Daniel Hurley

List of Publications by Year
in descending order

22 papers	600 citations	687363 13 h-index	642732 23 g-index
25 all docs	25 docs citations	25 times ranked	1039 citing authors

#	Article	IF	Citations
1	Enriching antimicrobial peptides from milk hydrolysates using pectin/alginate food-gels. Food Chemistry, 2021, 352, 129220.	8.2	18
2	Characterisation of Early Positive mcr-1 Resistance Gene and Plasmidome in Escherichia coli Pathogenic Strains Associated with Variable Phylogroups under Colistin Selection. Antibiotics, 2021, 10, 1041.	3.7	7
3	Characterization of Carbapenem-Resistant Enterobacteriaceae Cultured From Retail Meat Products, Patients, and Porcine Excrement in China. Frontiers in Microbiology, 2021, 12, 743468.	3.5	8
4	Draft genome sequences of Salmonella Oslo isolated from seafood and its laboratory generated auxotrophic mutant. Journal of Genomics, 2020, 8, 7-10.	0.9	2
5	Molecular characterisation of multi-drug resistant Escherichia coli of bovine origin. Veterinary Microbiology, 2020, 242, 108566.	1.9	10
6	Atypical Salmonella enterica Serovars in Murine and Human Macrophage Infection Models. Infection and Immunity, 2020, 88, .	2.2	6
7	Yersinia canariae sp. nov., isolated from a human yersiniosis case. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2382-2387.	1.7	10
8	Whole-Genome Sequencing-Based Characterization of 100 Listeria monocytogenes Isolates Collected from Food Processing Environments over a Four-Year Period. MSphere, 2019, 4, .	2.9	82
9	Yersinia hibernica sp. nov., isolated from pig-production environments. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 2023-2027.	1.7	15
10	Increased Virulence of Bloodstream Over Peripheral Isolates of P. aeruginosa Identified Through Post-transcriptional Regulation of Virulence Factors. Frontiers in Cellular and Infection Microbiology, 2018, 8, 357.	3.9	16
11	A novel disrupted mcr-1 gene and a lysogenized phage P1-like sequence detected from a large conjugative plasmid, cultured from a human atypical enteropathogenic Escherichia coli (aEPEC) recovered in China. Journal of Antimicrobial Chemotherapy, 2017, 72, dkw564.	3.0	18
12	Complete genetic analysis of a Salmonella enterica serovar Indiana isolate accompanying four plasmids carrying mcr-1, ESBL and other resistance genes in China. Veterinary Microbiology, 2017, 210, 142-146.	1.9	38
13	Exploring the Genome and Phenotype of Multi-Drug Resistant Klebsiella pneumoniae of Clinical Origin. Frontiers in Microbiology, 2017, 8, 1913.	3.5	35
14	Draft Genome Sequence of Escherichia coli 26R 793, a Plasmid-Free Recipient Strain Commonly Used in Conjugation Assays. Genome Announcements, 2016, 4, .	0.8	1
15	Molecular Characterization of Salmonella Serovars Anatum and Ealing Associated with Two Historical Outbreaks, Linked to Contaminated Powdered Infant Formula. Frontiers in Microbiology, 2016, 7, 1664.	3.5	2
16	Complete Genome Sequence of Clostridium estertheticum DSM 8809, a Microbe Identified in Spoiled Vacuum Packed Beef. Frontiers in Microbiology, 2016, 7, 1764.	3.5	19
17	Complete Genome Sequence of Leptospira alstonii Serovar Room22 Strain GWTS #1. Genome Announcements, 2016, 4, .	0.8	7
18	Characterisation of multidrug-resistant Shiga toxin-producing Escherichia coli cultured from pigs in China: co-occurrence of extended-spectrum Î²-lactamase- and mcr-1-encoding genes on plasmids. International Journal of Antimicrobial Agents, 2016, 48, 445-448.	2.5	44

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19	SalmonellaÃ¢â‚¬â€œHost Interactions Ã¢â‚¬â€œ Modulation of the Host Innate Immune System. Frontiers in Immunology, 2014, 5, 481.	4.8	124
20	Comparison of Listeria monocytogenes Isolates across the Island of Ireland. Journal of Food Protection, 2014, 77, 1402-1406.	1.7	4
21	A Model System for Studying the Transcriptomic and Physiological Changes Associated with Mammalian Host-Adaptation by Leptospira interrogans Serovar Copenhageni. PLoS Pathogens, 2014, 10, e1004004.	4.7	101
22	Potential of known and short prokaryotic protein motifs as a basis for novel peptide-based antibacterial therapeutics: a computational survey. Frontiers in Microbiology, 2014, 5, 4.	3.5	18