 2687-2694.	1.4	146
42	Two site-specific recombinases are implicated in phenotypic variation and competitive rhizosphere colonization in Pseudomonas fluorescens. Microbiology (United Kingdom), 2005, 151, 975-983.	0.7	65
43	Analysis of Pseudomonas fluorescens F113 genes implicated in flagellar filament synthesis and their role in competitive root colonization. Microbiology (United Kingdom), 2004, 150, 3889-3897.	0.7	129
44	Fluorescence Resonance Energy Transfer (FRET) based molecular detection of a genetically modified PCB degrader in soil. FEMS Microbiology Letters, 2004, 236, 349-357.	0.7	7
45	Cell Surface Interactions of Rhizobium Bacteroids and Other Bacterial Strains with Symbiosomal and Peribacteroid Membrane Components from Pea Nodules. Molecular Plant-Microbe Interactions, 2004, 17, 216-223.	1.4	37
46	Fluorescence Resonance Energy Transfer (FRET) based molecular detection of a genetically modified PCB degrader in soil. FEMS Microbiology Letters, 2004, 236, 349-357.	0.7	7
47	Influence of boron and calcium on the tolerance to salinity of nitrogen-fixing pea plants. Plant and Soil, 2003, 251, 93-103.	1.8	34
48	Title is missing!. Plant and Soil, 2003, 251, 47-54.	1.8	81
49	Effects of boron and calcium nutrition on the establishment of the Rhizobium leguminosarum -pea (Pisum sativum) symbiosis and nodule development under salt stress. Plant, Cell and Environment, 2003, 26, 1003-1011.	2.8	41
50	Phenotypic Selection and Phase Variation Occur during Alfalfa Root Colonization by Pseudomonas fluorescens F113. Journal of Bacteriology, 2002, 184, 1587-1596.	1.0	134
51	MucR and MucS Activate exp Genes Transcription and Galactoglucan Production in Sinorhizobium meliloti EFB1. Molecular Plant-Microbe Interactions, 2002, 15, 54-59.	1.4	6
52	Lectin-Like Glycoprotein PsNLEC-1 Is Not Correctly Glycosylated and Targeted in Boron-Deficient Pea Nodules. Molecular Plant-Microbe Interactions, 2001, 14, 663-670.	1.4	44
53	Research Note: Boron deficiency affects early infection events in the pea-Rhizobium symbiotic interaction. Functional Plant Biology, 2001, 28, 819.	1.1	12
54	MucR Is Necessary for Galactoglucan Production in Sinorhizobium meliloti EFB1. Molecular Plant-Microbe Interactions, 2000, 13, 129-135.	1.4	14

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55	PCR Use of Highly Conserved DNA Regions for Identification of Sinorhizobium meliloti. Applied and Environmental Microbiology, 2000, 66, 3621-3623.	1.4	11
56	Exopolysaccharide II Production Is Regulated by Salt in the Halotolerant Strain Rhizobium meliloti EFB1. Applied and Environmental Microbiology, 1998, 64, 1024-1028.	1.4	64
57	Rhizobium leguminosarum NodT is related to a family of outer-membrane transport proteins that includes TolC, PrtF, CyaE and AprF. Gene, 1995, 161, 27-31.	1.0	50
58	Ionic Stress and Osmotic Pressure Induce Different Alterations in the Lipopolysaccharide of a Rhizobium meliloti Strain. Applied and Environmental Microbiology, 1995, 61, 3701-3704.	1.4	89
59	Identification of a Rhizobium leguminosarum gene homologous to nodT but located outside the symbiotic plasmid. Gene, 1994, 144, 87-91.	1.0	19
60	Host recognition in the Rhizobium leguminosarumâ€“pea symbiosis. , 1992, , 257-266.		0
61	A note on the isolation of psychrotrophic coliform organisms from faecalâ€polluted environments. Journal of Applied Bacteriology, 1991, 70, 522-524.	1.1	1
62	Seasonal variations of pollution indicators in a wildfowl reserve (Doaˆ¼nana National Park, Spain). Journal of Applied Bacteriology, 1989, 67, 219-223.	1.1	5
63	Simplified methods for the microbiological evaluation of bottled natural mineral waters. Journal of Applied Bacteriology, 1988, 64, 273-278.	1.1	10