Denis Faure

List of Publications by Year
in descending order

95 papers	5,274 citations	81743 39 h-index	91712 69 g-index
97 all docs	97 docs citations	97 times ranked	5123 citing authors

#	Article	IF	Citations
1	<i>Agrobacterium tumefaciens</i> fitness genes involved in the colonization of plant tumors and roots. New Phytologist, 2022, 233, 905-918.	3.5	21
2	Pattern and causes of the establishment of the invasive bacterial potato pathogen Dickeya solani and of the maintenance of the resident pathogen D.Âdianthicola. Molecular Ecology, 2021, 30, 608-624.	2.0	13
3	Pectobacterium brasiliense: Genomics, Host Range and Disease Management. Microorganisms, 2021, 9, 106.	1.6	25
4	Is there a unique integration mechanism of <i>Agrobacterium</i> Tâ€DNA into a plant genome?. New Phytologist, 2021, 229, 2386-2388.	3.5	3
5	European Population of Pectobacterium punjabense: Genomic Diversity, Tuber Maceration Capacity and a Detection Tool for This Rarely Occurring Potato Pathogen. Microorganisms, 2021, 9, 781.	1.6	10
6	Species Diversity of <i>Dickeya</i> and <i>Pectobacterium</i> Causing Potato Blackleg Disease in Pakistan. Plant Disease, 2020, 104, 1492-1499.	0.7	16
7	Complete Genome Sequence of the Type Strain Pectobacterium punjabense SS95, Isolated from a Potato Plant with Blackleg Symptoms. Microbiology Resource Announcements, 2020, 9, .	0.3	1
8	Diversity of Pectobacteriaceae Species in Potato Growing Regions in Northern Morocco. Microorganisms, 2020, 8, 895.	1.6	14
9	Integrative and deconvolution omics approaches to uncover the Agrobacterium tumefaciens lifestyle in plant tumors. Plant Signaling and Behavior, 2019, 14, e1581562.	1.2	1
10	The biotrophAgrobacterium tumefacienstthrives in tumors by exploiting a wide spectrum of plant host metabolites. New Phytologist, 2019, 222, 455-467.	3.5	26
11	Common and distinctive adaptive traits expressed in <i>Dickeya dianthicola</i> and <i>Dickeya solani</i> pathogens when exploiting potato plant host. Environmental Microbiology, 2019, 21, 1004-1018.	1.8	42
12	First Report of <i>Pectobacterium parmentieri</i> and <i>Pectobacterium polaris</i> Causing Potato Blackleg Disease in Punjab, Pakistan. Plant Disease, 2019, 103, 1405-1405.	0.7	5
13	Transfer of the waterfall source isolate Pectobacterium carotovorum M022 to Pectobacterium fontis sp. nov., a deep-branching species within the genus Pectobacterium. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 470-475.	0.8	44
14	Dickeya undicola sp. nov., a novel species for pectinolytic isolates from surface waters in Europe and Asia. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 2440-2444.	0.8	53
15	Elevation of Pectobacterium carotovorum subsp. odoriferum to species level as Pectobacterium odoriferum sp. nov., proposal of Pectobacterium brasiliense sp. nov. and Pectobacterium actinidiae sp. nov., emended description of Pectobacterium carotovorum and description of Pectobacterium versatile sp. nov., isolated from streams and symptoms on diverse plants. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 3207-3216.	0.8	148
16	First Report of <i>Dickeya dianthicola</i> Causing Blackleg Disease on Potato Plants in Pakistan. Plant Disease, 2018, 102, 2027.	0.7	10
17	Complete Genome Sequences of the Plant Pathogens <i>Dickeya solani</i> RNS 08.23.3.1.A and <i>Dickeya dianthicola</i> RNS04.9. Genome Announcements, 2018, 6, .	0.8	4
