

Robert Jackson

List of Publications by Year in descending order

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Version: 2024-02-01

83
papers

5,414
citations

101543

36
h-index

85541

71
g-index

88
all docs

88
docs citations

88
times ranked

5664
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of novel aphid-killing bacteria to protect plants. <i>Microbial Biotechnology</i> , 2022, 15, 1203-1220.	4.2	6
2	Identifying resistance in wild and ornamental cherry towards bacterial canker caused by <i>Pseudomonas syringae</i> . <i>Plant Pathology</i> , 2022, 71, 949-965.	2.4	6
3	Natural selection on crosstalk between gene regulatory networks facilitates bacterial adaptation to novel environments. <i>Current Opinion in Microbiology</i> , 2022, 67, 102140.	5.1	14
4	Scaling-up to understand tree-pathogen interactions: A steep, tough climb or a walk in the park?. <i>Current Opinion in Plant Biology</i> , 2022, 68, 102229.	7.1	3
5	Rapid impact of <i>Impatiens glandulifera</i> control on above- and belowground invertebrate communities. <i>Weed Research</i> , 2021, 61, 35-44.	1.7	4
6	Transposon Mutagenesis of <i>Pseudomonas syringae</i> Pathovars <i>syringae</i> and <i>morsprunorum</i> to Identify Genes Involved in Bacterial Canker Disease of Cherry. <i>Microorganisms</i> , 2021, 9, 1328.	3.6	3
7	The role of l-arabinose metabolism for <i>Escherichia coli</i> O157:H7 in edible plants. <i>Microbiology (United Kingdom)</i> 180, 1801-1811. doi:10.1099/mic/0/000000.0	0.784314	1
8	Seeing the forest for the trees: Use of phages to treat bacterial tree diseases. <i>Plant Pathology</i> , 2021, 70, 1987-2004.	2.4	7
9	A mutational hotspot that determines highly repeatable evolution can be built and broken by silent genetic changes. <i>Nature Communications</i> , 2021, 12, 6092.	12.8	27
10	Genomic Characterisation of Mushroom Pathogenic <i>Pseudomonads</i> and Their Interaction with Bacteriophages. <i>Viruses</i> , 2020, 12, 1286.	3.3	3
11	An improved conjugation method for <i>Pseudomonas syringae</i> . <i>Journal of Microbiological Methods</i> , 2020, 177, 106025.	1.6	1
12	Phage biocontrol to combat <i>Pseudomonas syringae</i> pathogens causing disease in cherry. <i>Microbial Biotechnology</i> , 2020, 13, 1428-1445.	4.2	44
13	Genotypic and phenotypic analyses reveal distinct population structures and ecotypes for sugar beet-associated <i>Pseudomonas</i> in Oxford and Auckland. <i>Ecology and Evolution</i> , 2020, 10, 5963-5975.	1.9	2
14	Isolation, Characterisation and Experimental Evolution of Phage that Infect the Horse Chestnut Tree Pathogen, <i>Pseudomonas syringae</i> pv. <i>aesculi</i> . <i>Current Microbiology</i> , 2020, 77, 1438-1447.	2.2	10
15	Cherry picking by pseudomonads: After a century of research on canker, genomics provides insights into the evolution of pathogenicity towards stone fruits. <i>Plant Pathology</i> , 2020, 69, 962-978.	2.4	16
16	Editorial: Environmental Bacteriophages: From Biological Control Applications to Directed Bacterial Evolution. <i>Frontiers in Microbiology</i> , 2019, 10, 1830.	3.5	8
17	Endophytes vs tree pathogens and pests: can they be used as biological control agents to improve tree health?. <i>European Journal of Plant Pathology</i> , 2019, 155, 711-729.	1.7	87
18	Characterization of the pathogenicity of strains of <i>Pseudomonas syringae</i> towards cherry and plum. <i>Plant Pathology</i> , 2018, 67, 1177-1193.	2.4	40

