

Craig Parker

List of Publications by Year in descending order

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104
papers

3,968
citations

117453

34
h-index

133063

59
g-index

111
all docs

111
docs citations

111
times ranked

3748
citing authors

#	ARTICLE	IF	CITATIONS
1	Major Structural Differences and Novel Potential Virulence Mechanisms from the Genomes of Multiple <i>Campylobacter</i> Species. <i>PLoS Biology</i> , 2005, 3, e15.	2.6	483
2	Prevalence, Distribution, and Diversity of <i>Salmonella enterica</i> in a Major Produce Region of California. <i>Applied and Environmental Microbiology</i> , 2011, 77, 2734-2748.	1.4	216
3	The Complete Genome Sequence and Analysis of the Epsilonproteobacterium <i>Arcobacter butzleri</i> . <i>PLoS ONE</i> , 2007, 2, e1358.	1.1	203
4	Differentiation of <i>Campylobacter coli</i> , <i>Campylobacter jejuni</i> , <i>Campylobacter lari</i> , and <i>Campylobacter upsaliensis</i> by a Multiplex PCR Developed from the Nucleotide Sequence of the Lipid A Gene <i>lpxA</i> . <i>Journal of Clinical Microbiology</i> , 2004, 42, 5549-5557.	1.8	170
5	Comparison of <i>Campylobacter jejuni</i> Lipooligosaccharide Biosynthesis Loci from a Variety of Sources. <i>Journal of Clinical Microbiology</i> , 2005, 43, 2771-2781.	1.8	119
6	Transcriptome Analysis of <i>Escherichia coli</i> O157:H7 Exposed to Lysates of Lettuce Leaves. <i>Applied and Environmental Microbiology</i> , 2010, 76, 1375-1387.	1.4	116
7	Comparative Genomic Analysis of <i>Campylobacter jejuni</i> Strains Reveals Diversity Due to Genomic Elements Similar to Those Present in <i>C. jejuni</i> Strain RM1221. <i>Journal of Clinical Microbiology</i> , 2006, 44, 4125-4135.	1.8	115
8	Culture of <i>Campylobacter jejuni</i> with Sodium Deoxycholate Induces Virulence Gene Expression. <i>Journal of Bacteriology</i> , 2008, 190, 2286-2297.	1.0	110
9	The <i>Salmonella</i> Transcriptome in Lettuce and Cilantro Soft Rot Reveals a Niche Overlap with the Animal Host Intestine. <i>Applied and Environmental Microbiology</i> , 2013, 79, 250-262.	1.4	95
10	Comparative genomics of enterohemorrhagic <i>Escherichia coli</i> O145:H28 demonstrates a common evolutionary lineage with <i>Escherichia coli</i> O157:H7. <i>BMC Genomics</i> , 2014, 15, 17.	1.2	84
11	Characterization of Lipooligosaccharide-Biosynthetic Loci of <i>Campylobacter jejuni</i> Reveals New Lipooligosaccharide Classes: Evidence of Mosaic Organizations. <i>Journal of Bacteriology</i> , 2008, 190, 5681-5689.	1.0	82
12	Whole-Genome Sequencing-Based Characterization of 100 <i>Listeria monocytogenes</i> Isolates Collected from Food Processing Environments over a Four-Year Period. <i>MSphere</i> , 2019, 4, .	1.3	82
13	<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, 1885-1896.	1.0	76
14	Hyperosmotic Stress Response of <i>Campylobacter jejuni</i> . <i>Journal of Bacteriology</i> , 2012, 194, 6116-6130.	1.0	69
15	Comparative Genomics of the <i>Campylobacter lari</i> Group. <i>Genome Biology and Evolution</i> , 2014, 6, 3252-3266.	1.1	69
16	Microbiota-Derived Short-Chain Fatty Acids Modulate Expression of <i>Campylobacter jejuni</i> Determinants Required for Commensalism and Virulence. <i>MBio</i> , 2017, 8, .	1.8	68
17	The <i>Campylobacter jejuni</i> <i>PhoS</i> S/ <i>PhoS</i> R operon represents a non-classical phosphate-sensitive two-component system. <i>Molecular Microbiology</i> , 2006, 62, 278-291.	1.2	59
18	Diversity within the <i>Campylobacter jejuni</i> type I restriction modification loci. <i>Microbiology (United Kingdom)</i> , 2007, 157, 107-115.	0.7	55

