

Craig Parker

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/6089923/craig-parker-publications-by-year.pdf>

Version: 2024-04-26

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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 | Utilization efficiency of human milk oligosaccharides by human-associated is strain-dependent. <i>Applied and Environmental Microbiology</i> , 2021 , AEM0148721 | 4.8 | 6 |
| 97 | Genomic Characterization of Adapted to the Guinea Pig () Host. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021 , 11, 607747 | 5.9 | 1 |
| 96 | Genomic Characterization of DT104 Strains Associated with Cattle and Beef Products. <i>Pathogens</i> , 2021 , 10, | 4.5 | 3 |
| 95 | DNA adenine methylase, not the PstI restriction-modification system, regulates virulence gene expression in Shiga toxin-producing Escherichia coli. <i>Food Microbiology</i> , 2021 , 96, 103722 | 6 | 2 |
| 94 | Complete Genome Sequence of Pantoea agglomerans ASB05 Using Illumina and PacBio Sequencing. <i>Microbiology Resource Announcements</i> , 2021 , 10, e0050121 | 1.3 | 1 |
| 93 | 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 |
| 92 | Complete Genome Sequence of Enterobacter asburiae Strain AEB30, Determined Using Illumina and PacBio Sequencing. <i>Microbiology Resource Announcements</i> , 2021 , 10, e0056221 | 1.3 | 1 |
| 91 | Campylobacter jejuni genotypes are associated with post-infection irritable bowel syndrome in humans. <i>Communications Biology</i> , 2021 , 4, 1015 | 6.7 | 6 |
| 90 | Genomic population structure associated with repeated escape of Salmonella enterica ATCC14028s from the laboratory into nature. <i>PLoS Genetics</i> , 2021 , 17, e1009820 | 6 | 3 |
| 89 | 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 |
| 88 | The transcriptome of Escherichia coli O157: H7 reveals a role for oxidative stress resistance in its survival from predation by Tetrahymena. <i>FEMS Microbiology Ecology</i> , 2020 , 96, | 4.3 | 3 |
| 87 | Abundance in Breastfed Infants and Identification of a New Species in the Global Enterics Multicenter Study. <i>MSphere</i> , 2020 , 5, | 5 | 9 |
| 86 | Dataset of the phospholipidome and transcriptome of under different growth conditions. <i>Data in Brief</i> , 2020 , 33, 106349 | 1.2 | 1 |
| 85 | Unique inducible filamentous motility identified in pathogenic Bacillus cereus group species. <i>ISME Journal</i> , 2020 , 14, 2997-3010 | 11.9 | 3 |
| 84 | 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 |
| 83 | 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 |
| 82 | 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 |

| | | | |
|----|---|-----|----|
| 81 | 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 |
| 80 | 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 |
| 79 | 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, | 5 | 47 |
| 78 | Catabolite repression in <i>Campylobacter jejuni</i> correlates with intracellular succinate levels. <i>Environmental Microbiology</i> , 2018 , 20, 1374-1388 | 5-2 | 9 |
| 77 | 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 | 3-3 | 11 |
| 76 | 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 |
| 75 | Draft Genome Sequences of Nine <i>Campylobacter hyointestinalis</i> subsp. <i>lawsonii</i> Strains. <i>Microbiology Resource Announcements</i> , 2018 , 7, | 1-3 | 3 |
| 74 | 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, | 1-3 | 5 |
| 73 | 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 |
| 72 | Complete Genome Sequence of the <i>Arcobacter marinus</i> Type Strain JCM 15502. <i>Microbiology Resource Announcements</i> , 2018 , 7, | 1-3 | 1 |
| 71 | 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 |
| 70 | 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 |
| 69 | Genomic Sequence of subsp. HS:19 Penner Serotype Reference Strain RM3420. <i>Genome Announcements</i> , 2017 , 5, | | 2 |
| 68 | 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 |
| 67 | 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 |
| 66 | Microbiota-Derived Short-Chain Fatty Acids Modulate Expression of Determinants Required for Commensalism and Virulence. <i>MBio</i> , 2017 , 8, | 7-8 | 45 |
| 65 | 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 |
| 64 | Morphology heterogeneity within a <i>Campylobacter jejuni</i> helical population: the use of calcofluor white to generate rod-shaped <i>C. jejuni</i> 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 |

