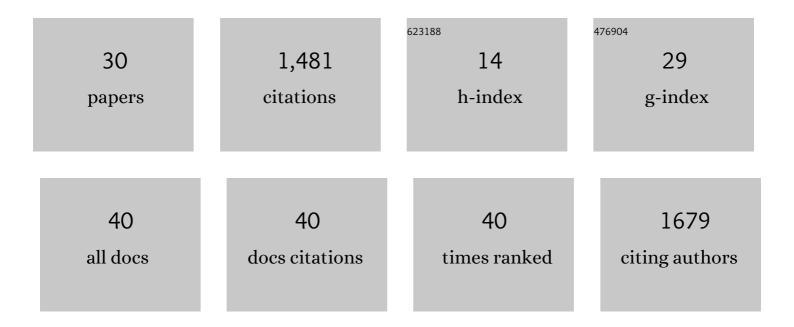
## Laura M Carroll

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Keeping up with the <i>Bacillus cereus</i> group: taxonomy through the genomics era and beyond. Critical Reviews in Food Science and Nutrition, 2022, 62, 7677-7702.	5.4	49
2	Associations between Listeria monocytogenes genomic characteristics and adhesion to polystyrene at 8°C. Food Microbiology, 2022, 102, 103915.	2.1	12
3	Genomic Sequencing of Bacillus cereus Sensu Lato Strains Isolated from Meat and Poultry Products in South Africa Enables Inter- and Intranational Surveillance and Source Tracking. Microbiology Spectrum, 2022, 10, e0070022.	1.2	4
4	Antibiotic Resistance in Shiga Toxigenic Escherichia coli Isolates from Surface Waters and Sediments in a Mixed Use Urban Agricultural Landscape. Antibiotics, 2021, 10, 237.	1.5	12
5	Recent Evolution and Genomic Profile of Salmonella enterica Serovar Heidelberg Isolates from Poultry Flocks in Brazil. Applied and Environmental Microbiology, 2021, 87, e0103621.	1.4	16
6	Genomic Characterization of Endemic and Ecdemic Non-typhoidal Salmonella enterica Lineages Circulating Among Animals and Animal Products in South Africa. Frontiers in Microbiology, 2021, 12, 748611.	1.5	10
7	Characterization of Basal Transcriptomes Identifies Potential Metabolic and Virulence-Associated Adaptations Among Diverse Nontyphoidal Salmonella enterica Serovars. Frontiers in Microbiology, 2021, 12, 730411.	1.5	4
8	Monitoring the Microevolution of Salmonella enterica in Healthy Dairy Cattle Populations at the Individual Farm Level Using Whole-Genome Sequencing. Frontiers in Microbiology, 2021, 12, 763669.	1.5	10
9	No Assembly Required: Using BTyper3 to Assess the Congruency of a Proposed Taxonomic Framework for the Bacillus cereus Group With Historical Typing Methods. Frontiers in Microbiology, 2020, 11, 580691.	1.5	32
10	Genomic Characterization of Salmonella Minnesota Clonal Lineages Associated with Poultry Production in Brazil. Animals, 2020, 10, 2043.	1.0	10
11	Twentieth-century emergence of antimicrobial resistant human- and bovine-associated Salmonella enterica serotype Typhimurium lineages in New York State. Scientific Reports, 2020, 10, 14428.	1.6	10
12	Cereulide Synthetase Acquisition and Loss Events within the Evolutionary History of Group III <i>Bacillus cereus Sensu Lato</i> Facilitate the Transition between Emetic and Diarrheal Foodborne Pathogens. MBio, 2020, 11, .	1.8	23
13	Novel Effective Bacillus cereus Group Species " <i>Bacillus clarus</i> ―Is Represented by Antibiotic-Producing Strain ATCC 21929 Isolated from Soil. MSphere, 2020, 5, .	1.3	13
14	Paenibacillus odorifer, the Predominant <i>Paenibacillus</i> Species Isolated from Milk in the United States, Demonstrates Genetic and Phenotypic Conservation of Psychrotolerance but Clade-Associated Differences in Nitrogen Metabolic Pathways. MSphere, 2020, 5, .	1.3	9
15	Proposal of a Taxonomic Nomenclature for the Bacillus cereus Group Which Reconciles Genomic Definitions of Bacterial Species with Clinical and Industrial Phenotypes. MBio, 2020, 11, .	1.8	127
16	Comparative genomics reveals different population structures associated with host and geographic origin in antimicrobialâ€resistant <scp><i>Salmonella enterica</i></scp> . Environmental Microbiology, 2020, 22, 2811-2828.	1.8	12
17	Assembly and Characterization of a Pathogen Strain Collection for Produce Safety Applications: Pre-growth Conditions Have a Larger Effect on Peroxyacetic Acid Tolerance Than Strain Diversity. Frontiers in Microbiology, 2019, 10, 1223.	1.5	17
18	Serotype-specific evolutionary patterns of antimicrobial-resistant Salmonella enterica. BMC Evolutionary Biology, 2019, 19, 132.	3.2	20

