

Ludovic Vial

List of Publications by Year in descending order

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38
papers

1,449
citations

394421

19
h-index

361022

35
g-index

41
all docs

41
docs citations

41
times ranked

1885
citing authors

#	ARTICLE	IF	CITATIONS
1	Phylogeny of the Rhizobium–Allorhizobium–Agrobacterium clade supports the delineation of Neorhizobium gen. nov.. Systematic and Applied Microbiology, 2014, 37, 208-215.	2.8	205
2	The various lifestyles of the <i>Burkholderia cepacia</i> complex species: a tribute to adaptation. Environmental Microbiology, 2011, 13, 1-12.	3.8	151
3	<i>Burkholderia pseudomallei</i> , <i>B. thailandensis</i> , and <i>B. ambifaria</i> Produce 4-Hydroxy-2-Alkylquinoline Analogues with a Methyl Group at the 3 Position That Is Required for Quorum-Sensing Regulation. Journal of Bacteriology, 2008, 190, 5339-5352.	2.2	128
4	Genomic Species Are Ecological Species as Revealed by Comparative Genomics in <i>Agrobacterium tumefaciens</i> . Genome Biology and Evolution, 2011, 3, 762-781.	2.5	110
5	Physical organization and phylogenetic analysis of <i>acdR</i> as leucine-responsive regulator of the 1-aminocyclopropane-1-carboxylate deaminase gene <i>acdS</i> in phytobeneficial <i>Azospirillum lipoferum</i> 4B and other Proteobacteria. FEMS Microbiology Ecology, 2008, 65, 202-219.	2.7	78
6	<i>Burkholderia</i> diversity and versatility: an inventory of the extracellular products. Journal of Microbiology and Biotechnology, 2007, 17, 1407-29.	2.1	75
7	Phase and antigenic variation mediated by genome modifications. Antonie Van Leeuwenhoek, 2008, 94, 493-515.	1.7	69
8	Phase Variation and Genomic Architecture Changes in <i>Azospirillum</i> . Journal of Bacteriology, 2006, 188, 5364-5373.	2.2	57
9	Plasmid–chromosome cross-talks. Environmental Microbiology, 2020, 22, 540-556.	3.8	46
10	Single acquisition of protelomerase gave rise to speciation of a large and diverse clade within the <i>Agrobacterium/Rhizobium</i> supercluster characterized by the presence of a linear chromid. Molecular Phylogenetics and Evolution, 2014, 73, 202-207.	2.7	44
11	N-acyl-homoserine lactone-mediated quorum-sensing in <i>Azospirillum</i> : an exception rather than a rule. FEMS Microbiology Ecology, 2006, 58, 155-168.	2.7	42
12	Identification of quorum sensing–controlled genes in <i>Burkholderia ambifaria</i> . MicrobiologyOpen, 2013, 2, 226-242.	3.0	39
13	Phase variation has a role in <i>Burkholderia ambifaria</i> niche adaptation. ISME Journal, 2010, 4, 49-60.	9.8	35
14	Analysis of Hydroxycinnamic Acid Degradation in <i>Agrobacterium fabrum</i> Reveals a Coenzyme A-Dependent, Beta-Oxidative Deacetylation Pathway. Applied and Environmental Microbiology, 2014, 80, 3341-3349.	3.1	35
15	Rapid and accurate species and genomic species identification and exhaustive population diversity assessment of <i>Agrobacterium</i> spp. using <i>recA</i> -based PCR. Systematic and Applied Microbiology, 2013, 36, 351-358.	2.8	33
16	<i>Drosophila melanogaster</i> as a Model Host for the <i>Burkholderia cepacia</i> Complex. PLoS ONE, 2010, 5, e11467.	2.5	32
17	Ancestral Genome Estimation Reveals the History of Ecological Diversification in <i>Agrobacterium</i> . Genome Biology and Evolution, 2017, 9, 3413-3431.	2.5	31
18	Small RNA Deep-Sequencing Analyses Reveal a New Regulator of Virulence in <i>Agrobacterium fabrum</i> C58. Molecular Plant-Microbe Interactions, 2015, 28, 580-589.	2.6	28

