

Toni A Chapman

List of Publications by Year in descending order

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Version: 2024-02-01

62
papers

2,190
citations

236612

25
h-index

233125

45
g-index

70
all docs

70
docs citations

70
times ranked

2395
citing authors

#	ARTICLE	IF	CITATIONS
1	Safety of raw meat and shellfish in Vietnam: An analysis of <i>Escherichia coli</i> isolations for antibiotic resistance and virulence genes. <i>International Journal of Food Microbiology</i> , 2008, 124, 217-223.	2.1	255
2	Comparison of Virulence Gene Profiles of <i>Escherichia coli</i> Strains Isolated from Healthy and Diarrheic Swine. <i>Applied and Environmental Microbiology</i> , 2006, 72, 4782-4795.	1.4	246
3	Synonymization of key pest species within the <i>Bactrocera dorsalis</i> species complex (Diptera: Tephritidae): taxonomic changes based on a review of 20 years of integrative morphological, molecular, cytogenetic, behavioural and chemoeological data. <i>Systematic Entomology</i> , 2015, 40, 456-471.	1.7	175
4	Porcine commensal <i>Escherichia coli</i> : a reservoir for class 1 integrons associated with IS26. <i>Microbial Genomics</i> , 2017, 3, .	1.0	89
5	Near full-length 16S rRNA gene next-generation sequencing revealed <i>Asaia</i> as a common midgut bacterium of wild and domesticated Queensland fruit fly larvae. <i>Microbiome</i> , 2018, 6, 85.	4.9	82
6	Population structure of <i>Bactrocera dorsalis</i> s.s., <i>B. papayae</i> and <i>B. philippinensis</i> (Diptera: Tephritidae) in southeast Asia: evidence for a single species hypothesis using mitochondrial DNA and wing-shape data. <i>BMC Evolutionary Biology</i> , 2012, 12, 130.	3.2	75
7	Antimicrobial resistance and virulence gene profiles in multi-drug resistant enterotoxigenic <i>Escherichia coli</i> isolated from pigs with post-weaning diarrhoea. <i>Veterinary Microbiology</i> , 2010, 145, 299-307.	0.8	74
8	Piecing together an integrative taxonomic puzzle: microsatellite, wing shape and aedeagus length analyses of <i>Bactrocera dorsalis</i> s.l. (Diptera: Tephritidae) find no evidence of multiple lineages in a proposed contact zone along the Thai/Malay Peninsula. <i>Systematic Entomology</i> , 2013, 38, 2-13.	1.7	70
9	Multi-gene phylogenetic analysis of south-east Asian pest members of the <i>Bactrocera dorsalis</i> species complex (Diptera: Tephritidae) does not support current taxonomy. <i>Journal of Applied Entomology</i> , 2014, 138, 235-253.	0.8	67
10	Human-associated fluoroquinolone-resistant <i>Escherichia coli</i> clonal lineages, including ST354, isolated from canine feces and extraintestinal infections in Australia. <i>Microbes and Infection</i> , 2015, 17, 266-274.	1.0	55
11	Diversity analysis of commensal porcine <i>Escherichia coli</i> associations between genotypes and habitat in the porcine gastrointestinal tract. <i>Microbiology (United Kingdom)</i> , 2004, 150, 1735-1740.	0.7	54
12	Genomic Microbial Epidemiology Is Needed to Comprehend the Global Problem of Antibiotic Resistance and to Improve Pathogen Diagnosis. <i>Frontiers in Microbiology</i> , 2016, 7, 843.	1.5	53
13	Comparative Analysis of Virulence Genes, Genetic Diversity, and Phylogeny of Commensal and Enterotoxigenic <i>Escherichia coli</i> Isolates from Weaned Pigs. <i>Applied and Environmental Microbiology</i> , 2007, 73, 83-91.	1.4	51
14	<i>Salmonella enterica</i> isolated from infections in Australian livestock remain susceptible to critical antimicrobials. <i>International Journal of Antimicrobial Agents</i> , 2014, 43, 126-130.	1.1	48
15	Phylogenetic and molecular insights into the evolution of multidrug-resistant porcine enterotoxigenic <i>Escherichia coli</i> in Australia. <i>International Journal of Antimicrobial Agents</i> , 2014, 44, 105-111.	1.1	44
16	Tephritid-microbial interactions to enhance fruit fly performance in sterile insect technique programs. <i>BMC Microbiology</i> , 2019, 19, 287.	1.3	39
17	Genetic relatedness and virulence gene profiles of <i>Escherichia coli</i> strains isolated from septicaemic and uroseptic patients. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2010, 29, 15-23.	1.3	37
18	Comparative genomic analysis of a multiple antimicrobial resistant enterotoxigenic <i>E. coli</i> O157 lineage from Australian pigs. <i>BMC Genomics</i> , 2015, 16, 165.	1.2	34