| | | | |
|----|---|-----|----|
| 63 | Comparative Genomic Analysis Identifies a Campylobacter Clade Deficient in Selenium Metabolism. <i>Genome Biology and Evolution</i> , 2017 , 9, 1843-1858 | 3.9 | 14 |
| 62 | Regulation of Energy Metabolism by the Extracytoplasmic function (ECF) [Factors of Arcobacter butzleri 2016 , 311-320 | | |
| 61 | Complete Genomic Sequence of Campylobacter jejuni subsp. jejuni HS:19 Strain RM1285 Isolated from Packaged Chicken. <i>Genome Announcements</i> , 2016 , 4, | | 2 |
| 60 | The Majority of Genotypes of the Virulence Gene inlA Are Intact among Natural Watershed Isolates of Listeria monocytogenes from the Central California Coast. <i>PLoS ONE</i> , 2016 , 11, e0167566 | 3.7 | 14 |
| 59 | Complete Genome Sequence of Campylobacter iguaniorum Strain RM11343, Isolated from an Alpaca. <i>Genome Announcements</i> , 2016 , 4, | | 5 |
| 58 | 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 |
| 57 | Campylobacter jejuni capsular genotypes are related to Guillain-Barré Syndrome. <i>Clinical Microbiology and Infection</i> , 2015 , 21, 852.e1-9 | 9.5 | 30 |
| 56 | 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 |
| 55 | 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 |
| 54 | Complete Genome Sequences of Two Outbreak Strains of Salmonella enterica subsp. enterica Serovar Thompson Associated with Cilantro. <i>Genome Announcements</i> , 2015 , 3, | | 1 |
| 53 | Complete Genome Sequences of Campylobacter jejuni Strains RM3196 (233.94) and RM3197 (308.95) Isolated from Patients with Guillain-Barré Syndrome. <i>Genome Announcements</i> , 2015 , 3, | | 3 |
| 52 | 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 |
| 51 | The Campylobacter jejuni RacRS system regulates fumarate utilization in a low oxygen environment. <i>Environmental Microbiology</i> , 2015 , 17, 1049-64 | 5.2 | 16 |
| 50 | Updated Campylobacter jejuni 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 |
| 49 | Natural rpoS mutations contribute to population heterogeneity in Escherichia coli O157:H7 strains linked to the 2006 US spinach-associated outbreak. <i>Food Microbiology</i> , 2014 , 44, 108-18 | 6 | 23 |
| 48 | Campylobacter jejuni Lipooligosaccharides: Structures and Biosynthesis 2014 , 483-504 | | 13 |
| 47 | Complete Genome Sequences of Two Escherichia coli O145:H28 Outbreak Strains of Food Origin. <i>Genome Announcements</i> , 2014 , 2, | | 15 |
| 46 | Complete Genome Sequence and Annotation of a Campylobacter jejuni Strain, MTVDSJCj20, Isolated from a Naturally Colonized Farm-Raised Chicken. <i>Genome Announcements</i> , 2014 , 2, | | 2 |

| | | |
|----|---|---------|
| 45 | Comparative genomics of the <i>Campylobacter lari</i> group. <i>Genome Biology and Evolution</i> , 2014 , 6, 3252-663.9 | 44 |
| 44 | 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 | 4.5 58 |
| 43 | Complete Genome Sequence of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Thompson Strain RM6836. <i>Genome Announcements</i> , 2013 , 1, | 2 |
| 42 | 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 |
| 41 | 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, 7706-194.8 | 35 |
| 40 | 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 |
| 39 | <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 |
| 38 | Hyperosmotic stress response of <i>Campylobacter jejuni</i> . <i>Journal of Bacteriology</i> , 2012 , 194, 6116-30 | 3.5 58 |
| 37 | 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, 455-48 | 35 |
| 36 | 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, 3803-135 | 26 |
| 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, 262-73 | 11.9 25 |
| 34 | Prevalence, distribution, and diversity of <i>Salmonella enterica</i> in a major produce region of California. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 2734-48 | 4.8 175 |
| 33 | 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 |
| 32 | 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, 3685-95 | 4.8 49 |
| 31 | <i>Salmonella</i> biofilm formation on <i>Aspergillus niger</i> involves cellulose--chitin interactions. <i>PLoS ONE</i> , 2011 , 6, e25553 | 3.7 47 |
| 30 | 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 |
| 29 | 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 |
| 28 | Growth phase-dependent activation of the DccRS regulon of <i>Campylobacter jejuni</i> . <i>Journal of Bacteriology</i> , 2010 , 192, 2729-36 | 3.5 13 |

