

# Chad R Laing

## List of Publications by Year in descending order

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35  
papers

1,791  
citations

393982

19  
h-index

377514

34  
g-index

36  
all docs

36  
docs citations

36  
times ranked

2284  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Salmonella In Silico Typing Resource (SISTR): An Open Web-Accessible Tool for Rapidly Typing and Subtyping Draft Salmonella Genome Assemblies. PLoS ONE, 2016, 11, e0147101.	1.1	426
2	Pan-genome sequence analysis using Panseq: an online tool for the rapid analysis of core and accessory genomic regions. BMC Bioinformatics, 2010, 11, 461.	1.2	249
3	Genotypes Associated with <i>Listeria monocytogenes</i> Isolates Displaying Impaired or Enhanced Tolerances to Cold, Salt, Acid, or Desiccation Stress. Frontiers in Microbiology, 2017, 8, 369.	1.5	147
4	Genome evolution in major <i>Escherichia coli</i> O157:H7 lineages. BMC Genomics, 2007, 8, 121.	1.2	138
5	Exploiting the explosion of information associated with whole genome sequencing to tackle Shiga toxin-producing <i>Escherichia coli</i> (STEC) in global food production systems. International Journal of Food Microbiology, 2014, 187, 57-72.	2.1	83
6	Pan-genome Analyses of the Species <i>Salmonella enterica</i> , and Identification of Genomic Markers Predictive for Species, Subspecies, and Serovar. Frontiers in Microbiology, 2017, 8, 1345.	1.5	74
7	In silico genomic analyses reveal three distinct lineages of <i>Escherichia coli</i> O157:H7, one of which is associated with hyper-virulence. BMC Genomics, 2009, 10, 287.	1.2	68
8	Spatial and Temporal Drivers of Zoonotic Pathogen Contamination of an Agricultural Watershed. Journal of Environmental Quality, 2012, 41, 242-252.	1.0	59
9	Lineage and Host Source Are Both Correlated with Levels of Shiga Toxin 2 Production by <i>Escherichia coli</i> O157:H7 Strains. Applied and Environmental Microbiology, 2010, 76, 474-482.	1.4	51
10	Whole Genome Sequencing demonstrates that Geographic Variation of <i>Escherichia coli</i> O157 Genotypes Dominates Host Association. Scientific Reports, 2015, 5, 14145.	1.6	49
11	Genotypic Characterization and Prevalence of Virulence Factors among Canadian <i>Escherichia coli</i> O157:H7 Strains. Applied and Environmental Microbiology, 2008, 74, 4314-4323.	1.4	48
12	A Comparison of Shiga-Toxin 2 Bacteriophage from Classical Enterohemorrhagic <i>Escherichia coli</i> Serotypes and the German <i>E. coli</i> O104:H4 Outbreak Strain. PLoS ONE, 2012, 7, e37362.	1.1	47
13	Comparative Genomic Analysis of <i>Mannheimia haemolytica</i> from Bovine Sources. PLoS ONE, 2016, 11, e0149520.	1.1	41
14	Identification of a novel prophage regulator in <i>Escherichia coli</i> controlling the expression of type III secretion. Molecular Microbiology, 2012, 83, 208-223.	1.2	33
15	Rapid Determination of <i>Escherichia coli</i> O157:H7 Lineage Types and Molecular Subtypes by Using Comparative Genomic Fingerprinting. Applied and Environmental Microbiology, 2008, 74, 6606-6615.	1.4	30
16	ECTyper: in silico <i>Escherichia coli</i> serotype and species prediction from raw and assembled whole-genome sequence data. Microbial Genomics, 2021, 7, .	1.0	27
17	Phylogeographic Analysis Reveals Multiple International transmission Events Have Driven the Global Emergence of <i>Escherichia coli</i> O157:H7. Clinical Infectious Diseases, 2019, 69, 428-437.	2.9	26
18	Phenotypic and Genotypic Characteristics of Shiga Toxin-Producing <i>Escherichia coli</i> Isolated from Surface Waters and Sediments in a Canadian Urban-Agricultural Landscape. Frontiers in Cellular and Infection Microbiology, 2016, 6, 36.	1.8	25

#	ARTICLE	IF	CITATIONS
19	Genomic Analysis of Third Generation Cephalosporin Resistant Escherichia coli from Dairy Cow Manure. <i>Veterinary Sciences</i> , 2017, 4, 57.	0.6	20
20	SuperPhy: predictive genomics for the bacterial pathogen Escherichia coli. <i>BMC Microbiology</i> , 2016, 16, 65.	1.3	18
21	Comparative Genomic Analysis of Escherichia coli O157:H7 Isolated from Super-Shedder and Low-Shedder Cattle. <i>PLoS ONE</i> , 2016, 11, e0151673.	1.1	17
22	Multi-Year Persistence of Verotoxigenic Escherichia coli (VTEC) in a Closed Canadian Beef Herd: A Cohort Study. <i>Frontiers in Microbiology</i> , 2018, 9, 2040.	1.5	15
23	Genomic Regions Conserved in Lineage II Escherichia coli O157:H7 Strains. <i>Applied and Environmental Microbiology</i> , 2009, 75, 3271-3280.	1.4	13
24	Phylotyper: in silico predictor of gene subtypes. <i>Bioinformatics</i> , 2017, 33, 3638-3641.	1.8	13
25	Everything at once: Comparative analysis of the genomes of bacterial pathogens. <i>Veterinary Microbiology</i> , 2011, 153, 13-26.	0.8	12
26	Two distinct groups of porcine enteropathogenic Escherichia coli strains of serogroup O45 are revealed by comparative genomic hybridization and virulence gene microarray. <i>BMC Genomics</i> , 2009, 10, 402.	1.2	11
27	A new pyrosequencing assay for rapid detection and genotyping of Shiga toxin, intimin and O157-specific rfbE genes of Escherichia coli. <i>Journal of Microbiological Methods</i> , 2015, 109, 167-179.	0.7	11
28	Identification of Salmonella enterica species- and subgroup-specific genomic regions using Panseq 2.0. <i>Infection, Genetics and Evolution</i> , 2011, 11, 2151-2161.	1.0	10
29	Characteristics of Clinical Shiga Toxin-Producing Escherichia coli isolated from British Columbia. <i>BioMed Research International</i> , 2013, 2013, 1-11.	0.9	7
30	Targeting discriminatory SNPs in Salmonella enterica serovar Heidelberg genomes using RNase H2-dependent PCR. <i>Journal of Microbiological Methods</i> , 2019, 157, 81-87.	0.7	5
31	Rapid and accurate SNP genotyping of clonal bacterial pathogens with BioHansel. <i>Microbial Genomics</i> , 2021, 7, .	1.0	4
32	Assessing the genomic relatedness and evolutionary rates of persistent verotoxigenic Escherichia coli serotypes within a closed beef herd in Canada. <i>Microbial Genomics</i> , 2020, 6, .	1.0	4
33	Eleven High-Quality Reference Genome Sequences and 360 Draft Assemblies of Shiga Toxin-Producing Escherichia coli Isolates from Human, Food, Animal, and Environmental Sources in Canada. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	4
34	Spfy: an integrated graph database for real-time prediction of bacterial phenotypes and downstream comparative analyses. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, 1-10.	1.4	3
35	Insights from Genomic Studies of the Foodborne and Waterborne Pathogen Escherichia coli O157:H7. , 0, , 1-21.		0