

Chad R Laing

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

36
papers

1,212
citations

16
h-index

34
g-index

36
ext. papers

1,623
ext. citations

4.4
avg, IF

3.94
L-index

#	Paper	IF	Citations
36	ECTyper: serotype and species prediction from raw and assembled whole-genome sequence data. <i>Microbial Genomics</i> , 2021 , 7,	4.4	2
35	Rapid and accurate SNP genotyping of clonal bacterial pathogens with BioHansel. <i>Microbial Genomics</i> , 2021 , 7,	4.4	3
34	Assessing the genomic relatedness and evolutionary rates of persistent verotoxigenic serotypes within a closed beef herd in Canada. <i>Microbial Genomics</i> , 2020 , 6,	4.4	1
33	Eleven High-Quality Reference Genome Sequences and 360 Draft Assemblies of Shiga Toxin-Producing <i>Escherichia coli</i> Isolates from Human, Food, Animal, and Environmental Sources in Canada. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	1
32	Targeting discriminatory SNPs in <i>Salmonella enterica</i> serovar Heidelberg genomes using RNase H2-dependent PCR. <i>Journal of Microbiological Methods</i> , 2019 , 157, 81-87	2.8	3
31	Phylogeographic Analysis Reveals Multiple International transmission Events Have Driven the Global Emergence of <i>Escherichia coli</i> O157:H7. <i>Clinical Infectious Diseases</i> , 2019 , 69, 428-437	11.6	16
30	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	5	3
29	Multi-Year Persistence of Verotoxigenic (VTEC) in a Closed Canadian Beef Herd: A Cohort Study. <i>Frontiers in Microbiology</i> , 2018 , 9, 2040	5.7	7
28	Genomic Analysis of Third Generation Cephalosporin Resistant <i>Escherichia coli</i> from Dairy Cow Manure. <i>Veterinary Sciences</i> , 2017 , 4,	2.4	6
27	Pan-genome Analyses of the Species , and Identification of Genomic Markers Predictive for Species, Subspecies, and Serovar. <i>Frontiers in Microbiology</i> , 2017 , 8, 1345	5.7	38
26	Phylotyper: in silico predictor of gene subtypes. <i>Bioinformatics</i> , 2017 , 33, 3638-3641	7.2	3
25	Genotypes Associated with Isolates Displaying Impaired or Enhanced Tolerances to Cold, Salt, Acid, or Desiccation Stress. <i>Frontiers in Microbiology</i> , 2017 , 8, 369	5.7	73
24	SuperPhy: predictive genomics for the bacterial pathogen <i>Escherichia coli</i> . <i>BMC Microbiology</i> , 2016 , 16, 65	4.5	9
23	The <i>Salmonella</i> In Silico Typing Resource (SISTR): An Open Web-Accessible Tool for Rapidly Typing and Subtyping Draft <i>Salmonella</i> Genome Assemblies. <i>PLoS ONE</i> , 2016 , 11, e0147101	3.7	235
22	Comparative Genomic Analysis of <i>Mannheimia haemolytica</i> from Bovine Sources. <i>PLoS ONE</i> , 2016 , 11, e0149520	3.7	30
21	Phenotypic and Genotypic Characteristics of Shiga Toxin-Producing <i>Escherichia coli</i> Isolated from Surface Waters and Sediments in a Canadian Urban-Agricultural Landscape. <i>Frontiers in Cellular and Infection Microbiology</i> , 2016 , 6, 36	5.9	11
20	Comparative Genomic Analysis of <i>Escherichia coli</i> O157:H7 Isolated from Super-Shedder and Low-Shedder Cattle. <i>PLoS ONE</i> , 2016 , 11, e0151673	3.7	10

19	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, 167-79	2.8	7
18	Whole Genome Sequencing demonstrates that Geographic Variation of Escherichia coli O157 Genotypes Dominates Host Association. <i>Scientific Reports</i> , 2015 , 5, 14145	4.9	32
17	Exploiting the explosion of information associated with whole genome sequencing to tackle Shiga toxin-producing Escherichia coli (STEC) in global food production systems. <i>International Journal of Food Microbiology</i> , 2014 , 187, 57-72	5.8	58
16	Characteristics of clinical Shiga toxin-producing Escherichia coli isolated from British Columbia. <i>BioMed Research International</i> , 2013 , 2013, 878956	3	5
15	A comparison of Shiga-toxin 2 bacteriophage from classical enterohemorrhagic Escherichia coli serotypes and the German E. coli O104:H4 outbreak strain. <i>PLoS ONE</i> , 2012 , 7, e37362	3.7	43
14	Spatial and temporal drivers of zoonotic pathogen contamination of an agricultural watershed. <i>Journal of Environmental Quality</i> , 2012 , 41, 242-52	3.4	42
13	Identification of a novel prophage regulator in Escherichia coli controlling the expression of type III secretion. <i>Molecular Microbiology</i> , 2012 , 83, 208-23	4.1	28
12	Identification of Salmonella enterica species- and subgroup-specific genomic regions using Panseq 2.0. <i>Infection, Genetics and Evolution</i> , 2011 , 11, 2151-61	4.5	9
11	Everything at once: comparative analysis of the genomes of bacterial pathogens. <i>Veterinary Microbiology</i> , 2011 , 153, 13-26	3.3	11
10	Lineage and host source are both correlated with levels of Shiga toxin 2 production by Escherichia coli O157:H7 strains. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 474-82	4.8	48
9	Pan-genome sequence analysis using Panseq: an online tool for the rapid analysis of core and accessory genomic regions. <i>BMC Bioinformatics</i> , 2010 , 11, 461	3.6	200
8	Genomic regions conserved in lineage II Escherichia coli O157:H7 strains. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 3271-80	4.8	12
7	In silico genomic analyses reveal three distinct lineages of Escherichia coli O157:H7, one of which is associated with hyper-virulence. <i>BMC Genomics</i> , 2009 , 10, 287	4.5	59
6	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	4.5	8
5	Genotypic characterization and prevalence of virulence factors among Canadian Escherichia coli O157:H7 strains. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 4314-23	4.8	46
4	Rapid determination of Escherichia coli O157:H7 lineage types and molecular subtypes by using comparative genomic fingerprinting. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 6606-15	4.8	29
3	Genome evolution in major Escherichia coli O157:H7 lineages. <i>BMC Genomics</i> , 2007 , 8, 121	4.5	123
2	Rapid and accurate SNP genotyping of clonal bacterial pathogens with BioHansel		1

1 Insights from Genomic Studies of the Foodborne and Waterborne Pathogen *Escherichia coli* O157:H71-21