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19	Complete Sequences of Multiple-Drug Resistant IncHI2 ST3 Plasmids in <i>Escherichia coli</i> of Porcine Origin in Australia. <i>Frontiers in Sustainable Food Systems</i> , 2019, 3, .	1.8	31
20	Molecular Techniques for the Detection and Differentiation of Host and Parasitoid Species and the Implications for Fruit Fly Management. <i>Insects</i> , 2012, 3, 763-788.	1.0	28
21	The genome of <i>Clostridium difficile</i> 5.3. <i>Gut Pathogens</i> , 2014, 6, 4.	1.6	27
22	Rapid identification of virulence genes in enterotoxigenic <i>Escherichia coli</i> isolates associated with diarrhoea in Queensland piggeries. <i>Australian Veterinary Journal</i> , 2005, 83, 293-299.	0.5	26
23	<i>Staphylococcus aureus</i> ST398 detected in pigs in Australia. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 1426-1428.	1.3	26
24	Next-Generation Sequencing reveals relationship between the larval microbiome and food substrate in the polyphagous Queensland fruit fly. <i>Scientific Reports</i> , 2019, 9, 14292.	1.6	26
25	Diet and irradiation effects on the bacterial community composition and structure in the gut of domesticated teneral and mature Queensland fruit fly, <i>Bactrocera tryoni</i> (Diptera: Tephritidae). <i>BMC Microbiology</i> , 2019, 19, 281.	1.3	26
26	Molecular Characterization of <i>Escherichia coli</i> Strains That Cause Symptomatic and Asymptomatic Urinary Tract Infections. <i>Journal of Clinical Microbiology</i> , 2012, 50, 1027-1030.	1.8	25
27	Microbiome of the Queensland Fruit Fly through Metamorphosis. <i>Microorganisms</i> , 2020, 8, 795.	1.6	25
28	Yeast: An Overlooked Component of <i>Bactrocera tryoni</i> (Diptera: Tephritidae) Larval Gut Microbiota. <i>Journal of Economic Entomology</i> , 2016, 110, tow262.	0.8	24
29	Interactions between ecological factors in the developmental environment modulate pupal and adult traits in a polyphagous fly. <i>Ecology and Evolution</i> , 2019, 9, 6342-6352.	0.8	24
30	Whole Genome Sequencing Analysis of Porcine Faecal Commensal <i>Escherichia coli</i> Carrying Class 1 Integrons from Sows and Their Offspring. <i>Microorganisms</i> , 2020, 8, 843.	1.6	22
31	Molecular Characterization of Commensal <i>Escherichia coli</i> Adapted to Different Compartments of the Porcine Gastrointestinal Tract. <i>Applied and Environmental Microbiology</i> , 2012, 78, 6799-6803.	1.4	19
32	Comparative genomics reveals signature regions used to develop a robust and sensitive multiplex TaqMan real-time qPCR assay to detect the genus <i>Dickeya</i> and <i>Dickeya dianthicola</i> . <i>Journal of Applied Microbiology</i> , 2020, 128, 1703-1719.	1.4	19
33	Molecular serogrouping of porcine enterotoxigenic <i>Escherichia coli</i> from Australia. <i>Journal of Microbiological Methods</i> , 2012, 88, 73-76.	0.7	18
34	Fluoroquinolone-resistant extraintestinal pathogenic <i>Escherichia coli</i> , including O25b-ST131, isolated from faeces of hospitalized dogs in an Australian veterinary referral centre. <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 1025-1031.	1.3	17
35	Genomic sequence analysis reveals diversity of Australian <i>Xanthomonas</i> species associated with bacterial leaf spot of tomato, capsicum and chilli. <i>BMC Genomics</i> , 2019, 20, 310.	1.2	17
36	Colonisation dynamics and virulence of two clonal groups of multidrug-resistant <i>Escherichia coli</i> isolated from dogs. <i>Microbes and Infection</i> , 2009, 11, 100-107.	1.0	16

