

Craig Parker

List of Publications by Citations

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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.

98
papers

3,054
citations

31
h-index

53
g-index

111
ext. papers

3,671
ext. citations

4.5
avg, IF

4.78
L-index

#	Paper	IF	Citations
98	Major structural differences and novel potential virulence mechanisms from the genomes of multiple campylobacter species. <i>PLoS Biology</i> , 2005 , 3, e15	9.7	440
97	Prevalence, distribution, and diversity of Salmonella enterica in a major produce region of California. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 2734-48	4.8	175
96	The complete genome sequence and analysis of the epsilonproteobacterium Arcobacter butzleri. <i>PLoS ONE</i> , 2007 , 2, e1358	3.7	155
95	Differentiation of Campylobacter coli, Campylobacter jejuni, Campylobacter lari, and Campylobacter upsaliensis by a multiplex PCR developed from the nucleotide sequence of the lipid A gene lpxA. <i>Journal of Clinical Microbiology</i> , 2004 , 42, 5549-57	9.7	142
94	Comparison of Campylobacter jejuni lipooligosaccharide biosynthesis loci from a variety of sources. <i>Journal of Clinical Microbiology</i> , 2005 , 43, 2771-81	9.7	111
93	Comparative genomic analysis of Campylobacter jejuni strains reveals diversity due to genomic elements similar to those present in C. jejuni strain RM1221. <i>Journal of Clinical Microbiology</i> , 2006 , 44, 4125-35	9.7	105
92	Transcriptome analysis of Escherichia coli O157:H7 exposed to lysates of lettuce leaves. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 1375-87	4.8	90
91	Culture of Campylobacter jejuni with sodium deoxycholate induces virulence gene expression. <i>Journal of Bacteriology</i> , 2008 , 190, 2286-97	3.5	88
90	The salmonella transcriptome in lettuce and cilantro soft rot reveals a niche overlap with the animal host intestine. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 250-62	4.8	74
89	Characterization of lipooligosaccharide-biosynthetic loci of Campylobacter jejuni reveals new lipooligosaccharide classes: evidence of mosaic organizations. <i>Journal of Bacteriology</i> , 2008 , 190, 5681-93	3.5	73
88	Comparative genomics of enterohemorrhagic Escherichia coli O145:H28 demonstrates a common evolutionary lineage with Escherichia coli O157:H7. <i>BMC Genomics</i> , 2014 , 15, 17	4.5	58
87	Hyperosmotic stress response of Campylobacter jejuni. <i>Journal of Bacteriology</i> , 2012 , 194, 6116-30	3.5	58
86	Distinct acid resistance and survival fitness displayed by Curli variants of enterohemorrhagic Escherichia coli O157:H7. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 3685-95	4.8	49
85	Detection and genotyping of Arcobacter and Campylobacter isolates from retail chicken samples by use of DNA oligonucleotide arrays. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 3645-55	4.8	49
84	Diversity within the Campylobacter jejuni type I restriction-modification loci. <i>Microbiology (United Kingdom)</i> , 2005 , 151, 337-351	2.9	49
83	Salmonella biofilm formation on Aspergillus niger involves cellulose--chitin interactions. <i>PLoS ONE</i> , 2011 , 6, e25553	3.7	47
82	Whole-Genome Sequencing-Based Characterization of 100 Listeria monocytogenes Isolates Collected from Food Processing Environments over a Four-Year Period. <i>MSphere</i> , 2019 , 4,	5	47

