

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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docs citations

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times ranked

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#	ARTICLE	IF	CITATIONS
1	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, D86005â€“D86019 and AB039381â€“AB039492; <i>rpoD</i> , D86020â€“D86036 and AB039493â€“AB039624.. <i>Microbiology (United Kingdom)</i> , 2000, 146, 2385-2394.	1.8	458
2	The influence of the accessory genome on bacterial pathogen evolution. <i>Mobile Genetic Elements</i> , 2011, 1, 55-65.	1.8	125
3	Exposure to Host Resistance Mechanisms Drives Evolution of Bacterial Virulence in Plants. <i>Current Biology</i> , 2005, 15, 2230-2235.	3.9	111
4	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
5	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
6	<i>Rahnella victoriana</i> sp. nov., <i>Rahnella bruchi</i> sp. nov., <i>Rahnella woolbedingensis</i> sp. nov., classification of <i>Rahnella</i> genospecies 2 and 3 as <i>Rahnella variigena</i> sp. nov. and <i>Rahnella inusitata</i> sp. nov., respectively and emended description of the genus <i>Rahnella</i> . <i>Systematic and Applied Microbiology</i> , 2014, 37, 545-552.	2.8	93
7	<i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> : from â€“has beanâ€™ to supermodel. <i>Molecular Plant Pathology</i> , 2011, 12, 617-627.	4.2	85
8	Bacterial Evolution by Genomic Island Transfer Occurs via DNA Transformation In Planta. <i>Current Biology</i> , 2009, 19, 1586-1590.	3.9	82
9	Evolution of microbial virulence: the benefits of stress. <i>Trends in Genetics</i> , 2007, 23, 293-300.	6.7	77
10	Pathogenicity and other genomic islands in plant pathogenic bacteria. <i>Molecular Plant Pathology</i> , 2003, 4, 407-420.	4.2	70
11	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
12	Bacterial pathogen evolution: breaking news. <i>Trends in Genetics</i> , 2011, 27, 32-40.	6.7	55
13	In planta 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
14	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
15	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
16	Description of <i>Brenneria roseae</i> sp. nov. and two subspecies, <i>Brenneria roseae</i> subspecies <i>roseae</i> ssp. nov. and <i>Brenneria roseae</i> subspecies <i>americana</i> ssp. nov. isolated from symptomatic oak. <i>Systematic and Applied Microbiology</i> , 2014, 37, 396-401.	2.8	45
17	<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
18	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

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19	<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
20	Taxonomy and identification of bacteria associated with acute oak decline. <i>World Journal of Microbiology and Biotechnology</i> , 2017, 33, 143.	3.6	32
21	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
22	<i>Pseudomonas syringae</i> : enterprising epiphyte and stealthy parasite. <i>Microbiology (United Kingdom)</i> , 2019, 165, 251-253.	1.8	25
23	<i>Gibbsiella greigii</i> sp. nov., a novel species associated with oak decline in the USA. <i>Systematic and Applied Microbiology</i> , 2014, 37, 417-422.	2.8	24
24	Bacterial genomes: evolution of pathogenicity. <i>Current Opinion in Plant Biology</i> , 2011, 14, 385-391.	7.1	23
25	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
26	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
27	<i>Pseudomonas kirkiae</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
28	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
29	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
30	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
31	In planta induced changes in the native plasmid profile of <i>Pseudomonas syringae</i> pathovar <i>phaseolicola</i> strain 1302A. <i>Plasmid</i> , 2013, 70, 420-424.	1.4	9
32	<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
33	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
34	<i>Gibbsiella papilionis</i> Kim et al. 2013 is a later heterotypic synonym of <i>Gibbsiella dentisursi</i> Saito et al. 2013. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 4788-4791.	1.7	6
35	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
36	<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

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37	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
38	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
39	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
40	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
41	An improved conjugation method for <i>Pseudomonas syringae</i> . <i>Journal of Microbiological Methods</i> , 2020, 177, 106025.	1.6	1