William G Miller

List of Publications by Year in Descending Order

81 papers	1,345 citations	18 h-index	35 g-index
87 ext. papers	1,774 ext. citations	3.5 avg, IF	4.23 L-index

#	Paper	IF	Citations
81	Detecting Glucose Fluctuations in the N-Glycan Structure. *ACS Chemical Biology*, **2021**, 16, 2690-2701	4.9	0
80	, , , and are later synonyms of : transfer of , , Ψand Ψto as comb. nov., comb. nov., comb. nov. and comb. nov. *International Journal of Systematic and Evolutionary Microbiology*, **2021**, 71,	2.2	1
79	Genomic Characterization of Adapted to the Guinea Pig () Host. *Frontiers in Cellular and Infection Microbiology*, **2021**, 11, 607747	5.9	1
78	Genetic characterisation of Campylobacter concisus: Strategies for improved genomospecies discrimination. *Systematic and Applied Microbiology*, **2021**, 44, 126187	4.2	2
77	Campylobacter vulpis sp. nov. isolated from wild red foxes. *Systematic and Applied Microbiology*, **2021**, 44, 126204	4.2	4
76	Identification of colonies of cultured shellfish-associated species by Elastic Light Scatter Analysis. *Current Research in Microbial Sciences*, **2021**, 2, 100033	3.3	
75	A critical rebuttal of the proposed division of the genus Arcobacter into six genera using comparative genomic, phylogenetic, and phenotypic criteria. *Systematic and Applied Microbiology*, **2020**, 43, 126108	4.2	15
74	Complete Genome Sequencing of Four Arcobacter Species Reveals a Diverse Suite of Mobile Elements. *Genome Biology and Evolution*, **2020**, 12, 3850-3856	3.9	
73	Antimicrobial resistance patterns and molecular resistance markers of Campylobacter jejuni isolates from human diarrheal cases. *PLoS ONE*, **2020**, 15, e0227833	3.7	21
72	Abundance in Breastfed Infants and Identification of a New Species in the Global Enterics Multicenter Study. *MSphere*, **2020**, 5,	5	9
71	An emended description of Sasi Jyothsna . 2013: genomic and phenotypic insights. *International Journal of Systematic and Evolutionary Microbiology*, **2020**, 70, 3921-3923	2.2	2
70	Search for spp. Reveals High Prevalence and Pronounced Genetic Diversity of Arcobacter butzleri in Floodwater Samples Associated with Hurricane Florence in North Carolina, USA. *Applied and Environmental Microbiology*, **2020**, 86,	4.8	3
69	Antimicrobial resistance patterns and molecular resistance markers of Campylobacter jejuni isolates from human diarrheal cases **2020**, 15, e0227833		
68	Antimicrobial resistance patterns and molecular resistance markers of Campylobacter jejuni isolates from human diarrheal cases **2020**, 15, e0227833		
67	Antimicrobial resistance patterns and molecular resistance markers of Campylobacter jejuni isolates from human diarrheal cases **2020**, 15, e0227833		
66	Antimicrobial resistance patterns and molecular resistance markers of Campylobacter jejuni isolates from human diarrheal cases **2020**, 15, e0227833		
65	Strain-Specific Differences in Survival of spp. in Naturally Contaminated Turkey Feces and Water. *Applied and Environmental Microbiology*, **2019**, 85,	4.8	2

