Yvan MoÃ«nne-Loccoz

List of Publications by Year
in descending order

87 papers	7,612 citations	71102 41 h-index	53230 85 g-index
88 all docs	88 docs citations	88 times ranked	7275 citing authors

#	Article	IF	Citations
1	The rhizosphere: a playground and battlefield for soilborne pathogens and beneficial microorganisms. Plant and Soil, 2009, 321, 341-361.	3.7	1,318
2	Plant growth-promoting rhizobacteria and root system functioning. Frontiers in Plant Science, 2013, 4, 356.	3.6	1,020
3	Let the Core Microbiota Be Functional. Trends in Plant Science, 2017, 22, 583-595.	8.8	317
4	Pseudomonas protegens sp. nov., widespread plant-protecting bacteria producing the biocontrol compounds 2,4-diacetylphloroglucinol and pyoluteorin. Systematic and Applied Microbiology, 2011, 34, 180-188.	2.8	304
5	Phylogeny of the 1-aminocyclopropane-1-carboxylic acid deaminase-encoding gene acdS in phytobeneficial and pathogenic Proteobacteria and relation with strain biogeography. FEMS Microbiology Ecology, 2006, 56, 455-470.	2.7	237
6	Root microbiome relates to plant host evolution in maize and other <scp>P</scp>oaceae. Environmental Microbiology, 2014, 16, 2804-2814.	3.8	233
7	Analysis of genes contributing to plant-beneficial functions in plant growth-promoting rhizobacteria and related Proteobacteria. Scientific Reports, 2014, 4, 6261.	3.3	210
8	Comparison of rhizobacterial community composition in soil suppressive or conducive to tobacco black root rot disease. ISME Journal, 2009, 3, 1127-1138.	9.8	180
9	Breeding for increased nitrogenâ€use efficiency: a review for wheat (<i><scp>T</scp>.Âaestivum) Tj ETQq1 1 0.784314 rgBT /Overlock	1.9	164
10	Phylogeny of HCN Synthase-Encoding hcnBC Genes in Biocontrol Fluorescent Pseudomonads and Its Relationship with Host Plant Species and HCN Synthesis Ability. Molecular Plant-Microbe Interactions, 2003, 16, 525-535.	2.6	163
11	Host plant secondary metabolite profiling shows a complex, strainâ€dependent response of maize to plant growthâ€promoting rhizobacteria of the genus <i>Azospirillum</i>. New Phytologist, 2011, 189, 494-506.	7.3	147
12	The <i>Pseudomonas</i> Secondary Metabolite 2,4-Diacetylphloroglucinol Is a Signal Inducing Rhizoplane Expression of <i>Azospirillum</i> Genes Involved in Plant-Growth Promotion. Molecular Plant-Microbe Interactions, 2011, 24, 271-284.	2.6	134
13	Is diversification history of maize influencing selection of soil bacteria by roots?. Molecular Ecology, 2012, 21, 195-206.	3.9	124
14	The Type III Secretion System of Biocontrol Pseudomonas fluorescens KD Targets the Phytopathogenic Chromista Pythium ultimum and Promotes Cucumber Protection. Molecular Plant-Microbe Interactions, 2005, 18, 991-1001.	2.6	123
15	Variation of secondary metabolite levels in maize seedling roots induced by inoculation with Azospirillum, Pseudomonas and Glomus consortium under field conditions. Plant and Soil, 2012, 356, 151-163.	3.7	118
16	Potential of a 16S rRNA-Based Taxonomic Microarray for Analyzing the Rhizosphere Effects of Maize on Agrobacterium spp. and Bacterial Communities. Applied and Environmental Microbiology, 2006, 72, 4302-4312.	3.1	111
17	Prevalence of fluorescent pseudomonads producing antifungal phloroglucinols and/or hydrogen cyanide in soils naturally suppressive or conducive to tobacco black root rot. FEMS Microbiology Ecology, 2003, 44, 35-43.	2.7	105
18	Is the ability of biocontrol fluorescent pseudomonads to produce the antifungal metabolite 2,4â€diacetylphloroglucinol really synonymous with higher plant protection?. New Phytologist, 2007, 173, 861-872.	7.3	98