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19	Salmonella Biofilm Formation on <i>Aspergillus niger</i> Involves Cellulose-Cellulose Chitin Interactions. <i>PLoS ONE</i> , 2011, 6, e25553.	1.1	55
20	Detection and Genotyping of <i>Arcobacter</i> and <i>Campylobacter</i> Isolates from Retail Chicken Samples by Use of DNA Oligonucleotide Arrays. <i>Applied and Environmental Microbiology</i> , 2007, 73, 3645-3655.	1.4	54
21	Distinct Acid Resistance and Survival Fitness Displayed by Curli Variants of Enterohemorrhagic <i>Escherichia coli</i> O157:H7. <i>Applied and Environmental Microbiology</i> , 2011, 77, 3685-3695.	1.4	52
22	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, 7706-7719.	1.4	52
23	Contribution of flagella and invasion proteins to pathogenesis of <i>Salmonella enterica</i> serovar enteritidis in chicks. <i>FEMS Microbiology Letters</i> , 2001, 204, 287-291.	0.7	51
24	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, 3123-3136.	1.4	51
25	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, 455-463.	1.4	50
26	Agricultural intensification and the evolution of host specialism in the enteric pathogen <i>Campylobacter jejuni</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 11018-11028.	3.3	50
27	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.	1.1	50
28	A DNase Encoded by Integrated Element CJIE1 Inhibits Natural Transformation of <i>Campylobacter jejuni</i> . <i>Journal of Bacteriology</i> , 2009, 191, 2296-2306.	1.0	49
29	Lipooligosaccharide of <i>Campylobacter jejuni</i> . <i>Journal of Biological Chemistry</i> , 2011, 286, 12361-12370.	1.6	49
30	Lipopolysaccharide O-chain microheterogeneity of <i>Salmonella</i> serotypes Enteritidis and Typhimurium. <i>Environmental Microbiology</i> , 2001, 3, 332-342.	1.8	46
31	The Complete Genome Sequence and Analysis of the Human Pathogen <i>Campylobacter lari</i> . <i>Foodborne Pathogens and Disease</i> , 2008, 5, 371-386.	0.8	44
32	Nucleases Encoded by the Integrated Elements CJIE2 and CJIE4 Inhibit Natural Transformation of <i>Campylobacter jejuni</i> . <i>Journal of Bacteriology</i> , 2010, 192, 936-941.	1.0	40
33	<i>Campylobacter jejuni</i> capsular genotypes are related to Guillain-Barré syndrome. <i>Clinical Microbiology and Infection</i> , 2015, 21, 852.e1-852.e9.	2.8	40
34	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, 3723-3731.	1.4	37
35	<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, 262-273.	4.4	37
36	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.	2.0	36

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37	Structural Analysis of the Capsular Polysaccharide from <i>Campylobacter jejuni</i> RM1221. <i>ChemBioChem</i> , 2007, 8, 625-631.	1.3	34
38	<i>Campylobacter</i> Abundance in Breastfed Infants and Identification of a New Species in the Global Enterics Multicenter Study. <i>MSphere</i> , 2020, 5, .	1.3	34
39	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.	1.3	33
40	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, 3803-3813.	1.0	32
41	Microarray-based comparative genomic indexing of the <i>Cronobacter</i> genus (<i>Enterobacter sakazakii</i>). <i>International Journal of Food Microbiology</i> , 2009, 136, 159-164.	2.1	29
42	Utilization Efficiency of Human Milk Oligosaccharides by Human-Associated <i>Akkermansia</i> Is Strain Dependent. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0148721.	1.4	29
43	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, 108-118.	2.1	27
44	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.	1.2	27
45	Egg contamination by <i>Salmonella</i> serovar enteritidis following vaccination with "aroA" <i>Salmonella</i> serovar typhimurium. <i>FEMS Microbiology Letters</i> , 2001, 195, 73-78.	0.7	26
46	The <i>Campylobacter jejuni</i> <i>RacRS</i> system regulates fumarate utilization in a low oxygen environment. <i>Environmental Microbiology</i> , 2015, 17, 1049-1064.	1.8	26
47	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.	1.3	25
48	Complete Genome Sequences of Two <i>Escherichia coli</i> O145:H28 Outbreak Strains of Food Origin. <i>Genome Announcements</i> , 2014, 2, .	0.8	25
49	Comparative Genomic Analysis of Clinical Strains of <i>Campylobacter jejuni</i> from South Africa. <i>PLoS ONE</i> , 2008, 3, e2015.	1.1	24
50	<i>Campylobacter jejuni</i> genotypes are associated with post-infection irritable bowel syndrome in humans. <i>Communications Biology</i> , 2021, 4, 1015.	2.0	24
51	Growth Phase-Dependent Activation of the <i>DccRS</i> Regulon of <i>Campylobacter jejuni</i> . <i>Journal of Bacteriology</i> , 2010, 192, 2729-2736.	1.0	23
52	Mitigation of avian reproductive tract function by <i>Salmonella enteritidis</i> producing high-molecular-mass lipopolysaccharide. <i>Environmental Microbiology</i> , 2002, 4, 538-545.	1.8	22
53	Complete Genome Sequences of Multidrug-Resistant <i>Campylobacter jejuni</i> Strain 14980A (Turkey Feces) and <i>Campylobacter coli</i> Strain 14983A (Housefly from a Turkey Farm), Harboring a Novel Gentamicin Resistance Mobile Element. <i>Genome Announcements</i> , 2016, 4, .	0.8	22
54	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.	1.2	22