81	The <i>Campylobacter jejuni</i> PhosS/PhosR operon represents a non-classical phosphate-sensitive two-component system. <i>Molecular Microbiology</i> , 2006 , 62, 278-91	4.1	46
80	Contribution of flagella and invasion proteins to pathogenesis of <i>Salmonella enterica</i> serovar enteritidis in chicks. <i>FEMS Microbiology Letters</i> , 2001 , 204, 287-91	2.9	46
79	Microbiota-Derived Short-Chain Fatty Acids Modulate Expression of Determinants Required for Commensalism and Virulence. <i>MBio</i> , 2017 , 8,	7.8	45
78	<i>Escherichia coli</i> serotype O55:H7 diversity supports parallel acquisition of bacteriophage at Shiga toxin phage insertion sites during evolution of the O157:H7 lineage. <i>Journal of Bacteriology</i> , 2012 , 194, 1885-96	3.5	45
77	Characterization of genetically matched isolates of <i>Campylobacter jejuni</i> reveals that mutations in genes involved in flagellar biosynthesis alter the organism's virulence potential. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 3123-36	4.8	45
76	Lipopolysaccharide O-chain microheterogeneity of <i>Salmonella</i> serotypes Enteritidis and Typhimurium. <i>Environmental Microbiology</i> , 2001 , 3, 332-42	5.2	45
75	Comparative genomics of the <i>Campylobacter lari</i> group. <i>Genome Biology and Evolution</i> , 2014 , 6, 3252-66	3.9	44
74	Lipooligosaccharide of <i>Campylobacter jejuni</i> : similarity with multiple types of mammalian glycans beyond gangliosides. <i>Journal of Biological Chemistry</i> , 2011 , 286, 12361-70	5.4	41
73	A DNase encoded by integrated element CJIE1 inhibits natural transformation of <i>Campylobacter jejuni</i> . <i>Journal of Bacteriology</i> , 2009 , 191, 2296-306	3.5	40
72	RcsB contributes to the distinct stress fitness among <i>Escherichia coli</i> O157:H7 curli variants of the 1993 hamburger-associated outbreak strains. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 7706-19	4.8	35
71	Distinct transcriptional profiles and phenotypes exhibited by <i>Escherichia coli</i> O157:H7 isolates related to the 2006 spinach-associated outbreak. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 455-63	4.8	35
70	The complete genome sequence and analysis of the human pathogen <i>Campylobacter lari</i> . <i>Foodborne Pathogens and Disease</i> , 2008 , 5, 371-86	3.8	34
69	Updated <i>Campylobacter jejuni</i> Capsule PCR Multiplex Typing System and Its Application to Clinical Isolates from South and Southeast Asia. <i>PLoS ONE</i> , 2015 , 10, e0144349	3.7	34
68	Nucleases encoded by the integrated elements CJIE2 and CJIE4 inhibit natural transformation of <i>Campylobacter jejuni</i> . <i>Journal of Bacteriology</i> , 2010 , 192, 936-41	3.5	32
67	Common genomic features of <i>Campylobacter jejuni</i> subsp. <i>doylei</i> strains distinguish them from <i>C. jejuni</i> subsp. <i>jejuni</i> . <i>BMC Microbiology</i> , 2007 , 7, 50	4.5	31
66	<i>Campylobacter jejuni</i> capsular genotypes are related to Guillain-Barré syndrome. <i>Clinical Microbiology and Infection</i> , 2015 , 21, 852.e1-9	9.5	30
65	Structural analysis of the capsular polysaccharide from <i>Campylobacter jejuni</i> RM1221. <i>ChemBioChem</i> , 2007 , 8, 625-31	3.8	29
64	Comparison of genotypes of <i>Salmonella enterica</i> serovar Enteritidis phage type 30 and 9c strains isolated during three outbreaks associated with raw almonds. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 3723-31	4.8	28