18	Complete Chromosome and Plasmid Sequences of Two Plant Pathogens, Dickeya solani Strains D s0432-1 and PPO 9019. Genome Announcements, 2018, 6, .	0.8	5

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19	Lifestyle of the biotroph <i>Agrobacterium tumefaciens</i> in the ecological niche constructed on its host plant. New Phytologist, 2018, 219, 350-362.	3.5	20
20	Quorum Sensing and Quorum Quenching in Agrobacterium: A â€œGo/No Go Systemâ€?. Genes, 2018, 9, 210.	1.0	33
21	Pectobacterium punjabense sp. nov., isolated from blackleg symptoms of potato plants in Pakistan. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3551-3556.	0.8	53
22	Quorum-quenching limits quorum-sensing exploitation by signal-negative invaders. Scientific Reports, 2017, 7, 40126.	1.6	18
23	A <i>gapA</i> PCR-sequencing Assay for Identifying the <i>Dickeya</i> and <i>Pectobacterium</i> Potato Pathogens. Plant Disease, 2017, 101, 1278-1282.	0.7	62
24	Phenotypic and genomic survey on organic acid utilization profile of Pseudomonas mendocina strain S5.2, a vineyard soil isolate. AMB Express, 2017, 7, 138.	1.4	7
25	Fitness costs restrict niche expansion by generalist niche-constructing pathogens. ISME Journal, 2017, 11, 374-385.	4.4	12
26	Structural basis for high specificity of octopine binding in the plant pathogen Agrobacterium tumefaciens. Scientific Reports, 2017, 7, 18033.	1.6	15
27	Pseudomonas lini Strain ZBG1 Revealed Carboxylic Acid Utilization and Copper Resistance Features Required for Adaptation to Vineyard Soil Environment: A Draft Genome Analysis. Journal of Genomics, 2016, 4, 26-28.	0.6	3
28	The plant <scp>GABA</scp> signaling downregulates horizontal transfer of the <i>Agrobacterium tumefaciens</i> virulence plasmid. New Phytologist, 2016, 210, 974-983.	3.5	34
29	Comprehensive genomic and phenotypic metal resistance profile of Pseudomonas putida strain S13.1.2 isolated from a vineyard soil. AMB Express, 2016, 6, 95.	1.4	28
30	Plant GABA:proline ratio modulates dissemination of the virulence Ti plasmid within the <i>Agrobacterium tumefaciens</i> hosted population. Plant Signaling and Behavior, 2016, 11, e1178440.	1.2	5
31	Structural Basis for High Specificity of Amadori Compound and Mannopine Opine Binding in Bacterial Pathogens. Journal of Biological Chemistry, 2016, 291, 22638-22649.	1.6	17
32	Transcriptome analysis revealed that a quorum sensing system regulates the transfer of the pAt megaplasmid in Agrobacterium tumefaciens. BMC Genomics, 2016, 17, 661.	1.2	13
33	Complete genome anatomy of the emerging potato pathogen Dickeya solani type strain IPO 2222T. Standards in Genomic Sciences, 2016, 11, 87.	1.5	44
34	Engineering the Rhizosphere. Trends in Plant Science, 2016, 21, 266-278.	4.3	203
35	Quorum quenching: role in nature and applied developments. FEMS Microbiology Reviews, 2016, 40, 86-116.	3.9	493
36	Biocontrol of the Potato Blackleg and Soft Rot Diseases Caused by Dickeya dianthicola. Applied and Environmental Microbiology, 2016, 82, 268-278.	1.4	51

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37	Transfer of the potato plant isolates of Pectobacterium wasabiae to Pectobacterium parmentieri sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 5379-5383.	0.8	108
38	REVIEW: Predictive ecology in a changing world. Journal of Applied Ecology, 2015, 52, 1293-1310.	1.9	237
39	A Pyranose-2-Phosphate Motif Is Responsible for Both Antibiotic Import and Quorum-Sensing Regulation in Agrobacterium tumefaciens. PLoS Pathogens, 2015, 11, e1005071.	2.1	29
