

João F Pothier

List of Publications by Year in descending order

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75
papers

1,790
citations

304368

22
h-index

315357

38
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79
all docs

79
docs citations

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times ranked

2119
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#	ARTICLE	IF	CITATIONS
1	Complete Genome and Plasmid Sequence Data of Three Strains of <i>Xanthomonas arboricola</i> pv. <i>corylina</i> , the Bacterium Responsible for Bacterial Blight of Hazelnut. <i>Phytopathology</i> , 2022, 112, 956-960.	1.1	4
2	<i>Xanthomonas hortorum</i> “ beyond gardens: Current taxonomy, genomics, and virulence repertoires. <i>Molecular Plant Pathology</i> , 2022, 23, 597-621.	2.0	20
3	Taxonomic Refinement of <i>Xanthomonas arboricola</i> . <i>Phytopathology</i> , 2022, 112, 1630-1639.	1.1	8
4	Complete Genome Sequence Data of Two <i>Xanthomonas arboricola</i> Strains Isolated from Blueberry Plants Displaying Bacterial Leaf Blight in Poland. <i>Phytopathology</i> , 2022, 112, 1814-1818.	1.1	1
5	Comparative Genomics of Prunus-Associated Members of the <i>Pseudomonas syringae</i> Species Complex Reveals Traits Supporting Co-evolution and Host Adaptation. <i>Frontiers in Microbiology</i> , 2022, 13, 804681.	1.5	0
6	DNA Markers for Detection and Genotyping of <i>Xanthomonas euroxantha</i> . <i>Microorganisms</i> , 2022, 10, 1078.	1.6	1
7	Differentiation of the <i>Xanthomonas hortorum</i> “ <i>Xanthomonas hydrangeae</i> Species Complex Using Sensitive and Selective LAMP Assays. <i>Frontiers in Agronomy</i> , 2022, 4, .	1.5	3
8	Comparative Genomics of <i>Xanthomonas euroxantha</i> and <i>Xanthomonas arboricola</i> pv. <i>juglandis</i> Strains Isolated from a Single Walnut Host Tree. <i>Microorganisms</i> , 2021, 9, 624.	1.6	10
9	First report of bacterial leaf spot of <i>Hydrangea</i> in retail nurseries in Belgium caused by strains assigned to a new <i>Xanthomonas hortorum</i> clade. <i>New Disease Reports</i> , 2021, 43, e12008.	0.4	4
10	Trends in Molecular Diagnosis and Diversity Studies for Phytosanitary Regulated <i>Xanthomonas</i> . <i>Microorganisms</i> , 2021, 9, 862.	1.6	22
11	<i>Xanthomonas arboricola</i> pv. <i>juglandis</i> and pv. <i>corylina</i> : Brothers or distant relatives? Genetic clues, epidemiology, and insights for disease management. <i>Molecular Plant Pathology</i> , 2021, 22, 1481-1499.	2.0	19
12	Integrating science on <i>Xanthomonadaceae</i> for sustainable plant disease management in Europe. <i>Molecular Plant Pathology</i> , 2021, 22, 1461-1463.	2.0	6
13	<i>Xanthomonas hydrangeae</i> sp. nov., a novel plant pathogen isolated from <i>Hydrangea arborescens</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	15
14	Complete or High-Quality Draft Genome Sequences of Six <i>Xanthomonas hortorum</i> Strains Sequenced with Short- and Long-Read Technologies. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	12
15	Comparative genomics of <i>Xanthomonas fragariae</i> and <i>Xanthomonas arboricola</i> pv. <i>fragariae</i> reveals intra- and interspecies variations. <i>Phytopathology Research</i> , 2020, 2, .	0.9	8
16	Host-Pathogen Interactions between <i>Xanthomonas fragariae</i> and Its Host <i>Fragaria</i> — ananassa Investigated with a Dual RNA-Seq Analysis. <i>Microorganisms</i> , 2020, 8, 1253.	1.6	11
17	Transcriptome analysis of <i>Xanthomonas fragariae</i> in strawberry leaves. <i>Scientific Reports</i> , 2020, 10, 20582.	1.6	7
18	Isolation and Identification of Actinomycetes Strains from Switzerland and their Biotechnological Potential. <i>Chimia</i> , 2020, 74, 382.	0.3	6