63	Agricultural intensification and the evolution of host specialism in the enteric pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 11018-11028	11.5	27
62	FdhTU-modulated formate dehydrogenase expression and electron donor availability enhance recovery of <i>Campylobacter jejuni</i> following host cell infection. <i>Journal of Bacteriology</i> , 2012 , 194, 3803-1335	3.5	26
61	<i>Salmonella</i> transcriptional signature in <i>Tetrahymena</i> phagosomes and role of acid tolerance in passage through the protist. <i>ISME Journal</i> , 2011 , 5, 262-73	11.9	25
60	Identification of genomic differences between <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> and <i>C. jejuni</i> subsp. <i>doylei</i> at the <i>nap</i> locus leads to the development of a <i>C. jejuni</i> subspeciation multiplex PCR method. <i>BMC Microbiology</i> , 2007 , 7, 11	4.5	25
59	Microarray-based comparative genomic indexing of the <i>Cronobacter</i> genus (<i>Enterobacter sakazakii</i>). <i>International Journal of Food Microbiology</i> , 2009 , 136, 159-64	5.8	24
58	Natural <i>rpoS</i> mutations contribute to population heterogeneity in <i>Escherichia coli</i> O157:H7 strains linked to the 2006 US spinach-associated outbreak. <i>Food Microbiology</i> , 2014 , 44, 108-18	6	23
57	Comparative genomic analysis of clinical strains of <i>Campylobacter jejuni</i> from South Africa. <i>PLoS ONE</i> , 2008 , 3, e2015	3.7	21
56	Local genes for local bacteria: Evidence of allopatry in the genomes of transatlantic <i>Campylobacter</i> populations. <i>Molecular Ecology</i> , 2017 , 26, 4497-4508	5.7	20
55	Egg contamination by <i>Salmonella</i> serovar enteritidis following vaccination with Delta-aroA <i>Salmonella</i> serovar typhimurium. <i>FEMS Microbiology Letters</i> , 2001 , 195, 73-8	2.9	20
54	Molecular diversity of the genetic loci responsible for lipopolysaccharide core oligosaccharide assembly within the genus <i>Salmonella</i> . <i>Molecular Microbiology</i> , 2002 , 46, 1305-18	4.1	18
53	The <i>Campylobacter jejuni</i> helical to coccoid transition involves changes to peptidoglycan and the ability to elicit an immune response. <i>Molecular Microbiology</i> , 2019 , 112, 280-301	4.1	17
52	Mitigation of avian reproductive tract function by <i>Salmonella enteritidis</i> producing high-molecular-mass lipopolysaccharide. <i>Environmental Microbiology</i> , 2002 , 4, 538-45	5.2	17
51	The <i>Campylobacter jejuni</i> RacRS system regulates fumarate utilization in a low oxygen environment. <i>Environmental Microbiology</i> , 2015 , 17, 1049-64	5.2	16
50	Complete Genome Sequences of Two <i>Escherichia coli</i> O145:H28 Outbreak Strains of Food Origin. <i>Genome Announcements</i> , 2014 , 2,		15
49	Comparative Genomic Analysis Identifies a <i>Campylobacter</i> Clade Deficient in Selenium Metabolism. <i>Genome Biology and Evolution</i> , 2017 , 9, 1843-1858	3.9	14
48	The Majority of Genotypes of the Virulence Gene <i>inlA</i> Are Intact among Natural Watershed Isolates of <i>Listeria monocytogenes</i> from the Central California Coast. <i>PLoS ONE</i> , 2016 , 11, e0167566	3.7	14
47	Generation of the membrane potential and its impact on the motility, ATP production and growth in <i>Campylobacter jejuni</i> . <i>Molecular Microbiology</i> , 2017 , 105, 637-651	4.1	13
46	Demonstrates Conserved Proteomic and Transcriptomic Responses When Co-cultured With Human INT 407 and Caco-2 Epithelial Cells. <i>Frontiers in Microbiology</i> , 2019 , 10, 755	5.7	13