| | | | |
|----|---|-----|-----|
| 27 | 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 |
| 26 | 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 |
| 25 | A DNase encoded by integrated element CJIE1 inhibits natural transformation of Campylobacter jejuni. <i>Journal of Bacteriology</i> , 2009 , 191, 2296-306 | 3.5 | 40 |
| 24 | Microarray-based comparative genomic indexing of the Cronobacter genus (Enterobacter sakazakii). <i>International Journal of Food Microbiology</i> , 2009 , 136, 159-64 | 5.8 | 24 |
| 23 | The complete genome sequence and analysis of the human pathogen Campylobacter lari. <i>Foodborne Pathogens and Disease</i> , 2008 , 5, 371-86 | 3.8 | 34 |
| 22 | Culture of Campylobacter jejuni with sodium deoxycholate induces virulence gene expression. <i>Journal of Bacteriology</i> , 2008 , 190, 2286-97 | 3.5 | 88 |
| 21 | 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 |
| 20 | Comparative genomic analysis of clinical strains of Campylobacter jejuni from South Africa. <i>PLoS ONE</i> , 2008 , 3, e2015 | 3.7 | 21 |
| 19 | The complete genome sequence and analysis of the epsilonproteobacterium Arcobacter butzleri. <i>PLoS ONE</i> , 2007 , 2, e1358 | 3.7 | 155 |
| 18 | Structural analysis of the capsular polysaccharide from Campylobacter jejuni RM1221. <i>ChemBioChem</i> , 2007 , 8, 625-31 | 3.8 | 29 |
| 17 | Identification of genomic differences between Campylobacter jejuni subsp. jejuni and C. jejuni subsp. doylei at the nap locus leads to the development of a C. jejuni subspeciation multiplex PCR method. <i>BMC Microbiology</i> , 2007 , 7, 11 | 4.5 | 25 |
| 16 | Common genomic features of Campylobacter jejuni subsp. doylei strains distinguish them from C. jejuni subsp. jejuni. <i>BMC Microbiology</i> , 2007 , 7, 50 | 4.5 | 31 |
| 15 | Characterization of genetically matched isolates of Campylobacter jejuni 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 |
| 14 | 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 |
| 13 | 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 |
| 12 | The Campylobacter jejuni PhosS/PhosR operon represents a non-classical phosphate-sensitive two-component system. <i>Molecular Microbiology</i> , 2006 , 62, 278-91 | 4.1 | 46 |
| 11 | 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 |
| 10 | 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 |

| | | | |
|---|---|-----|-----|
| 9 | Diversity within the <i>Campylobacter jejuni</i> type I restriction-modification loci. <i>Microbiology (United Kingdom)</i> , 2005 , 151, 337-351 | 2.9 | 49 |
| 8 | 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, 5549-57 | 9.7 | 142 |
| 7 | 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 |
| 6 | 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 |
| 5 | Lipopolysaccharide O-chain microheterogeneity of <i>Salmonella</i> serotypes Enteritidis and Typhimurium. <i>Environmental Microbiology</i> , 2001 , 3, 332-42 | 5.2 | 45 |
| 4 | 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 |
| 3 | 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 |
| 2 | <i>Campylobacter</i> and <i>Arcobacter</i> 49-65 | | 3 |
| 1 | Contribution of flagella and invasion proteins to pathogenesis of <i>Salmonella enterica</i> serovar enteritidis in chicks | | 1 |