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19	<i>Bradyrhizobium ivorense</i> sp. nov. as a potential local bioinoculant for <i>Cajanus cajan</i> cultures in Côte d'Ivoire. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1421-1430.	0.8	17
20	<i>Xanthomonas euroxanthea</i> sp. nov., a new xanthomonad species including pathogenic and non-pathogenic strains of walnut. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 6024-6031.	0.8	25
21	Typing Plasmids with Distributed Sequence Representation. <i>Lecture Notes in Computer Science</i> , 2020, , 200-210.	1.0	1
22	Comparative Genomic Analysis of the Biotechnological Potential of the Novel Species <i>Pseudomonas wadenswilerensis</i> CCOS 864T and <i>Pseudomonas reidholzensis</i> CCOS 865T. <i>Diversity</i> , 2019, 11, 204.	0.7	3
23	Mixotrophic Growth Under Micro-Oxic Conditions in the Purple Sulfur Bacterium <i>Thiodictyon syntrophicum</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 384.	1.5	16
24	Subspecies Typing of <i>Streptococcus agalactiae</i> Based on Ribosomal Subunit Protein Mass Variation by MALDI-TOF MS. <i>Frontiers in Microbiology</i> , 2019, 10, 471.	1.5	17
25	Comparative genomics and pathogenicity potential of members of the <i>Pseudomonas syringae</i> species complex on <i>Prunus</i> spp. <i>BMC Genomics</i> , 2019, 20, 172.	1.2	30
26	Draft Genome Sequence of <i>Chromatium okenii</i> Isolated from the Stratified Alpine Lake Cadagno. <i>Scientific Reports</i> , 2019, 9, 1936.	1.6	16
27	High-Quality Draft Genome Sequence of <i>Pseudomonas reidholzensis</i> Strain CCOS 865 T. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
28	Updated Genome Sequence and Annotation for the Full Genome of <i>Pseudomonas protegens</i> CHA0. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
29	Qualitative microbiome profiling along a wastewater system in Kampala, Uganda. <i>Scientific Reports</i> , 2019, 9, 17334.	1.6	3
30	High-Quality Draft Genome Sequence of <i>Xanthomonas</i> sp. Strain CPBF 424, a Walnut-Pathogenic Strain with Atypical Features. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	7
31	High-Quality Draft Genome Sequence of <i>Xanthomonas arboricola</i> pv. <i>juglandis</i> CPBF 1521, Isolated from Leaves of a Symptomatic Walnut Tree in Portugal without a Past of Phytosanitary Treatment. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	5
32	High-Quality Draft Genome Sequences of Five <i>Xanthomonas arboricola</i> pv. <i>fragariae</i> Isolates. <i>Genome Announcements</i> , 2018, 6, .	0.8	6
33	High-Quality Draft Genome Sequence of <i>Pseudomonas wadenswilerensis</i> CCOS 864 T. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	5
34	Complete Genome Sequences of <i>Erwinia amylovora</i> Phages vB_EamP-S2 and vB_EamM-Bue1. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	10
35	Complete genome sequence of <i>Thiodictyon syntrophicum</i> sp. nov. strain Cad16T, a photolithoautotrophic purple sulfur bacterium isolated from the alpine meromictic Lake Cadagno. <i>Standards in Genomic Sciences</i> , 2018, 13, 14.	1.5	12
36	<i>Frankia canadensis</i> sp. nov., isolated from root nodules of <i>Alnus incana</i> subspecies <i>rugosa</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3001-3011.	0.8	33