45	Campylobacter jejuni Lipooligosaccharides: Structures and Biosynthesis 2014 , 483-504		13
44	Growth phase-dependent activation of the DccRS regulon of Campylobacter jejuni. <i>Journal of Bacteriology</i> , 2010 , 192, 2729-36	3.5	13
43	The Campylobacter jejuni CprRS two-component regulatory system regulates aspects of the cell envelope. <i>Molecular Microbiology</i> , 2015 , 96, 189-209	4.1	12
42	Multi-drug resistant Escherichia coli in diarrhoeagenic foals: Pulsotyping, phylotyping, serotyping, antibiotic resistance and virulence profiling. <i>Veterinary Microbiology</i> , 2018 , 223, 144-152	3.3	11
41	Analysis of the activity and regulon of the two-component regulatory system composed by Cjj81176_1484 and Cjj81176_1483 of Campylobacter jejuni. <i>Journal of Bacteriology</i> , 2015 , 197, 1592-605	3.5	10
40	Complete Genome Sequences of Multidrug-Resistant Campylobacter jejuni Strain 14980A (Turkey Feces) and Campylobacter coli Strain 14983A (Housefly from a Turkey Farm), Harboring a Novel Gentamicin Resistance Mobile Element. <i>Genome Announcements</i> , 2016 , 4,		10
39	Abundance in Breastfed Infants and Identification of a New Species in the Global Enterics Multicenter Study. <i>MSphere</i> , 2020 , 5,	5	9
38	Catabolite repression in Campylobacter jejuni correlates with intracellular succinate levels. <i>Environmental Microbiology</i> , 2018 , 20, 1374-1388	5.2	9
37	Genomic epidemiology of Campylobacter jejuni associated with asymptomatic pediatric infection in the Peruvian Amazon. <i>PLoS Neglected Tropical Diseases</i> , 2020 , 14, e0008533	4.8	9
36	Morphology heterogeneity within a Campylobacter jejuni helical population: the use of calcofluor white to generate rod-shaped C. jejuni 81-176 clones and the genetic determinants responsible for differences in morphology within 11168 strains. <i>Molecular Microbiology</i> , 2017 , 104, 948-971	4.1	8
35	The Unique Phospholipidome of the Enteric Pathogen Campylobacter jejuni: Lysophospholipids Are Required for Motility at Low Oxygen Availability. <i>Journal of Molecular Biology</i> , 2020 , 432, 5244-5258	6.5	8
34	High-Frequency Variation of Purine Biosynthesis Genes Is a Mechanism of Success in Campylobacter jejuni. <i>MBio</i> , 2015 , 6, e00612-15	7.8	7
33	Utilization efficiency of human milk oligosaccharides by human-associated is strain-dependent. <i>Applied and Environmental Microbiology</i> , 2021 , AEM0148721	4.8	6
32	Campylobacter jejuni genotypes are associated with post-infection irritable bowel syndrome in humans. <i>Communications Biology</i> , 2021 , 4, 1015	6.7	6
31	Genotyping Campylobacter jejuni by comparative genome indexing: an evaluation with pulsed-field gel electrophoresis and flaA SVR sequencing. <i>Foodborne Pathogens and Disease</i> , 2009 , 6, 337-49	3.8	5
30	A porcine ligated loop model reveals new insight into the host immune response against. <i>Gut Microbes</i> , 2020 , 12, 1-25	8.8	5
29	Complete Genome Sequence of Campylobacter iguaniorum Strain RM11343, Isolated from an Alpaca. <i>Genome Announcements</i> , 2016 , 4,		5
28	Genome Sequences of Eight Shiga Toxin-Producing Escherichia coli Strains Isolated from a Produce-Growing Region in California. <i>Microbiology Resource Announcements</i> , 2018 , 7,	1.3	5