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19	Coping with Environmental Eukaryotes; Identification of <i>Pseudomonas syringae</i> Genes during the Interaction with Alternative Hosts or Predators. <i>Microorganisms</i> , 2018, 6, 32.	3.6	6
20	Comparative genomics of <i>Pseudomonas syringae</i> reveals convergent gene gain and loss associated with specialization onto cherry (<i>Prunus avium</i>). <i>New Phytologist</i> , 2018, 219, 672-696.	7.3	52
21	Supercoiling of an excised genomic island represses effector gene expression to prevent activation of host resistance. <i>Molecular Microbiology</i> , 2018, 110, 444-454.	2.5	10
22	Is there sufficient Ensifer and Rhizobium species diversity in UK farmland soils to support red clover (<i>Trifolium pratense</i>), white clover (<i>T. repens</i>), lucerne (<i>Medicago sativa</i>) and black medic (<i>M. Tj ETQq0 0 0 rgBT /Owblock 10Tf 50 617</i>).		
23	Whole-Transcriptome Analysis of Verocytotoxigenic <i>Escherichia coli</i> O157:H7 (Sakai) Suggests Plant-Species-Specific Metabolic Responses on Exposure to Spinach and Lettuce Extracts. <i>Frontiers in Microbiology</i> , 2016, 7, 1088.	3.5	34
24	Throwing down the gauntlet for molecular plant pathology in the 21st century—what are the new challenges for bacterial research?. <i>Molecular Plant Pathology</i> , 2016, 17, 1163-1164.	4.2	0
25	Early changes in apoplast composition associated with defence and disease in interactions between <i>Phaseolus vulgaris</i> and the halo blight pathogen <i>Pseudomonas syringae</i> Pv. <i>phaseolicola</i> . <i>Plant, Cell and Environment</i> , 2016, 39, 2172-2184.	5.7	102
26	Wheat seed embryo excision enables the creation of axenic seedlings and Koch's postulates testing of putative bacterial endophytes. <i>Scientific Reports</i> , 2016, 6, 25581.	3.3	45
27	A low frequency persistent reservoir of a genomic island in a pathogen population ensures island survival and improves pathogen fitness in a susceptible host. <i>Environmental Microbiology</i> , 2016, 18, 4144-4152.	3.8	22
28	Endophytic bacterial community composition in wheat (<i>Triticum aestivum</i>) is determined by plant tissue type, developmental stage and soil nutrient availability. <i>Plant and Soil</i> , 2016, 405, 381-396.	3.7	128
29	Rapid, automated detection of stem canker symptoms in woody perennials using artificial neural network analysis. <i>Plant Methods</i> , 2015, 11, 57.	4.3	21
30	Editorial on plants as alternative hosts for human and animal pathogens. <i>Frontiers in Microbiology</i> , 2015, 6, 397.	3.5	22
31	Evolutionary resurrection of flagellar motility via rewiring of the nitrogen regulation system. <i>Science</i> , 2015, 347, 1014-1017.	12.6	61
32	The Identification of Genes Important in <i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> Plant Colonisation Using In Vitro Screening of Transposon Libraries. <i>PLoS ONE</i> , 2015, 10, e0137355.	2.5	10
33	An optimized method for the extraction of bacterial mRNA from plant roots infected with <i>Escherichia coli</i> O157:H7. <i>Frontiers in Microbiology</i> , 2014, 5, 286.	3.5	13
34	Evidence that nematodes may vector the soft rot causing enterobacterial phytopathogens. <i>Plant Pathology</i> , 2014, 63, 747-757.	2.4	17
35	The <i>ruIB</i> gene of plasmid <i>pWW</i> is a hotspot for the site-specific insertion of integron-like elements found in the chromosomes of environmental <i>Pseudomonas fluorescens</i> group bacteria. <i>Environmental Microbiology</i> , 2014, 16, 2374-2388.	3.8	9
36	The biosurfactant viscosin produced by <i>Pseudomonas fluorescens</i> SBW25 aids spreading motility and plant growth promotion. <i>Environmental Microbiology</i> , 2014, 16, 2267-2281.	3.8	103