LAURA M CARROLL

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19	Identification of Novel Mobilized Colistin Resistance Gene <i>mcr-9</i> in a Multidrug-Resistant, Colistin-Susceptible Salmonella enterica Serotype Typhimurium Isolate. MBio, 2019, 10, .	1.8	406
20	Characterization of Emetic and Diarrheal Bacillus cereus Strains From a 2016 Foodborne Outbreak Using Whole-Genome Sequencing: Addressing the Microbiological, Epidemiological, and Bioinformatic Challenges. Frontiers in Microbiology, 2019, 10, 144.	1.5	101
21	Next-Generation Sequencing. , 2019, , 376-383.		1
22	Impacts of feeding preweaned calves milk containing drug residues on the functional profile of the fecal microbiota. Scientific Reports, 2018, 8, 554.	1.6	29
23	First report of an mcr-1-harboring Salmonella enterica subsp. enterica serotype 4,5,12:i:- strain isolated from blood of a patient in Switzerland. International Journal of Antimicrobial Agents, 2018, 52, 740-741.	1.1	10
24	Whole-Genome Sequencing of Drug-Resistant Salmonella enterica Isolates from Dairy Cattle and Humans in New York and Washington States Reveals Source and Geographic Associations. Applied and Environmental Microbiology, 2017, 83, .	1.4	89
25	Precision food safety: A systems approach to food safety facilitated byÂgenomics tools. TrAC - Trends in Analytical Chemistry, 2017, 96, 52-61.	5.8	74
26	Rapid, High-Throughput Identification of Anthrax-Causing and Emetic Bacillus cereus Group Genome Assemblies via BTyper, a Computational Tool for Virulence-Based Classification of Bacillus cereus Group Isolates by Using Nucleotide Sequencing Data. Applied and Environmental Microbiology, 2017, 83, .	1.4	80
27	Temporal Genomic Phylogeny Reconstruction Indicates a Geospatial Transmission Path of Salmonella Cerro in the United States and a Clade-Specific Loss of Hydrogen Sulfide Production. Frontiers in Microbiology, 2017, 8, 737.	1.5	31
28	Bacillus wiedmannii sp. nov., a psychrotolerant and cytotoxic Bacillus cereus group species isolated from dairy foods and dairy environments. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 4744-4753.	0.8	157
29	Application of a Nonlinear Model to Transcript Levels of Upregulated Stress Response Gene ibpA in Stationary-Phase Salmonella enterica Subjected to Sublethal Heat Stress. Journal of Food Protection, 2016, 79, 1089-1096.	0.8	4
30	Production of hemolysin BL by Bacillus cereus group isolates of dairy origin is associated with whole-genome phylogenetic clade. BMC Genomics, 2016, 17, 581.	1.2	77