27	Complete Annotated Genome Sequences of Three <i>Campylobacter jejuni</i> Strains Isolated from Naturally Colonized Farm-Raised Chickens. <i>Genome Announcements</i> , 2017 , 5,		4
26	Regulation of energy metabolism by the extracytoplasmic function (ECF) [Factors of <i>Arcobacter butzleri</i> . <i>PLoS ONE</i> , 2012 , 7, e44796	3-7	4
25	The transcriptome of <i>Escherichia coli</i> O157: H7 reveals a role for oxidative stress resistance in its survival from predation by <i>Tetrahymena</i> . <i>FEMS Microbiology Ecology</i> , 2020 , 96,	4-3	3
24	Complete Genome Sequences of <i>Campylobacter jejuni</i> Strains RM3196 (233.94) and RM3197 (308.95) Isolated from Patients with Guillain-Barré Syndrome. <i>Genome Announcements</i> , 2015 , 3,		3
23	<i>Campylobacter</i> and <i>Arcobacter</i> 49-65		3
22	Unique inducible filamentous motility identified in pathogenic <i>Bacillus cereus</i> group species. <i>ISME Journal</i> , 2020 , 14, 2997-3010	11-9	3
21	Genomic Characterization of DT104 Strains Associated with Cattle and Beef Products. <i>Pathogens</i> , 2021 , 10,	4-5	3
20	Draft Genome Sequences of Nine <i>Campylobacter hyointestinalis</i> subsp. <i>lawsonii</i> Strains. <i>Microbiology Resource Announcements</i> , 2018 , 7,	1-3	3
19	Complete Genome Sequence of <i>Acinetobacter radioresistens</i> Strain LH6, a Multidrug-Resistant Bacteriophage-Propagating Strain. <i>Microbiology Resource Announcements</i> , 2018 , 7,	1-3	3
18	Genomic population structure associated with repeated escape of <i>Salmonella enterica</i> ATCC14028s from the laboratory into nature. <i>PLoS Genetics</i> , 2021 , 17, e1009820	6	3
17	Genomic Sequence of subsp. HS:19 Penner Serotype Reference Strain RM3420. <i>Genome Announcements</i> , 2017 , 5,		2
16	Complete Genomic Sequence of <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> HS:19 Strain RM1285 Isolated from Packaged Chicken. <i>Genome Announcements</i> , 2016 , 4,		2
15	Complete Genome Sequence and Annotation of a <i>Campylobacter jejuni</i> Strain, MTVDSJ20, Isolated from a Naturally Colonized Farm-Raised Chicken. <i>Genome Announcements</i> , 2014 , 2,		2
14	Complete Genome Sequence of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Thompson Strain RM6836. <i>Genome Announcements</i> , 2013 , 1,		2
13	HIV retesting in pregnant women in South Africa: Outcomes of a quality improvement project targeting health systems Weaknesses. <i>Southern African Journal of HIV Medicine</i> , 2018 , 19, 784	1-4	2
12	DNA adenine methylase, not the PstI restriction-modification system, regulates virulence gene expression in Shiga toxin-producing <i>Escherichia coli</i> . <i>Food Microbiology</i> , 2021 , 96, 103722	6	2
11	Design and Operation of a Scaled-up Pilot Plant for the Removal of Sugar Beet Extract Colorants using Powdered Activated Carbon. <i>Sugar Tech</i> , 2021 , 23, 167-177	1-9	2
10	Complete Genome Sequences of Three <i>Bacillus amyloliquefaciens</i> Strains That Inhibit the Growth of <i>Listeria monocytogenes</i> . <i>Genome Announcements</i> , 2018 , 6,		2

9	Complete Genome Sequences of Two Outbreak Strains of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Thompson Associated with Cilantro. <i>Genome Announcements</i> , 2015 , 3,		1
8	Contribution of flagella and invasion proteins to pathogenesis of <i>Salmonella enterica</i> serovar enteritidis in chicks		1
7	Dataset of the phospholipidome and transcriptome of under different growth conditions. <i>Data in Brief</i> , 2020 , 33, 106349	1.2	1
6	Genomic Characterization of Adapted to the Guinea Pig () Host. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021 , 11, 607747	5.9	1
5	Complete Genome Sequence of <i>Pantoea agglomerans</i> ASB05 Using Illumina and PacBio Sequencing. <i>Microbiology Resource Announcements</i> , 2021 , 10, e0050121	1.3	1
4	Complete Genome Sequence of the <i>Arcobacter marinus</i> Type Strain JCM 15502. <i>Microbiology Resource Announcements</i> , 2018 , 7,	1.3	1
3	Complete Genome Sequence of <i>Lactococcus lactis</i> subsp Strain 14B4, Which Inhibits the Growth of <i>Salmonella enterica</i> Serotype Poona. <i>Microbiology Resource Announcements</i> , 2018 , 7,	1.3	1
2	Complete Genome Sequence of <i>Enterobacter asburiae</i> Strain AEB30, Determined Using Illumina and PacBio Sequencing. <i>Microbiology Resource Announcements</i> , 2021 , 10, e0056221	1.3	1
1	Regulation of Energy Metabolism by the Extracytoplasmic function (ECF) Factors of <i>Arcobacter butzleri</i> 2016 , 311-320		