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19	Genetic diversity and biocontrol potential of fluorescent pseudomonads producing phloroglucinols and hydrogen cyanide from Swiss soils naturally suppressive or conducive to Thielaviopsis basicola-mediated black root rot of tobacco. FEMS Microbiology Ecology, 2006, 55, 369-381.	2.7	91
20	Development and validation of a prototype 16S rRNA-based taxonomic microarray for Alphaproteobacteria. Environmental Microbiology, 2006, 8, 289-307.	3.8	89
21	Molecular characterization and PCR detection of a nitrogen-fixing Pseudomonas strain promoting rice growth. Biology and Fertility of Soils, 2006, 43, 163-170.	4.3	88
22	Comparison of prominent Azospirillum strains in Azospirillumâ€"Pseudomonasâ€"Glomus consortia for promotion of maize growth. Applied Microbiology and Biotechnology, 2013, 97, 4639-4649.	3.6	87
23	Physical organization and phylogenetic analysis of acdR as leucine-responsive regulator of the 1-aminocyclopropane-1-carboxylate deaminase gene acdS in phytobeneficial Azospirillum lipoferum 4B and other Proteobacteria. FEMS Microbiology Ecology, 2008, 65, 202-219.	2.7	78
24	Multilocus sequence analysis of biocontrol fluorescent Pseudomonas spp. producing the antifungal compound 2,4-diacetylphloroglucinol. Environmental Microbiology, 2007, 9, 1939-1955.	3.8	73
25	Polymorphism of the Polyketide Synthase Gene phlD in Biocontrol Fluorescent Pseudomonads Producing 2,4-Diacetylphloroglucinol and Comparison of PhlD with Plant Polyketide Synthases. Molecular Plant-Microbe Interactions, 2001, 14, 639-652.	2.6	68
26	Field survival of the phytostimulator Azospirillum lipoferum CRT1 and functional impact on maize crop, biodegradation of crop residues, and soil faunal indicators in a context of decreasing nitrogen fertilisation. Soil Biology and Biochemistry, 2006, 38, 1712-1726.	8.8	66
27	Exploitation of genetically modified inoculants for industrial ecology applications. Antonie Van Leeuwenhoek, 2002, 81, 599-606.	1.7	62
28	Effects of Azospirillum brasilense with genetically modified auxin biosynthesis gene ipdC upon the diversity of the indigenous microbiota of the wheat rhizosphere. Research in Microbiology, 2010, 161, 219-226.	2.1	62
29	Impact of inoculation with the phytostimulatory PGPR Azospirillum lipoferum CRT1 on the genetic structure of the rhizobacterial community of field-grown maize. Soil Biology and Biochemistry, 2009, 41, 409-413.	8.8	59
30	Actinobacterial community dominated by a distinct clade in acidic soil of a waterlogged deciduous forest. FEMS Microbiology Ecology, 2011, 78, 386-394.	2.7	59
31	Phase Variation and Genomic Architecture Changes in Azospirillum. Journal of Bacteriology, 2006, 188, 5364-5373.	2.2	57
32	Distribution of 2,4-Diacetylphloroglucinol Biosynthetic Genes among the Pseudomonas spp. Reveals Unexpected Polyphyletism. Frontiers in Microbiology, 2017, 8, 1218.	3.5	55
33	1-Aminocyclopropane-1-carboxylate deaminase producers associated to maize and other Poaceae species. Microbiome, 2018, 6, 114.	11.1	55
34	The role of the antimicrobial compound 2,4-diacetylphloroglucinol in the impact of biocontrol Pseudomonas fluorescens F113 on Azospirillum brasilense phytostimulators. Microbiology (United) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.8	52
35	Comparison of ATPase-Encoding Type III Secretion System hrcN Genes in Biocontrol Fluorescent Pseudomonads and in Phytopathogenic Proteobacteria. Applied and Environmental Microbiology, 2004, 70, 5119-5131.	3.1	51
36	Ancient wheat varieties have a higher ability to interact with plant growthâ€promoting rhizobacteria. Plant, Cell and Environment, 2020, 43, 246-260.	5.7	51