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19	Interplay between 4-Hydroxy-3-Methyl-2-Alkylquinoline and N-Acyl-Homoserine Lactone Signaling in a Burkholderia cepacia Complex Clinical Strain. <i>Frontiers in Microbiology</i> , 2017, 8, 1021.	3.5	24
20	Essential oils of <i>Origanum compactum</i> and <i>Thymus vulgaris</i> exert a protective effect against the phytopathogen <i>Allorhizobium vitis</i> . <i>Environmental Science and Pollution Research</i> , 2018, 25, 29943-29952.	5.3	22
21	Comparative Genomics of Novel <i>Agrobacterium</i> G3 Strains Isolated From the International Space Station and Description of <i>Agrobacterium tomkonis</i> sp. nov.. <i>Frontiers in Microbiology</i> , 2021, 12, 765943.	3.5	22
22	The plant defense signal galactinol is specifically used as a nutrient by the bacterial pathogen <i>Agrobacterium fabrum</i> . <i>Journal of Biological Chemistry</i> , 2018, 293, 7930-7941.	3.4	18
23	Characterization of the first tetrameric transcription factor of the GntR superfamily with allosteric regulation from the bacterial pathogen <i>Agrobacterium fabrum</i> . <i>Nucleic Acids Research</i> , 2021, 49, 529-546.	14.5	15
24	Regulation of Hydroxycinnamic Acid Degradation Drives <i>Agrobacterium fabrum</i> Lifestyles. <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 814-822.	2.6	14
25	Coordinated Regulation of Species-Specific Hydroxycinnamic Acid Degradation and Siderophore Biosynthesis Pathways in <i>Agrobacterium fabrum</i> . <i>Applied and Environmental Microbiology</i> , 2016, 82, 3515-3524.	3.1	12
26	Ecological Conditions and Molecular Determinants Involved in <i>Agrobacterium</i> Lifestyle in Tumors. <i>Frontiers in Plant Science</i> , 2019, 10, 978.	3.6	11
27	Construction of a <i>recA</i> mutant of <i>Azospirillum lipoferum</i> and involvement of <i>recA</i> in phase variation. <i>FEMS Microbiology Letters</i> , 2004, 236, 291-299.	1.8	9
28	Construction of a <i>recA</i> mutant of <i>Azospirillum lipoferum</i> and involvement of <i>recA</i> in phase variation*1. <i>FEMS Microbiology Letters</i> , 2004, 236, 291-299.	1.8	9
29	Automatic quantitation of vacuolar lesions in the brain of mice infected with transmissible spongiform encephalopathies. <i>Journal of Virological Methods</i> , 2005, 124, 197-202.	2.1	9
30	A novel plasmid-encoded transcribed regulatory sRNA, QfsR, controls chromosomal polycistronic gene expression in <i>Agrobacterium fabrum</i> . <i>Environmental Microbiology</i> , 2019, 21, 3063-3075.	3.8	9
31	Rapid and Efficient Methods to Isolate, Type Strains and Determine Species of <i>Agrobacterium</i> spp. in Pure Culture and Complex Environments. , 0, , .		8
32	Biofilm-Constructing Variants of <i>Burkholderia phytofirmans</i> PsJN Outcompete the Wild-Type Form in Free-Living and Static Conditions but Not <i>In Planta</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	6
33	The Fruit Fly as a Meeting Place for Microbes. <i>Cell Host and Microbe</i> , 2008, 4, 505-507.	11.0	5
34	Evolutionary classification of tumor- and root-inducing plasmids based on T-DNAs and virulence regions. <i>Molecular Phylogenetics and Evolution</i> , 2022, 169, 107388.	2.7	5
35	Characterization and phylogenetic diversity of <i>Allorhizobium vitis</i> isolated from grapevine in Morocco. <i>Journal of Applied Microbiology</i> , 2020, 128, 828-839.	3.1	4
36	<i>Agrobacterium fabrum</i> C58 involved nitrate reductase NapA and antisense RNA NorR to denitrify. <i>FEMS Microbiology Ecology</i> , 2020, 97, .	2.7	3

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37	Cell-Cell Communication in Azospirillum and Related PGPR. , 2015, , 263-285.		2
38	Import pathways of the mannityl-opines into the bacterial pathogen <i>Agrobacterium tumefaciens</i> : structural, affinity and <i>in vivo</i> approaches. Biochemical Journal, 2020, 477, 615-628.	3.7	0