40	Genome Sequence of the Potato Plant Pathogen Dickeya dianthicola Strain RNS04.9. Genome Announcements, 2015, 3, .	0.8	9
41	Draft Genome Sequences of the Three Pectobacterium-Antagonistic Bacteria Pseudomonas brassicacearum PP1-210F and PA1G7 and Bacillus simplex BA2H3. Genome Announcements, 2015, 3, .	0.8	18
42	Population genomics reveals additive and replacing horizontal gene transfers in the emerging pathogen Dickeya solani. BMC Genomics, 2015, 16, 788.	1.2	63
43	Draft Genome Sequences of Pseudomonas fluorescens Strains PA4C2 and PA3G8 and Pseudomonas putida PA14H7, Three Biocontrol Bacteria against Dickeya Phytopathogens. Genome Announcements, 2015, 3, .	0.8	10
44	Next-generation sequencing as a powerful motor for advances in the biological and environmental sciences. Genetica, 2015, 143, 129-132.	0.5	24
45	Environmental microbiology reveals the Earth secret life. Environmental Science and Pollution Research, 2015, 22, 13573-13576.	2.7	3
46	Environmental microbiology as a mosaic of explored ecosystems and issues. Environmental Science and Pollution Research, 2015, 22, 13577-13598.	2.7	10
47	Natural Guided Genome Engineering Reveals Transcriptional Regulators Controlling Quorum-Sensing Signal Degradation. PLoS ONE, 2015, 10, e0141718.	1.1	11
48	Functions and regulation of quorum-sensing in Agrobacterium tumefaciens. Frontiers in Plant Science, 2014, 5, 14.	1.7	91
49	Agrobacterium Uses a Unique Ligand-Binding Mode for Trapping Opines and Acquiring A Competitive Advantage in the Niche Construction on Plant Host. PLoS Pathogens, 2014, 10, e1004444.	2.1	32
50	Genome Sequence of the Emerging Plant Pathogen Dickeya solani Strain RNS 08.23.3.1A. Genome Announcements, 2014, 2, .	0.8	22
51	An increasing opine carbon bias in artificial exudation systems and genetically modified plant rhizospheres leads to an increasing reshaping of bacterial populations. Molecular Ecology, 2014, 23, 4846-4861.	2.0	33
52	Genomic and metabolic comparison with Dickeya dadantii 3937 reveals the emerging Dickeya solani potato pathogen to display distinctive metabolic activities and T5SS/T6SS-related toxin repertoire. BMC Genomics, 2014, 15, 283.	1.2	61
53	Concerted transfer of the virulence <scp>T</scp>i plasmid and companion <scp>A</scp>t plasmid in the <i><scp>A</scp>grobacterium tumefaciens</i>â€induced plant tumour. Molecular Microbiology, 2013, 90, 1178-1189.	1.2	36
54	Genome Sequence of the Pectobacterium atrosepticum Strain CFBP6276, Causing Blackleg and Soft Rot Diseases on Potato Plants and Tubers. Genome Announcements, 2013, 1, .	0.8	8

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55	A Metagenomic Study Highlights Phylogenetic Proximity of Quorum-Quenching and Xenobiotic-Degrading Amidases of the AS-Family. PLoS ONE, 2013, 8, e65473.	1.1	29
56	N,Nâ€™-alkylated Imidazolium-Derivatives Act as Quorum-Sensing Inhibitors Targeting the Pectobacterium atrosepticum-Induced Symptoms on Potato Tubers. International Journal of Molecular Sciences, 2013, 14, 19976-19986.	1.8	16
57	At a Supra-Physiological Concentration, Human Sexual Hormones Act as Quorum-Sensing Inhibitors. PLoS ONE, 2013, 8, e83564.	1.1	38
58	N-Acyl Homoserine Lactones in Diverse Pectobacterium and Dickeya Plant Pathogens: Diversity, Abundance, and Involvement in Virulence. Sensors, 2012, 12, 3484-3497.	2.1	42
