

Dawn L Arnold

List of Publications by Year in descending order

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41
papers

1,996
citations

304743

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276875

41
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42
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docs citations

42
times ranked

2172
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	<i>Brenneria goodwinii</i> growth in vitro is improved by competitive interactions with other bacterial species associated with Acute Oak Decline. <i>Current Research in Microbial Sciences</i> , 2022, 3, 100102.	2.3	4
3	<i>Rahnella perminowiae</i> sp. nov., <i>Rahnella bonaserana</i> sp. nov., <i>Rahnella rivi</i> sp. nov. and <i>Rahnella ecdela</i> sp. nov., isolated from diverse environmental sources, and emended description of the genus <i>Rahnella</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	1.7	9
4	Phosphite-mediated enhancement of defence responses in <i>Agrostis stolonifera</i> and <i>Poa annua</i> infected by <i>Microdochium nivale</i> . <i>Plant Pathology</i> , 2022, 71, 1486-1495.	2.4	3
5	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
6	An improved conjugation method for <i>Pseudomonas syringae</i> . <i>Journal of Microbiological Methods</i> , 2020, 177, 106025.	1.6	1
7	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
8	<i>Pseudomonas kirkieae</i> sp. nov., a novel species isolated from oak in the United Kingdom, and phylogenetic considerations of the genera <i>Pseudomonas</i> , <i>Azotobacter</i> and <i>Azomonas</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2426-2434.	1.7	15
9	<i>Pseudomonas syringae</i> : enterprising epiphyte and stealthy parasite. <i>Microbiology (United Kingdom)</i> , 2019, 165, 251-253.	1.8	25
10	<i>Pseudomonas daroniae</i> sp. nov. and <i>Pseudomonas dryadis</i> sp. nov., isolated from pedunculate oak affected by acute oak decline in the UK. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3368-3376.	1.7	34
11	Confocal microscopy reveals <i>in planta</i> dynamic interactions between pathogenic, avirulent and non-pathogenic <i>Pseudomonas syringae</i> strains. <i>Molecular Plant Pathology</i> , 2018, 19, 537-551.	4.2	31
12	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
13	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
14	Taxonomy and identification of bacteria associated with acute oak decline. <i>World Journal of Microbiology and Biotechnology</i> , 2017, 33, 143.	3.6	32
15	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
16	Multi-locus sequence typing of <i>Escherichia coli</i> isolates with acquired <i>ampC</i> genes and <i>ampC</i> promoter mutations. <i>Diagnostic Microbiology and Infectious Disease</i> , 2016, 86, 265-267.	1.8	1
17	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
18	<i>Pseudomonas syringae</i> Differentiates into Phenotypically Distinct Subpopulations During Colonization of a Plant Host. <i>Environmental Microbiology</i> , 2016, 18, 3593-3605.	3.8	41

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19	Gibbsiella papilionis Kim et al. 2013 is a later heterotypic synonym of Gibbsiella dentisursi Saito et al. 2013. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 4788-4791.	1.7	6
20	The Identification of Genes Important in Pseudomonas syringae pv. phaseolicola Plant Colonisation Using In Vitro Screening of Transposon Libraries. PLoS ONE, 2015, 10, e0137355.	2.5	10
21	Rahnella victoriana sp. nov., Rahnella bruchi sp. nov., Rahnella woolbedingensis sp. nov., classification of Rahnella genomospecies 2 and 3 as Rahnella variigena sp. nov. and Rahnella inusitata sp. nov., respectively and emended description of the genus Rahnella. Systematic and Applied Microbiology, 2014, 37, 545-552.	2.8	93
22	Description of Brenneria roseae sp. nov. and two subspecies, Brenneria roseae subspecies roseae ssp. nov and Brenneria roseae subspecies americana ssp. nov. isolated from symptomatic oak. Systematic and Applied Microbiology, 2014, 37, 396-401.	2.8	45
23	Gibbsiella greigii sp. nov., a novel species associated with oak decline in the USA. Systematic and Applied Microbiology, 2014, 37, 417-422.	2.8	24
24	In planta induced changes in the native plasmid profile of Pseudomonas syringae pathover phaseolicola strain 1302A. Plasmid, 2013, 70, 420-424.	1.4	9
25	<i>In planta</i> conditions induce genomic changes in <i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> . Molecular Plant Pathology, 2011, 12, 167-176.	4.2	47
26	<i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> : from 'has bean'™ to supermodel. Molecular Plant Pathology, 2011, 12, 617-627.	4.2	85
27	Bacterial pathogen evolution: breaking news. Trends in Genetics, 2011, 27, 32-40.	6.7	55
28	Bacterial genomes: evolution of pathogenicity. Current Opinion in Plant Biology, 2011, 14, 385-391.	7.1	23
29	The influence of the accessory genome on bacterial pathogen evolution. Mobile Genetic Elements, 2011, 1, 55-65.	1.8	125
30	The Stealth Episode: Suppression of Gene Expression on the Excised Genomic Island PPHGI-1 from Pseudomonas syringae pv. phaseolicola. PLoS Pathogens, 2011, 7, e1002010.	4.7	47
31	Comparative Genome Analysis Provides Insights into the Evolution and Adaptation of Pseudomonas syringae pv. aesculi on Aesculus hippocastanum. PLoS ONE, 2010, 5, e10224.	2.5	104
32	Bacterial Evolution by Genomic Island Transfer Occurs via DNA Transformation In Planta. Current Biology, 2009, 19, 1586-1590.	3.9	82
33	Evolution of microbial virulence: the benefits of stress. Trends in Genetics, 2007, 23, 293-300.	6.7	77
34	The Use of Bioluminescence for Monitoring in planta Growth Dynamics of a Pseudomonas syringae Plant Pathogen. European Journal of Plant Pathology, 2006, 115, 363-366.	1.7	11
35	Exposure to Host Resistance Mechanisms Drives Evolution of Bacterial Virulence in Plants. Current Biology, 2005, 15, 2230-2235.	3.9	111
36	Pathogenicity and other genomic islands in plant pathogenic bacteria. Molecular Plant Pathology, 2003, 4, 407-420.	4.2	70

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37	Location and activity of members of a family of virPphA 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
38	Highly conserved sequences flank avirulence genes: isolation of novel avirulence genes from <i>Pseudomonas syringae</i> pv. <i>psis</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
39	Evidence for the mobility of an avirulence gene, <i>avrPpiA1</i> , between the chromosome and plasmids of races of <i>Pseudomonas syringae</i> pv. <i>psis</i> . <i>Molecular Plant Pathology</i> , 2000, 1, 195-199.	4.2	16
40	Excision from tRNA genes of a large chromosomal region, carrying <i>avrPphB</i> , associated with race change in the bean pathogen, <i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> . <i>Molecular Microbiology</i> , 2000, 38, 186-197.	2.5	46
41	Phylogeny of the genus <i>Pseudomonas</i> : intrageneric structure reconstructed from the nucleotide sequences of <i>gyrB</i> and <i>rpoD</i> genes. The GenBank accession numbers for the sequences determined in this work are: <i>gyrB</i> , D37926, D37297, D86005, D86019 and AB039381, AB039492; <i>rpoD</i> , D86020, D86036 and AB039493, AB039624. <i>Microbiology (United Kingdom)</i> , 2000, 146, 2385-2394.	1.8	458