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55	Multi-drug resistant <i>Escherichia coli</i> in diarrhoeagenic foals: Pulsotyping, phylotyping, serotyping, antibiotic resistance and virulence profiling. <i>Veterinary Microbiology</i> , 2018, 223, 144-152.	0.8	22
56	Molecular diversity of the genetic loci responsible for lipopolysaccharide core oligosaccharide assembly within the genus <i>Salmonella</i> . <i>Molecular Microbiology</i> , 2002, 46, 1305-1318.	1.2	20
57	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.	1.1	20
58	Comparative Genomic Analysis Identifies a <i>Campylobacter</i> Clade Deficient in Selenium Metabolism. <i>Genome Biology and Evolution</i> , 2017, 9, 1843-1858.	1.1	20
59	Genomic epidemiology of <i>Campylobacter jejuni</i> associated with asymptomatic pediatric infection in the Peruvian Amazon. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008533.	1.3	20
60	<i>Campylobacter jejuni</i> Lipooligosaccharides: Structures and Biosynthesis. , 2014, , 483-504.		19
61	<i>Campylobacter jejuni</i> 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.	1.5	19
62	The <i>Campylobacter jejuni</i> CprRS two-component regulatory system regulates aspects of the cell envelope. <i>Molecular Microbiology</i> , 2015, 96, 189-209.	1.2	16
63	Analysis of the Activity and Regulon of the Two-Component Regulatory System Composed by Cjj81176_1484 and Cjj81176_1483 of <i>Campylobacter jejuni</i> . <i>Journal of Bacteriology</i> , 2015, 197, 1592-1605.	1.0	15
64	The Unique Phospholipidome of the Enteric Pathogen <i>Campylobacter jejuni</i> : Lysophospholipids Are Required for Motility at Low Oxygen Availability. <i>Journal of Molecular Biology</i> , 2020, 432, 5244-5258.	2.0	15
65	Morphology heterogeneity within a <i>Campylobacter jejuni</i> helical population: the use of calcofluor white to generate rod-shaped <i>C. jejuni</i> clones and the genetic determinants responsible for differences in morphology within 11168 strains. <i>Molecular Microbiology</i> , 2017, 104, 948-971.	1.2	14
66	High-Frequency Variation of Purine Biosynthesis Genes Is a Mechanism of Success in <i>Campylobacter jejuni</i> . <i>MBio</i> , 2015, 6, e00612-15.	1.8	13
67	Catabolite repression in <i>Campylobacter jejuni</i> correlates with intracellular succinate levels. <i>Environmental Microbiology</i> , 2018, 20, 1374-1388.	1.8	13
68	Genome Sequences of Eight Shiga Toxin-Producing <i>Escherichia coli</i> Strains Isolated from a Produce-Growing Region in California. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	11
69	Unique inducible filamentous motility identified in pathogenic <i>Bacillus cereus</i> group species. <i>ISME Journal</i> , 2020, 14, 2997-3010.	4.4	8
70	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.	1.5	8
71	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, .	0.8	7
72	Complete Genome Sequence of <i>Acinetobacter radioresistens</i> Strain LH6, a Multidrug-Resistant Bacteriophage-Propagating Strain. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	7

