

Perrine Portier

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

1,169
citations

516710

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414414

32
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all docs

38
docs citations

38
times ranked

1059
citing authors

#	ARTICLE	IF	CITATIONS
1	Using Ecology, Physiology, and Genomics to Understand Host Specificity in <i>Xanthomonas</i> . Annual Review of Phytopathology, 2016, 54, 163-187.	7.8	157
2	Elevation of <i>Pectobacterium carotovorum</i> subsp. <i>odoriferum</i> to species level as <i>Pectobacterium odoriferum</i> sp. nov., proposal of <i>Pectobacterium brasiliense</i> sp. nov. and <i>Pectobacterium actinidiae</i> sp. nov., emended description of <i>Pectobacterium carotovorum</i> and description of <i>Pectobacterium versatile</i> sp. nov., isolated from streams and symptoms on diverse plants. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 3207-3216.	1.7	148
3	Rapid and Efficient Identification of <i>Agrobacterium</i> Species by <i>recA</i> Allele Analysis. Microbial Ecology, 2010, 60, 862-872.	2.8	111
4	Identification of Genomic Species in <i>Agrobacterium</i> Biovar 1 by AFLP Genomic Markers. Applied and Environmental Microbiology, 2006, 72, 7123-7131.	3.1	66
5	<i>Pectobacterium aquaticum</i> sp. nov., isolated from waterways. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 745-751.	1.7	64
6	New Coffee Plant-Infecting <i>Xylella fastidiosa</i> Variants Derived via Homologous Recombination. Applied and Environmental Microbiology, 2016, 82, 1556-1568.	3.1	63
7	Genomics and transcriptomics of <i>Xanthomonas campestris</i> species challenge the concept of core type III effectome. BMC Genomics, 2015, 16, 975.	2.8	62
8	Clarifying the taxonomy of the causal agent of bacterial leaf spot of lettuce through a polyphasic approach reveals that <i>Xanthomonas cynarae</i> TrÃ©baol et al. 2000 emend. Timilsina et al. 2019 is a later heterotypic synonym of <i>Xanthomonas hortorum</i> Vauterin et al. 1995. Systematic and Applied Microbiology, 2020, 43, 126087.	2.8	59
9	Ancestral acquisitions, gene flow and multiple evolutionary trajectories of the type three secretion system and effectors in <i>Xanthomonas</i> plant pathogens. Molecular Ecology, 2017, 26, 5939-5952.	3.9	56
10	Genomic Changes Arising in Long-Term Stab Cultures of <i>Escherichia coli</i> . Journal of Bacteriology, 2004, 186, 6437-6442.	2.2	37
11	Comparative Genomics and Phylogenetic Analyses Suggest Several Novel Species within the Genus <i>Clavibacter</i> , Including Nonpathogenic Tomato-Associated Strains. Applied and Environmental Microbiology, 2020, 86, .	3.1	33
12	Updated Taxonomy of <i>Pectobacterium</i> Genus in the CIRM-CFBP Bacterial Collection: When Newly Described Species Reveal an Endemic Population. Microorganisms, 2020, 8, 1441.	3.6	31
13	High-Quality Draft Genome Sequence of the <i>Xanthomonas translucens</i> pv. <i>cerealis</i> Pathotype Strain CFBP 2541. Genome Announcements, 2015, 3, .	0.8	24
14	<i>Erwinia iniecta</i> sp. nov., isolated from Russian wheat aphid (<i>Diuraphis noxia</i>). International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 3625-3633.	1.7	23
15	Complete Genome Sequences of Six Copper-Resistant <i>Xanthomonas</i> Strains Causing Bacterial Spot of Solaneous Plants, Belonging to <i>X. gardneri</i> , <i>X. euvesicatoria</i> , and <i>X. vesicatoria</i> , Using Long-Read Technology. Genome Announcements, 2017, 5, .	0.8	22
16	<i>Xanthomonas citri</i> pv. <i>viticola</i> Affecting Grapevine in Brazil: Emergence of a Successful Monomorphic Pathogen. Frontiers in Plant Science, 2019, 10, 489.	3.6	19
17	<i>Xanthomonas prunicola</i> sp. nov., a novel pathogen that affects nectarine (<i>Prunus persica</i> var.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 1857-1866.	1.7	19
18	The Complete Genome Sequence of <i>Xanthomonas theicola</i> , the Causal Agent of Canker on Tea Plants, Reveals Novel Secretion Systems in Clade-1 <i>Xanthomonads</i> . Phytopathology, 2021, 111, 611-616.	2.2	17