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37	Draft genome sequence of <i>Pseudomonas corrugata</i> , a phytopathogenic bacterium with potential industrial applications. <i>Journal of Biotechnology</i> , 2014, 175, 65-66.	3.8	12
38	<i>Bdellovibrio bacteriovorus</i> HD100 guards against <i>Pseudomonas tolaasii</i> brown-blotch lesions on the surface of post-harvest <i>Agaricus bisporus</i> supermarket mushrooms. <i>BMC Microbiology</i> , 2014, 14, 163.	3.3	41
39	First steps in experimental cancer evolution. <i>Evolutionary Applications</i> , 2013, 6, 535-548.	3.1	25
40	Hcp2, a Secreted Protein of the Phytopathogen <i>Pseudomonas syringae</i> pv. Tomato DC3000, Is Required for Fitness for Competition against Bacteria and Yeasts. <i>Journal of Bacteriology</i> , 2012, 194, 4810-4822.	2.2	76
41	<i>In planta</i> conditions induce genomic changes in <i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> . <i>Molecular Plant Pathology</i> , 2011, 12, 167-176.	4.2	47
42	<i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> : from "has bean"™ to supermodel. <i>Molecular Plant Pathology</i> , 2011, 12, 617-627.	4.2	85
43	<i>Pseudomonas</i> genomes: diverse and adaptable. <i>FEMS Microbiology Reviews</i> , 2011, 35, 652-680.	8.6	765
44	Bacterial pathogen evolution: breaking news. <i>Trends in Genetics</i> , 2011, 27, 32-40.	6.7	55
45	Bacterial genomes: evolution of pathogenicity. <i>Current Opinion in Plant Biology</i> , 2011, 14, 385-391.	7.1	23
46	The influence of the accessory genome on bacterial pathogen evolution. <i>Mobile Genetic Elements</i> , 2011, 1, 55-65.	1.8	125
47	Influence of the <i>Photorhabdus luminescens</i> Phosphomannose Isomerase Gene, <i>manA</i> , on Mannose Utilization, Exopolysaccharide Structure, and Biofilm Formation. <i>Applied and Environmental Microbiology</i> , 2011, 77, 776-785.	3.1	10
48	The Stealth Episode: Suppression of Gene Expression on the Excised Genomic Island PPHGI-1 from <i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> . <i>PLoS Pathogens</i> , 2011, 7, e1002010.	4.7	47
49	Miniature Transposable Sequences Are Frequently Mobilized in the Bacterial Plant Pathogen <i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> . <i>PLoS ONE</i> , 2011, 6, e25773.	2.5	23
50	Testing temperature-induced proteomic changes in the plant-associated bacterium <i>Pseudomonas fluorescens</i> SBW25. <i>Environmental Microbiology Reports</i> , 2010, 2, 396-402.	2.4	5
51	Confocal Imaging of <i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> Colony Development in Bean Reveals Reduced Multiplication of Strains Containing the Genomic Island PPHGI-1. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 1294-1302.	2.6	17
52	Comparative Genome Analysis Provides Insights into the Evolution and Adaptation of <i>Pseudomonas syringae</i> pv. <i>aesculi</i> on <i>Aesculus hippocastanum</i> . <i>PLoS ONE</i> , 2010, 5, e10224.	2.5	104
53	Bacterial Evolution by Genomic Island Transfer Occurs via DNA Transformation In Planta. <i>Current Biology</i> , 2009, 19, 1586-1590.	3.9	82
54	Microbe-associated molecular pattern (MAMP) signatures, synergy, size and charge: influences on perception or mobility and host defence responses. <i>Molecular Plant Pathology</i> , 2009, 10, 375-387.	4.2	76