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73	A porcine ligated loop model reveals new insight into the host immune response against <i>Campylobacter jejuni</i> . <i>Gut Microbes</i> , 2020, 12, 1814121.	4.3	7
74	Genomic Characterization of <i>Salmonella typhimurium</i> DT104 Strains Associated with Cattle and Beef Products. <i>Pathogens</i> , 2021, 10, 529.	1.2	7
75	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.	2.1	7
76	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, .	1.3	6
77	Genotyping <i>Campylobacter jejuni</i> by Comparative Genome Indexing: An Evaluation with Pulsed-Field Gel Electrophoresis and <i>flaASVR</i> Sequencing. <i>Foodborne Pathogens and Disease</i> , 2009, 6, 337-349.	0.8	5
78	Regulation of Energy Metabolism by the Extracytoplasmic Function (ECF) ĩf Factors of <i>Arcobacter butzleri</i> . <i>PLoS ONE</i> , 2012, 7, e44796.	1.1	5
79	Complete Genome Sequence of <i>Campylobacter iguaniorum</i> Strain RM11343, Isolated from an Alpaca. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
80	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.	0.9	5
81	Genomic Characterization of <i>Campylobacter jejuni</i> Adapted to the Guinea Pig (<i>Cavia porcellus</i>) Host. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 607747.	1.8	5
82	Complete Annotated Genome Sequences of Three <i>Campylobacter jejuni</i> Strains Isolated from Naturally Colonized Farm-Raised Chickens. <i>Genome Announcements</i> , 2017, 5, .	0.8	4
83	Biomolecule sulphation and novel methylations related to Guillain-Barré syndrome-associated <i>Campylobacter jejuni</i> serotype HS:19. <i>Microbial Genomics</i> , 2021, 7, .	1.0	4
84	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, .	0.8	3
85	Genomic Sequence of <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> HS:19 Penner Serotype Reference Strain RM3420. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
86	Draft Genome Sequences of Nine <i>Campylobacter hyointestinalis</i> subsp. <i>lawsonii</i> Strains. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	3
87	Complete Genome Sequences of Three <i>Bacillus amyloliquefaciens</i> Strains That Inhibit the Growth of <i>Listeria monocytogenes</i> ĩn Vitro. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
88	Complete Genome Sequence of <i>Pantoea agglomerans</i> ASB05 Using Illumina and PacBio Sequencing. <i>Microbiology Resource Announcements</i> , 2021, 10, e0050121.	0.3	3
89	<i>Campylobacter</i> and <i>Arcobacter</i> . , 0, , 49-65.		3
90	HIV retesting in pregnant women in South Africa: Outcomes of a quality improvement project targeting health systemsâ€™ weaknesses. <i>Southern African Journal of HIV Medicine</i> , 2018, 19, 784.	0.3	3

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91	Complete Genome Sequence of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Thompson Strain RM6836. <i>Genome Announcements</i> , 2013, 1, .	0.8	2
92	Complete Genome Sequence and Annotation of a <i>Campylobacter jejuni</i> Strain, MTVDSCj20, Isolated from a Naturally Colonized Farm-Raised Chicken. <i>Genome Announcements</i> , 2014, 2, .	0.8	2
93	Complete Genome Sequence of <i>Lactococcus lactis</i> subsp. <i>lactis</i> Strain 14B4, Which Inhibits the Growth of <i>Salmonella enterica</i> Serotype Poona In Vitro. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	2
94	Complete Genome Sequence of <i>Enterobacter asburiae</i> Strain AEB30, Determined Using Illumina and PacBio Sequencing. <i>Microbiology Resource Announcements</i> , 2021, 10, e0056221.	0.3	2
95	RNA and Sugars, Unique Properties of Bacteriophages Infecting Multidrug Resistant <i>Acinetobacter radioresistens</i> Strain LH6. <i>Viruses</i> , 2021, 13, 1652.	1.5	2
96	Differences in the Propensity of Different Antimicrobial Resistance Determinants to Be Disseminated via Transformation in <i>Campylobacter jejuni</i> and <i>Campylobacter coli</i> . <i>Microorganisms</i> , 2022, 10, 1194.	1.6	2
97	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, .	0.8	1
98	Complete Genomic Sequences of Two <i>Salmonella enterica</i> subsp. <i>enterica</i> Serogroup C2 (O:6,8) Strains from Central California. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
99	Complete Genome Sequence of the <i>Arcobacter marinus</i> Type Strain JCM 15502. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	1
100	Dataset of the phospholipidome and transcriptome of <i>Campylobacter jejuni</i> under different growth conditions. <i>Data in Brief</i> , 2020, 33, 106349.	0.5	1
101	Contribution of flagella and invasion proteins to pathogenesis of <i>Salmonella enterica</i> serovar enteritidis in chicks. , 0, .		1
102	Complete Genome Sequences of Three Shiga Toxin-Producing <i>Escherichia coli</i> O111:H8 Strains Exhibiting an Aggregation Phenotype. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
103	Complete Genomic Sequences of Three <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Muenchen Strains from an Orchard in San Joaquin County, California. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
104	Complete Genome Sequences of Two <i>Bacillus velezensis</i> Strains Isolated from California Raisin Vineyard Soils. <i>Microbiology Resource Announcements</i> , 0, , .	0.3	0