59	Efficient Biostimulation of Native and Introduced Quorum-Quenching Rhodococcus erythropolis Populations Is Revealed by a Combination of Analytical Chemistry, Microbiology, and Pyrosequencing. Applied and Environmental Microbiology, 2012, 78, 481-492.	1.4	67
60	Catabolic Pathway of Gamma-caprolactone in the Biocontrol Agent <i>Rhodococcus erythropolis</i>. Journal of Proteome Research, 2012, 11, 206-216.	1.8	44
61	Structural basis for selective <scp>GABA</scp> binding in bacterial pathogens. Molecular Microbiology, 2012, 86, 1085-1099.	1.2	25
62	Biological control of pathogen communication in the rhizosphere: A novel approach applied to potato soft rot due to Pectobacterium atrosepticum. Plant and Soil, 2012, 358, 27-37.	1.8	40
63	Quorum Sensing Signaling Molecules Produced by Reference and Emerging Soft-Rot Bacteria (Dickeya) Tj ETQq1 1 0.784314 rgBT /Ov	1.1	54
64	Transgenic plants expressing the quorum quenching lactonase AttM do not significantly alter root-associated bacterial populations. Research in Microbiology, 2011, 162, 951-958.	1.0	15
65	Gamma-caprolactone stimulates growth of quorum-quenching Rhodococcus populations in a large-scale hydroponic system for culturing Solanum tuberosum. Research in Microbiology, 2011, 162, 945-950.	1.0	48
66	Multilocus Sequence-Based Analysis Delineates a Clonal Population of Agrobacterium (Rhizobium) radiobacter (Agrobacterium tumefaciens) of Human Origin. Journal of Bacteriology, 2011, 193, 2608-2618.	1.0	29
67	A Conserved Mechanism of GABA Binding and Antagonism Is Revealed by Structure-Function Analysis of the Periplasmic Binding Protein Atu2422 in Agrobacterium tumefaciens. Journal of Biological Chemistry, 2010, 285, 30294-30303.	1.6	42
68	A fine control of quorum-sensing communication in<i>Agrobacterium tumefaciens</i>. Communicative and Integrative Biology, 2010, 3, 84-88.	0.6	42
69	Molecular communication in the rhizosphere. Plant and Soil, 2009, 321, 279-303.	1.8	165
70	Different Regulation and Roles of Lactonases AiiB and AttM in <i>Agrobacterium tumefaciens</i> C58. Molecular Plant-Microbe Interactions, 2009, 22, 529-537.	1.4	68
71	A metagenomic analysis of soil bacteria extends the diversity of quorumâ€quenching lactonases. Environmental Microbiology, 2008, 10, 560-570.	1.8	100
72	Comparative transcriptome analysis of<i>Agrobacterium tumefaciens</i>in response to plant signal salicylic acid, indole-3-acetic acid and Î³-amino butyric acid reveals signalling cross-talk and<i>Agrobacterium</i>-plant co-evolution. Cellular Microbiology, 2008, 10, 2339-2354.	1.1	102

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73	A <i>Rhodococcus qsdA</i> -Encoded Enzyme Defines a Novel Class of Large-Spectrum Quorum-Quenching Lactonases. Applied and Environmental Microbiology, 2008, 74, 1357-1366.	1.4	177
74	Lutte contre les maladies bactÃ©riennes de la pomme de terre dues aux Pectobacterium spp. (ErwiniaÂcarotovora). Cahiers Agricultures, 2008, 17, 355-360.	0.4	18
75	Growth promotion of quorum-quenching bacteria in the rhizosphere of Solanum tuberosum. Environmental Microbiology, 2007, 9, 1511-1522.	1.8	97
76	Quorum sensing as a target for developing control strategies for the plant pathogen Pectobacterium. European Journal of Plant Pathology, 2007, 119, 353-365.	0.8	63
77	N-acyl-homoserine lactone-mediated quorum-sensing in Azospirillum: an exception rather than a rule. FEMS Microbiology Ecology, 2006, 58, 155-168.	1.3	42