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37	Commensal microbiota modulates larval foraging behaviour, development rate and pupal production in <i>Bactrocera tryoni</i> . <i>BMC Microbiology</i> , 2019, 19, 286.	1.3	16
38	Genomic Acquisitions in Emerging Populations of <i>Xanthomonas vasicola</i> pv. <i>vasculorum</i> Infecting Corn in the United States and Argentina. <i>Phytopathology</i> , 2020, 110, 1161-1173.	1.1	16
39	Genomic Characterisation of a Multiple Drug Resistant InCHI2 ST4 Plasmid in <i>Escherichia coli</i> ST744 in Australia. <i>Microorganisms</i> , 2020, 8, 896.	1.6	15
40	<i>Escherichia coli</i> ST302: Genomic Analysis of Virulence Potential and Antimicrobial Resistance Mediated by Mobile Genetic Elements. <i>Frontiers in Microbiology</i> , 2020, 10, 3098.	1.5	14
41	Spray-dried porcine plasma and yeast derived protein meal influence the adaption to weaning of primiparous and multiparous sow progeny in different ways. <i>Animal Production Science</i> , 2013, 53, 75.	0.6	13
42	Phenotypic and genotypic profiling of antimicrobial resistance in enteric <i>Escherichia coli</i> communities isolated from finisher pigs in Australia. <i>Australian Veterinary Journal</i> , 2016, 94, 371-376.	0.5	13
43	Comparative genomic analysis of toxin-negative strains of <i>Clostridium difficile</i> from humans and animals with symptoms of gastrointestinal disease. <i>BMC Microbiology</i> , 2016, 16, 41.	1.3	13
44	Pathogenicity and copper tolerance in Australian <i>Xanthomonas</i> species associated with bacterial leaf spot. <i>Crop Protection</i> , 2020, 127, 104923.	1.0	13
45	Multilocus sequence typing of Australian <i>Streptococcus suis</i> type 2 by MALDI-TOF mass spectrometry analysis of PCR amplicons. <i>Veterinary Microbiology</i> , 2015, 177, 394-397.	0.8	11
46	Artificial Larval Diet Mediates the Microbiome of Queensland Fruit Fly. <i>Frontiers in Microbiology</i> , 2020, 11, 576156.	1.5	11
47	First report of the presence of <i>Verticillium dahliae</i> VCG1A in Australia. <i>Australasian Plant Disease Notes</i> , 2016, 11, 1.	0.4	10
48	A large-scale metagenomic survey dataset of the post-weaning piglet gut lumen. <i>GigaScience</i> , 2021, 10, .	3.3	9
49	Post-weaning shifts in microbiome composition and metabolism revealed by over 25,000 pig gut metagenome-assembled genomes. <i>Microbial Genomics</i> , 2021, 7, .	1.0	9
50	Editorial: Genome-Wide Analyses of <i>Pectobacterium</i> and <i>Dickeya</i> Species. <i>Frontiers in Plant Science</i> , 2022, 13, 855262.	1.7	9
51	Fruit host-dependent fungal communities in the microbiome of wild Queensland fruit fly larvae. <i>Scientific Reports</i> , 2020, 10, 16550.	1.6	7
52	The <i>Verticillium</i> wilt problem in Australian cotton. <i>Australasian Plant Pathology</i> , 2021, 50, 129-135.	0.5	6
53	Selected culturable enteric bacterial populations are modified by diet acidification and the growth promotant Tylosin. <i>Letters in Applied Microbiology</i> , 2005, 41, 119-124.	1.0	5
54	Dynamics of the Queensland Fruit Fly Microbiome through the Transition from Nature to an Established Laboratory Colony. <i>Microorganisms</i> , 2022, 10, 291.	1.6	5

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55	Phylogenetic diversity analysis of shotgun metagenomic reads describes gut microbiome development and treatment effects in the post-weaned pig. PLoS ONE, 2022, 17, e0270372.	1.1	5
56	Green Fluorescent Protein-Based Biosensor To Detect and Quantify Stress Responses Induced by DNA-Degrading Colicins. Applied and Environmental Microbiology, 2011, 77, 6691-6693.	1.4	4
57	Virulence not linked with vegetative compatibility groups in Australian cotton <i>Verticillium dahliae</i> isolates. Australian Journal of Crop Science, 2020, , 633-640.	0.1	4
58	Comparative Genomics of <i>Xanthomonas citri</i> pv. <i>citri</i> A* Pathotype Reveals Three Distinct Clades with Varying Plasmid Distribution. Microorganisms, 2020, 8, 1947.	1.6	4
59	Virulence characteristics of translocating <i>Escherichia coli</i> and the interleukin-8 response to infection. Microbial Pathogenesis, 2011, 50, 81-86.	1.3	3
60	Building More Resilient Culture Collections: A Call for Increased Deposits of Plant-Associated Bacteria. Microorganisms, 2022, 10, 741.	1.6	2
61	Characterisation of <i>Verticillium dahliae</i> by inter-simple sequence repeats identified a virulent subpopulation affecting Australian cotton. Australasian Plant Pathology, 2022, 51, 409-418.	0.5	1
62	Using Genomics to Design a Pathovar-Specific Loop-Mediated Isothermal Amplification (LAMP) Assay, for the Improved Detection of <i>Xanthomonas citri</i> pv. <i>citri</i> . Microorganisms, 2022, 10, 1153.	1.6	0