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19	Xanthomonas bonasiae sp. nov. and Xanthomonas youngii sp. nov., isolated from crown gall tissues. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	1.7	16
20	First Report of Cassava Bacterial Blight Caused by <i>Xanthomonas axonopodis</i> pv. <i>manihotis</i> in Burkina Faso. Plant Disease, 2015, 99, 551-551.	1.4	15
21	Role of the acquisition of a type 3 secretion system in the emergence of novel pathogenic strains of <i>Xanthomonas</i> . Molecular Plant Pathology, 2019, 20, 33-50.	4.2	15
22	Genetic diversity of <i>Curtobacterium flaccumfaciens</i> revealed by multilocus sequence analysis. European Journal of Plant Pathology, 2019, 154, 189-202.	1.7	15
23	Draft Genome Sequences of the Type Strains of Three <i>Clavibacter</i> Subspecies and Atypical Peach-Colored Strains Isolated from Tomato. Microbiology Resource Announcements, 2018, 7, .	0.6	13
24	Phenotypic and Molecular-Phylogenetic Analyses Reveal Distinct Features of Crown Gall-Associated <i>Xanthomonas</i> Strains. Microbiology Spectrum, 2022, 10, e0057721.	3.0	11
25	Genome Sequences of the Race 1 and Race 4 <i>Xanthomonas campestris</i> pv. <i>campestris</i> Strains CFBP 1869 and CFBP 5817. Genome Announcements, 2015, 3, .	0.8	9
26	Draft Genome Sequence of the <i>Xanthomonas cassavae</i> Type Strain CFBP 4642. Genome Announcements, 2013, 1, .	0.8	7
27	High-Quality Draft Genome Sequence of <i>Xanthomonas alfalfae</i> subsp. <i>alfalfae</i> Strain CFBP 3836. Genome Announcements, 2013, 1, .	0.8	7
28	Draft Genome Sequence of the Flagellated <i>Xanthomonas fuscans</i> subsp. <i>fuscans</i> Strain CFBP 4884. Genome Announcements, 2014, 2, .	0.8	7
29	Draft Genome Sequence of <i>Xanthomonas translucens</i> pv. <i>graminis</i> Pathotype Strain CFBP 2053. Genome Announcements, 2015, 3, .	0.8	7
30	High-Quality Genome Resource of <i>Xanthomonas hyacinthi</i> Generated via Long-Read Sequencing. Plant Disease, 2020, 104, 1011-1012.	1.4	7
31	Pathogenicity and molecular phylogenetic analysis reveal a distinct position of the banana fingertip rot pathogen among the <i>Burkholderia cenocepacia</i> genomovars. Plant Pathology, 2019, 68, 804-815.	2.4	6
32	Yeast Plasma Membrane Fungal Oligopeptide Transporters Display Distinct Substrate Preferences despite Their High Sequence Identity. Journal of Fungi (Basel, Switzerland), 2021, 7, 963.	3.5	6
33	Whole Genome Resources of 17 <i>Curtobacterium flaccumfaciens</i> Strains Including Pathotypes of <i>C. flaccumfaciens</i> pv. <i>betae</i> , <i>C. flaccumfaciens</i> pv. <i>oortii</i> , and <i>C. flaccumfaciens</i> pv. <i>poinsettiae</i> . Molecular Plant-Microbe Interactions, 2022, 35, 352-356.	2.6	6
34	High-Quality Draft Genome Sequence of <i>Curtobacterium</i> sp. Strain Ferrero. Genome Announcements, 2017, 5, .	0.8	4
35	Building More Resilient Culture Collections: A Call for Increased Deposits of Plant-Associated Bacteria. Microorganisms, 2022, 10, 741.	3.6	2
36	The Broad Host Range Plant Pathogen <i>Dickeya dianthicola</i> Shows a High Genetic Diversity. Microorganisms, 2022, 10, 1024.	3.6	2

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37	Interannual population dynamics of the green spruce aphid <i>Elatobium abietinum</i> (Walker) in France. <i>Annals of Applied Biology</i> , 2020, 176, 233-240.	2.5	1