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55	Genomic and genetic analyses of diversity and plant interactions of <i>Pseudomonas fluorescens</i> . <i>Genome Biology</i> , 2009, 10, R51.	9.6	370
56	Bacterial Polysaccharides Suppress Induced Innate Immunity by Calcium Chelation. <i>Current Biology</i> , 2008, 18, 1078-1083.	3.9	212
57	Mutational activation of niche-specific genes provides insight into regulatory networks and bacterial function in a complex environment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 18247-18252.	7.1	79
58	Phylogenetic Analysis of the pPT23A Plasmid Family of <i>Pseudomonas syringae</i> . <i>Applied and Environmental Microbiology</i> , 2007, 73, 1287-1295.	3.1	41
59	Thioquinolobactin, a <i>Pseudomonas</i> siderophore with antifungal and anti- <i>Pythium</i> activity. <i>Environmental Microbiology</i> , 2007, 9, 425-434.	3.8	122
60	Evolution of microbial virulence: the benefits of stress. <i>Trends in Genetics</i> , 2007, 23, 293-300.	6.7	77
61	The Use of Bioluminescence for Monitoring in planta Growth Dynamics of a <i>Pseudomonas syringae</i> Plant Pathogen. <i>European Journal of Plant Pathology</i> , 2006, 115, 363-366.	1.7	11
62	Development and Application of In Vivo Expression Technology (IVET) for Analysing Microbial Gene Expression in Complex Environments. <i>Infectious Disorders - Drug Targets</i> , 2006, 6, 207-240.	0.8	16
63	<i>Pseudomonas syringae</i> pv. <i>coryli</i> , the Causal Agent of Bacterial Twig Dieback of <i>Corylus avellana</i> . <i>Phytopathology</i> , 2005, 95, 1316-1324.	2.2	37
64	Exposure to Host Resistance Mechanisms Drives Evolution of Bacterial Virulence in Plants. <i>Current Biology</i> , 2005, 15, 2230-2235.	3.9	111
65	Genetic Characterization of <i>Pseudomonas fluorescens</i> SBW25 <i>rsp</i> Gene Expression in the Phytosphere and In Vitro. <i>Journal of Bacteriology</i> , 2005, 187, 8477-8488.	2.2	48
66	Changes in Race-Specific Virulence in <i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> Are Associated with a Chimeric Transposable Element and Rare Deletion Events in a Plasmid-Borne Pathogenicity Island. <i>Applied and Environmental Microbiology</i> , 2005, 71, 3778-3785.	3.1	30
67	Whole-Genome Sequence Analysis of <i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> 1448A Reveals Divergence among Pathovars in Genes Involved in Virulence and Transposition. <i>Journal of Bacteriology</i> , 2005, 187, 6488-6498.	2.2	301
68	Pathogenicity and other genomic islands in plant pathogenic bacteria. <i>Molecular Plant Pathology</i> , 2003, 4, 407-420.	4.2	70
69	Location and activity of members of a family of <i>virPphA</i> homologues in pathovars of <i>Pseudomonas syringae</i> and <i>P. savastanoi</i> . <i>Molecular Plant Pathology</i> , 2002, 3, 205-216.	4.2	38
70	Molecular characterization of <i>avrPphD</i> , a widely-distributed gene from <i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> involved in non-host recognition by pea (<i>Pisum sativum</i>). <i>Physiological and Molecular Plant Pathology</i> , 2001, 58, 55-62.	2.5	33
71	The roles of plasmids in phytopathogenic bacteria: mobile arsenals?. <i>Microbiology (United Kingdom)</i> , 2001, 147, 763-780.	1.8	96
72	Highly conserved sequences flank avirulence genes: isolation of novel avirulence genes from <i>Pseudomonas syringae</i> pv. <i>pti</i> The GenBank accession numbers for the sequences determined in this work are AJ277495 and AJ277496.. <i>Microbiology (United Kingdom)</i> , 2001, 147, 1171-1182.	1.8	63

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73	Distribution and Characterisation of vir Gene Homologues in Pseudomonas syringae Pathovars. , 2001, , 212-215.		0
74	Isolation of Novel Avirulence Genes from Pseudomonas syringae pv. pisi. , 2001, , 216-219.		0
75	Evidence for the mobility of an avirulence gene, avrPpiA1 , between the chromosome and plasmids of races of Pseudomonas syringae pv. pisi. Molecular Plant Pathology, 2000, 1, 195-199.	4.2	16
76	Excision from tRNA genes of a large chromosomal region, carrying avrPphB, associated with race change in the bean pathogen, Pseudomonas syringae pv. phaseolicola. Molecular Microbiology, 2000, 38, 186-197.	2.5	46
77	Cultivar-specific avirulence and virulence functions assigned to avrPphF in Pseudomonas syringae pv. phaseolicola, the cause of bean halo-blight disease. EMBO Journal, 2000, 19, 3204-3214.	7.8	213
78	Phylogeny of the genus Pseudomonas: intrageneric structure reconstructed from the nucleotide sequences of gyrB and rpoD genes The GenBank accession numbers for the sequences determined in this work are: gyrB, D37926, D37297, D86005â€“D86019 and AB039381â€“AB039492; rpoD, D86020â€“D86036 and AB039493â€“AB039624.. Microbiology (United Kingdom), 2000, 146, 2385-2394.	1.8	458
79	Identification of a pathogenicity island, which contains genes for virulence and avirulence, on a large native plasmid in the bean pathogen Pseudomonas syringae pathovar phaseolicola. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 10875-10880.	7.1	325
80	A dispensable region of the chromosome which is associated with an avirulence gene in Pseudomonas syringae pv. pisi. Microbiology (United Kingdom), 1999, 145, 135-141.	1.8	6
81	Phylogenetic Evidence for a Diversification of Pseudomonas syringae pv. pisi Race 4 Strains into Two Distinct Lineages. Phytopathology, 1996, 86, 1051.	2.2	17
82	Molecular Mechanisms Underpinning Colonization of a Plant by Plant Growth-Promoting Rhizobacteria. , 0, , 111-128.		1
83	Genomic Islands in Plant-pathogenic Bacteria. , 0, , 137-158.		0