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37	Development of a real-time PCR method to quantify the PGPR strain Azospirillum lipoferum CRT1 on maize seedlings. Soil Biology and Biochemistry, 2010, 42, 2298-2305.	8.8	49
38	Development of bacterial community during spontaneous succession on spoil heaps after brown coal mining. FEMS Microbiology Ecology, 2011, 78, 59-69.	2.7	49
39	Genomic, phylogenetic and catabolic re-assessment of the Pseudomonas putida clade supports the delineation of Pseudomonas alloputida sp. nov., Pseudomonas inefficax sp. nov., Pseudomonas persica sp. nov., and Pseudomonas shirazica sp. nov. Systematic and Applied Microbiology, 2019, 42, 468-480.	2.8	48
40	Effect of Azospirillum brasilense inoculation on rhizobacterial communities analyzed by denaturing gradient gel electrophoresis and automated ribosomal intergenic spacer analysis. Soil Biology and Biochemistry, 2006, 38, 1212-1218.	8.8	47
41	Monitoring of the relation between 2,4-diacetylphloroglucinol-producing Pseudomonas and Thielaviopsis basicola populations by real-time PCR in tobacco black root-rot suppressive and conducive soils. Soil Biology and Biochemistry, 2013, 57, 144-155.	8.8	45
42	Rhizosphere microbial communities associated with Rhizoctonia damage at the field and disease patch scale. Applied Soil Ecology, 2014, 78, 37-47.	4.3	42
43	Fluorescent Pseudomonas Strains with only Few Plant-Beneficial Properties Are Favored in the Maize Rhizosphere. Frontiers in Plant Science, 2016, 7, 1212.	3.6	42
44	Comparison of Barley Succession and Take-All Disease as Environmental Factors Shaping the Rhizobacterial Community during Take-All Decline. Applied and Environmental Microbiology, 2010, 76, 4703-4712.	3.1	41
45	Duplication of Plasmid-Borne Nitrite Reductase Gene <i>nirK</i> in the Wheat-Associated Plant Growthâ€“Promoting Rhizobacterium <i>Azospirillum brasilense</i> Sp245. Molecular Plant-Microbe Interactions, 2008, 21, 831-842.	2.6	39
46	Rhizosphere ecology and phytoprotection in soils naturally suppressive to <scp>T</scp>hielaviopsis black root rot of tobacco. Environmental Microbiology, 2014, 16, 1949-1960.	3.8	38
47	Development of a 16S rRNA microarray approach for the monitoring of rhizosphere Pseudomonas populations associated with the decline of take-all disease of wheat. Soil Biology and Biochemistry, 2008, 40, 1028-1039.	8.8	37
48	Is plant evolutionary history impacting recruitment of diazotrophs and nifH expression in the rhizosphere?. Scientific Reports, 2016, 6, 21690.	3.3	37
49	Effect of Azospirillum inoculants on arbuscular mycorrhiza establishment in wheat and maize plants. Biology and Fertility of Soils, 2005, 41, 301-309.	4.3	36
50	Frequent, independent transfers of a catabolic gene from bacteria to contrasted filamentous eukaryotes. Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20140848.	2.6	35
51	Rock substrate rather than black stain alterations drives microbial community structure in the passage of Lascaux Cave. Microbiome, 2018, 6, 216.	11.1	34
52	Persistence of Culturable <i>Escherichia coli</i> Fecal Contaminants in Dairy Alpine Grassland Soils. Journal of Environmental Quality, 2008, 37, 2299-2310.	2.0	32
53	Comparison of Sandy Soils Suppressive or Conducive to Ectoparasitic Nematode Damage on Sugarcane. Phytopathology, 2003, 93, 1437-1444.	2.2	31
54	Persistence of a biocontrol Pseudomonas inoculant as high populations of culturable and non-culturable cells in 200-cm-deep soil profiles. Soil Biology and Biochemistry, 2012, 44, 122-129.	8.8	31

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55	Effect of Stress on the Ability of a phlA -Based Quantitative Competitive PCR Assay To Monitor Biocontrol Strain Pseudomonas fluorescens CHA0. Applied and Environmental Microbiology, 2003, 69, 686-690.	3.1	30
56	Anthropization level of Lascaux Cave microbiome shown by regionalâ€scale comparisons of pristine and anthropized caves. Molecular Ecology, 2019, 28, 3383-3394.	3.9	30
57	A new DGGE protocol targeting 2,4-diacetylphloroglucinol biosynthetic gene phlD from phylogenetically contrasted biocontrol pseudomonads for assessment of disease-suppressive soils. FEMS Microbiology Ecology, 2008, 64, 468-481.	2.7	29
58	Denaturing gradient gel electrophoretic analysis of dominant 2,4-diacetylphloroglucinol biosynthetic phlD alleles in fluorescent Pseudomonas from soils suppressive or conducive to black root rot of tobacco. Soil Biology and Biochemistry, 2010, 42, 649-656.	8.8	29
59	Evolutionary history of synthesis pathway genes for phloroglucinol and cyanide antimicrobials in plant-associated fluorescent pseudomonads. Molecular Phylogenetics and Evolution, 2012, 63, 877-890.	2.7	29
60	Evaluation of rhizobacterial indicators of tobacco black root rot suppressiveness in farmers' fields. Environmental Microbiology Reports, 2014, 6, 346-353.	2.4	27
61	Development of a 16S rRNA gene-based prototype microarray for the detection of selected actinomycetes genera. Antonie Van Leeuwenhoek, 2008, 94, 439-453.	1.7	26
62	Pseudomonas and other Microbes in Disease-Suppressive Soils. Sustainable Agriculture Reviews, 2012, , 93-140.	1.1	26
63	Nutrient deprivation and the subsequent survival of biocontrol Pseudomonas fluorescens CHA0 in soil. Soil Biology and Biochemistry, 1999, 31, 1181-1188.	8.8	25
64	Assessment of the relationship between geologic origin of soil, rhizobacterial community composition and soil receptivity to tobacco black root rot in Savoie region (France). Plant and Soil, 2013, 371, 397-408.	3.7	23
65	Effect of Clay Mineralogy on Iron Bioavailability and Rhizosphere Transcription of 2,4-Diacetylphloroglucinol Biosynthetic Genes in Biocontrol <i>Pseudomonas protegens</i>. Molecular Plant-Microbe Interactions, 2013, 26, 566-574.	2.6	23
66	Bacterial, archaeal and micro-eukaryotic communities characterize a disease-suppressive or conducive soil and a cultivar resistant or susceptible to common scab. Scientific Reports, 2019, 9, 14883.	3.3	23
67	Expression on roots and contribution to maize phytostimulation of 1-aminocyclopropane-1-decarboxylate deaminase gene acdS in Pseudomonas fluorescens F113. Plant and Soil, 2016, 407, 187-202.	3.7	21
68	Persistence and cell culturability of biocontrol strain Pseudomonas fluorescens CHA0 under plough pan conditions in soil and influence of the anaerobic regulator gene anr. Environmental Microbiology, 2003, 5, 103-115.	3.8	20
69	Unexpected Phytostimulatory Behavior for <i>Escherichia coli</i> and <i>Agrobacterium tumefaciens</i> Model Strains. Molecular Plant-Microbe Interactions, 2013, 26, 495-502.	2.6	20
70	Plasmid Profiles of Rhizobia Used in Inoculants and Isolated from Clover Fields. Agronomy Journal, 1994, 86, 117-121.	1.8	19
71	Microbial ecology of tourist Paleolithic caves. Science of the Total Environment, 2022, 816, 151492.	8.0	19
72	Effect of Inoculation Level on the Impact of the PGPR Azospirillum lipoferum CRT1 on Selected Microbial Functional Groups in the Rhizosphere of Field Maize. Microorganisms, 2022, 10, 325.	3.6	17