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37	Genome-based population structure analysis of the strawberry plant pathogen <i>Xanthomonas fragariae</i> reveals two distinct groups that evolved independently before its species description. <i>Microbial Genomics</i> , 2018, 4, .	1.0	23
38	Comparative genomics-informed design of two LAMP assays for detection of the kiwifruit pathogen <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> and discrimination of isolates belonging to the pandemic biovar 3. <i>Plant Pathology</i> , 2017, 66, 140-149.	1.2	24
39	A diagnostic tool for improved detection of <i>Xanthomonas fragariae</i> using a rapid and highly specific LAMP assay designed with comparative genomics. <i>Plant Pathology</i> , 2017, 66, 1094-1102.	1.2	14
40	Draft Genome Sequences of Seven <i>Streptococcus agalactiae</i> Strains Isolated from <i>Camelus dromedarius</i> at the Horn of Africa. <i>Genome Announcements</i> , 2017, 5, .	0.8	8
41	Complete Genome Sequences of Three Isolates of <i>Xanthomonas fragariae</i> , the Bacterium Responsible for Angular Leaf Spots on Strawberry Plants. <i>Genome Announcements</i> , 2017, 5, .	0.8	12
42	Complete Genome Sequence of <i>Pseudomonas viridiflava</i> CFBP 1590, Isolated from Diseased Cherry in France. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
43	Role of the type VI secretion systems during disease interactions of <i>Erwinia amylovora</i> with its plant host. <i>BMC Genomics</i> , 2017, 18, 628.	1.2	26
44	Development and evaluation of a bioinformatics approach for designing molecular assays for viral detection. <i>PLoS ONE</i> , 2017, 12, e0178195.	1.1	6
45	Bacterial diseases.. , 2017, , 365-385.		4
46	Diversity and host range of <i>Pseudomonas</i> in fruit tree species in Latvia. <i>Acta Horticulturae</i> , 2016, , 25-30.	0.1	1
47	Fire blight disease reactome: RNA-seq transcriptional profile of apple host plant defense responses to <i>Erwinia amylovora</i> pathogen infection. <i>Scientific Reports</i> , 2016, 6, 21600.	1.6	38
48	<i>Pararhizobium polonicum</i> sp. nov. isolated from tumors on stone fruit rootstocks. <i>Systematic and Applied Microbiology</i> , 2016, 39, 164-169.	1.2	18
49	<i>Pseudomonas cerasi</i> sp. nov. (non Griffin, 1911) isolated from diseased tissue of cherry. <i>Systematic and Applied Microbiology</i> , 2016, 39, 370-377.	1.2	42
50	Characterization and genetic diversity of causal agent of stone fruit bacterial canker <i>Pseudomonas cerasi</i> , a new pathogen of cherry. <i>Acta Horticulturae</i> , 2016, , 9-14.	0.1	1
51	Metagenomic diagnostics for the simultaneous detection of multiple pathogens in human stool specimens from Côte d'Ivoire: a proof-of-concept study. <i>Infection, Genetics and Evolution</i> , 2016, 40, 389-397.	1.0	34
52	Complete Genome Sequence of the Cyanogenic Phosphate-Solubilizing <i>Pseudomonas</i> sp. Strain CCOS 191, a Close Relative of <i>Pseudomonas mosselii</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	4
53	Evaluation of a real-time PCR and a loop-mediated isothermal amplification for detection of <i>Xanthomonas arboricola</i> pv. <i>pruni</i> in plant tissue samples. <i>Journal of Microbiological Methods</i> , 2015, 112, 36-39.	0.7	11
54	Ribosomal protein biomarkers provide root nodule bacterial identification by MALDI-TOF MS. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 5547-5562.	1.7	47