78	GABA controls the level of quorum-sensing signal in Agrobacterium tumefaciens. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 7460-7464.	3.3	235
79	Extracellular Î³-Aminobutyrate Mediates Communication between Plants and Other Organisms. Plant Physiology, 2006, 142, 1350-1352.	2.3	108
80	N-hexanoyl-l-homoserine lactone, a mediator of bacterial quorum-sensing regulation, exhibits plant-dependent stability and may be inactivated by germinating Lotus corniculatus seedlings. FEMS Microbiology Ecology, 2005, 52, 13-20.	1.3	107
81	Diversity of N-acyl homoserine lactone-producing and -degrading bacteria in soil and tobacco rhizosphere. Environmental Microbiology, 2005, 7, 1796-1808.	1.8	156
82	Bacterial populations in the rhizosphere of tobacco plants producing the quorum-sensing signals hexanoyl-homoserine lactone and 3-oxo-hexanoyl-homoserine lactone. FEMS Microbiology Ecology, 2004, 51, 19-29.	1.3	34
83	Involvement of N-acylhomoserine Lactones Throughout Plant Infection by Erwinia carotovora subsp. atroseptica (Pectobacterium atrosepticum). Molecular Plant-Microbe Interactions, 2004, 17, 1269-1278.	1.4	87
84	The Assimilation of Î³-Butyrolactone in Agrobacterium tumefaciens C58 Interferes with the Accumulation of the N-Acyl-Homoserine Lactone Signal. Molecular Plant-Microbe Interactions, 2004, 17, 951-957.	1.4	69
85	Novel bacteria degrading N-acylhomoserine lactones and their use as quenchers of quorum-sensing-regulated functions of plant-pathogenic bacteria. Microbiology (United Kingdom), 2003, 149, 1981-1989.	0.7	213
86	The Family-3 Glycoside Hydrolases: from Housekeeping Functions to Host-Microbe Interactions. Applied and Environmental Microbiology, 2002, 68, 1485-1490.	1.4	67
87	Detection and activity of insertion sequences in environmental strains of Burkholderia. Environmental Microbiology, 2001, 3, 766-773.	1.8	13
88	The celA Gene, Encoding a Glycosyl Hydrolase Family 3 Î²-Glucosidase in Azospirillum irakense, Is Required for Optimal Growth on Cellobiosides. Applied and Environmental Microbiology, 2001, 67, 2380-2383.	1.4	21
89	A Broad-Host-Range Plasmid for Isolating Mobile Genetic Elements in Gram-Negative Bacteria. Plasmid, 2000, 44, 201-207.	0.4	36
90	Growth of <i>Azospirillum irakense</i> KBC1 on the Aryl Î²-Glucoside Salicin Requires either <i>salA</i> or <i>salB</i>. Journal of Bacteriology, 1999, 181, 3003-3009.	1.0	17

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91	Development of a strain-specific probe to follow inoculated Azospirillum lipoferum CRT1 under field conditions and enhancement of maize root development by inoculation. FEMS Microbiology Ecology, 1998, 27, 43-51.	1.3	50
92	Isolation of<i>Azospirillum lipoferum</i>from the rhizosphere of rice by a new, simple method. Canadian Journal of Microbiology, 1997, 43, 486-490.	0.8	21
93	Population dynamics of a motile and a non-motile Azospirillum lipoferum strain during rice root colonization and motility variation in the rhizosphere. FEMS Microbiology Ecology, 1996, 19, 271-278.	1.3	34
94	Oligonucleotide probes based on 16S rRNA sequences for the identification of four <i>Azospirillum</i> species. Canadian Journal of Microbiology, 1995, 41, 1081-1087.	0.8	21
95	Polyphenol oxidase inAzospirillum lipoferumisolated from rice rhizosphere: Evidence for laccase activity in non-motile strains ofAzospirillum lipoferum. FEMS Microbiology Letters, 1993, 108, 205-210.	0.7	245