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73	Prevalence of type III secretion system in effective biocontrol pseudomonads. Research in Microbiology, 2014, 165, 300-304.	2.1	16
74	Phylogenetic diversity and antagonistic traits of root and rhizosphere pseudomonads of bean from Iran for controlling Rhizoctonia solani. Research in Microbiology, 2017, 168, 760-772.	2.1	16
75	Environmental mycobacteria closely related to the pathogenic species evidenced in an acidic forest wetland. Soil Biology and Biochemistry, 2011, 43, 697-700.	8.8	15
76	Inactivation of the Regulatory Gene algU or gacA Can Affect the Ability of Biocontrol Pseudomonas fluorescens CHA0 To Persist as Culturable Cells in Nonsterile Soil. Applied and Environmental Microbiology, 2002, 68, 2085-2088.	3.1	14
77	Effect of long-term vineyard monoculture on rhizosphere populations of pseudomonads carrying the antimicrobial biosynthetic genes phlD and/or hcnAB. FEMS Microbiology Ecology, 2009, 68, 25-36.	2.7	12
78	Physical organization of phytobeneficial genesnifHandipdCin the plant growth-promoting rhizobacteriumAzospirillum lipoferum4VI. FEMS Microbiology Letters, 2005, 244, 157-163.	1.8	11
79	Cell culturability ofPseudomonas protegensCHA0 depends on soil pH. FEMS Microbiology Ecology, 2014, 87, 441-450.	2.7	10
80	Construction of a recA mutant of Azospirillum lipoferum and involvement of recA in phase variation*1. FEMS Microbiology Letters, 2004, 236, 291-299.	1.8	9
81	Co-occurrence of rhizobacteria with nitrogen fixation and/or 1-aminocyclopropane-1-carboxylate deamination abilities in the maize rhizosphere. FEMS Microbiology Ecology, 2020, 96, .	2.7	9
82	Field Site-Specific Effects of an Azospirillum Seed Inoculant on Key Microbial Functional Groups in the Rhizosphere. Frontiers in Microbiology, 2021, 12, 760512.	3.5	8
83	Rhizosphere competence of fluorescent Pseudomonas sp. B24 genetically modified to utilise additional ferric siderophores. FEMS Microbiology Ecology, 1996, 19, 215-225.	2.7	7
84	Distribution of Pseudomonas populations harboring phlD or hcnAB biocontrol genes is related to depth in vineyard soils. Soil Biology and Biochemistry, 2010, 42, 466-472.	8.8	7
85	Significance of the Diversification of Wheat Species for the Assembly and Functioning of the Root-Associated Microbiome. Frontiers in Microbiology, 2021, 12, 782135.	3.5	7
86	Comparison of <i>Actinobacteria</i> communities from humanâ€impacted and pristine karst caves. MicrobiologyOpen, 2022, 11, e1276.	3.0	6
87	Rhizophere analysis of auxin producers harboring the phenylpyruvate decarboxylase pathway. Applied Soil Ecology, 2022, 173, 104363.	4.3	5