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55	Phylogeography and population structure of the biologically invasive phytopathogen <i>Erwinia amylovora</i> inferred using minisatellites. <i>Environmental Microbiology</i> , 2014, 16, 2112-2125.	1.8	49
56	Development of multilocus variable-number tandem repeat analysis (MLVA) for <i>Xanthomonas arboricola</i> pathovars. <i>Journal of Microbiological Methods</i> , 2014, 100, 84-90.	0.7	22
57	<i>Dickeya solani</i> sp. nov., a pectinolytic plant-pathogenic bacterium isolated from potato (<i>Solanum tuberosum</i>) Tj ETQq1 1 0.784314 rgBT/Overlook 0.8 228	0.8	228
58	Transcriptional profile of <i>Salmonella enterica</i> subsp. <i>enterica</i> serovar W eltevreden during alfalfa sprout colonization. <i>Microbial Biotechnology</i> , 2014, 7, 528-544.	2.0	21
59	Genomics-informed design of loop-mediated isothermal amplification for detection of phytopathogenic <i>Xanthomonas arboricola</i> pv. <i>pruni</i> at the intraspecific level. <i>Plant Pathology</i> , 2013, 62, 475-484.	1.2	38
60	<i>Erwinia amylovora</i> loop-mediated isothermal amplification (LAMP) assay for rapid pathogen detection and on-site diagnosis of fire blight. <i>Journal of Microbiological Methods</i> , 2013, 92, 332-339.	0.7	71
61	Identification of a major QTL for <i>Xanthomonas arboricola</i> pv. <i>pruni</i> resistance in apricot. <i>Tree Genetics and Genomes</i> , 2013, 9, 409-421.	0.6	12
62	Comparative RNA-Seq Analysis of Early-Infected Peach Leaves by the Invasive Phytopathogen <i>Xanthomonas arboricola</i> pv. <i>pruni</i> . <i>PLoS ONE</i> , 2013, 8, e54196.	1.1	46
63	<i>Xanthomonas arboricola</i> pv. <i>fragariae</i> : what's in a name?. <i>Plant Pathology</i> , 2013, 62, 1123-1131.	1.2	32
64	Type Three Effector Gene Distribution and Sequence Analysis Provide New Insights into the Pathogenicity of Plant-Pathogenic <i>Xanthomonas arboricola</i> . <i>Applied and Environmental Microbiology</i> , 2012, 78, 371-384.	1.4	58
65	Evolutionary history of synthesis pathway genes for phloroglucinol and cyanide antimicrobials in plant-associated fluorescent pseudomonads. <i>Molecular Phylogenetics and Evolution</i> , 2012, 63, 877-890.	1.2	29
66	The role of the antimicrobial compound 2,4-diacetylphloroglucinol in the impact of biocontrol <i>Pseudomonas fluorescens</i> F113 on <i>Azospirillum brasilense</i> phyto-stimulators. <i>Microbiology (United Kingdom)</i> Tj ETQq0 0 0 rgBT/Overlook 10 Tf 5	0.7	10
67	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. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 271-284.	1.4	134
68	A duplex-PCR method for species- and pathovar-level identification and detection of the quarantine plant pathogen <i>Xanthomonas arboricola</i> pv. <i>pruni</i> . <i>Journal of Microbiological Methods</i> , 2011, 86, 16-24.	0.7	48
69	The ubiquitous plasmid pXap41 in the invasive phytopathogen <i>Xanthomonas arboricola</i> pv. <i>pruni</i> : complete sequence and comparative genomic analysis. <i>FEMS Microbiology Letters</i> , 2011, 323, 52-60.	0.7	30
70	First report of the quarantine pathogen <i>Xanthomonas arboricola</i> pv. <i>pruni</i> on apricot and plum in Switzerland. <i>Plant Pathology</i> , 2010, 59, 404-404.	1.2	11
71	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 phyto-beneficial <i>Azospirillum lipoferum</i> 4B and other Proteobacteria. <i>FEMS Microbiology Ecology</i> , 2008, 65, 202-219.	1.3	78
72	Duplication of Plasmid-Borne Nitrite Reductase Gene <i>nirK</i> in the Wheat-Associated Plant Growth-Promoting Rhizobacterium <i>Azospirillum brasilense</i> Sp245. <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 831-842.	1.4	39

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73	Promoter-trap identification of wheat seed extract-induced genes in the plant-growth-promoting rhizobacterium <i>Azospirillum brasilense</i> Sp245. <i>Microbiology (United Kingdom)</i> , 2007, 153, 3608-3622.	0.7	77
74	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.	0.7	9
75	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.	0.7	9