64	Comparative genomics and genome biology of. *Emerging Microbes and Infections*, **2019**, 8, 827-840	18.9	4
63	Isolated From New Zealand Mussels Harbor a Putative Virulence Plasmid. *Frontiers in Microbiology*, **2019**, 10, 1802	5.7	5
62	Complete Genome Sequences of the Campylobacter fetus subsp. , Campylobacter lari subsp. , Campylobacter sputorum bv. sputorum, and Campylobacter volucris Type Strains. *Microbiology Resource Announcements*, **2019**, 8,	1.3	2
61	sp. nov., a novel member of the group isolated from surface water and stools from humans with enteric infection. *International Journal of Systematic and Evolutionary Microbiology*, **2019**, 69, 3969-3979	2.2	9
60	Molecular epidemiology and antimicrobial resistance mechanisms of Campylobacter coli from diarrhoeal patients and broiler carcasses in Belgium. *Transboundary and Emerging Diseases*, **2019**, 66, 463-475	4.2	16
59	Orthogonal typing methods identify genetic diversity among Belgian Campylobacter jejuni strains isolated over a decade from poultry and cases of sporadic human illness. *International Journal of Food Microbiology*, **2018**, 275, 66-75	5.8	9
58	Genetic Basis and Clonal Population Structure of Antibiotic Resistance in Isolated From Broiler Carcasses in Belgium. *Frontiers in Microbiology*, **2018**, 9, 1014	5.7	24
57	Proximity to Other Commercial Turkey Farms Affects Colonization Onset, Genotypes, and Antimicrobial Resistance Profiles of Campylobacter spp. in Turkeys: Suggestive Evidence from a Paired-Farm Model. *Applied and Environmental Microbiology*, **2018**, 84,	4.8	4
56	Draft Genome Sequences of Nine Campylobacter hyointestinalis subsp. lawsonii Strains. *Microbiology Resource Announcements*, **2018**, 7,	1.3	3
55	Complete Genome Sequence of the Arcobacter bivalviorum Type Strain LMG 26154. *Microbiology Resource Announcements*, **2018**, 7,	1.3	3
54	Complete Genome Sequence of the Arcobacter trophiarum Type Strain LMG 25534. *Microbiology Resource Announcements*, **2018**, 7,	1.3	3
53	Complete Genome Sequence of Acinetobacter radioresistens Strain LH6, a Multidrug-Resistant Bacteriophage-Propagating Strain. *Microbiology Resource Announcements*, **2018**, 7,	1.3	3
52	Complete Genome Sequence of the Arcobacter ellisii Type Strain LMG 26155. *Microbiology Resource Announcements*, **2018**, 7,	1.3	1
51	Complete Genome Sequence of the Arcobacter marinus Type Strain JCM 15502. *Microbiology Resource Announcements*, **2018**, 7,	1.3	1
50	Complete Genome Sequence of the Arcobacter molluscorum Type Strain LMG 25693. *Microbiology Resource Announcements*, **2018**, 7,	1.3	4
49	Complete Genome Sequences of the Arcobacter cryaerophilus Strains ATCC 43158 and ATCC 49615. *Microbiology Resource Announcements*, **2018**, 7,	1.3	3
48	Complete Genome Sequence of the Arcobacter halophilus Type Strain CCUG 53805. *Microbiology Resource Announcements*, **2018**, 7,	1.3	1
47	Complete Genome Sequence of the Arcobacter mytili Type Strain LMG 24559. *Microbiology Resource Announcements*, **2018**, 7,	1.3	3

46	Lack of Evidence for erm(B) Infiltration Into Erythromycin-Resistant Campylobacter coli and Campylobacter jejuni from Commercial Turkey Production in Eastern North Carolina: A Major Turkey-Growing Region in the United States. *Foodborne Pathogens and Disease*, **2018**, 15, 698-700	3.8	9
45	Complete Genome Sequence of ATCC 33237 and Draft Genome Sequences for an Additional Eight Well-Characterized Strains. *Genome Announcements*, **2017**, 5,		8
44	Complete Genome Sequence of the Type Strain LMG 24588. *Genome Announcements*, **2017**, 5,		1
43	Complete Genome Sequence of the Type Strain ATCC 51209. *Genome Announcements*, **2017**, 5,		2
42	Comparative Genomic Analysis Identifies a Campylobacter Clade Deficient in Selenium Metabolism. *Genome Biology and Evolution*, **2017**, 9, 1843-1858	3.9	14
41	Comparative Genomics of All Three Campylobacter sputorum Biovars and a Novel Cattle-Associated C. sputorum Clade. *Genome Biology and Evolution*, **2017**, 9, 1513-1518	3.9	11
40	Complete Genome Sequence of the Hippuricase-Positive Type Strain LMG 24591. *Genome Announcements*, **2017**, 5,		1
39	Campylobacter pinnipediorum sp. nov., isolated from pinnipeds, comprising Campylobacter pinnipediorum subsp. pinnipediorum subsp. nov. and Campylobacter pinnipediorum subsp. caledonicus subsp. nov. *International Journal of Systematic and Evolutionary Microbiology*, **2017**, 67, 1961-1968	2.2	12
38	Minimal standards for describing new species belonging to the families Campylobacteraceae and Helicobacteraceae: Campylobacter, Arcobacter, Helicobacter and Wolinella spp. *International Journal of Systematic and Evolutionary Microbiology*, **2017**, 67, 5296-5311	2.2	50
37	International Committee on Systematics of Prokaryotes Subcommittee on the Taxonomy of Campylobacter and Related Bacteria. Minutes of the meetings, August 27 and August 31 2011, Vancouver, Canada. *International Journal of Systematic and Evolutionary Microbiology*, **2017**, 67, 5312-5314	2.2	1
36	International Committee on Systematics of Prokaryotes Subcommittee on the Taxonomy of Campylobacter and Related Bacteria. Minutes of the meetings, September 15th and 18th 2013, Aberdeen, Scotland. *International Journal of Systematic and Evolutionary Microbiology*, **2017**, 67, 5315-5316	2.2	0
35	Regulation of Energy Metabolism by the Extracytoplasmic function (ECF) Factors of Arcobacter butzleri **2016**, 311-320		
34	Comparative Genomics of Campylobacter iguaniorum to Unravel Genetic Regions Associated with Reptilian Hosts. *Genome Biology and Evolution*, **2016**, 8, 3022-3029	3.9	6
33	Whole genome sequence analysis indicates recent diversification of mammal-associated Campylobacter fetus and implicates a genetic factor associated with H2S production. *BMC Genomics*, **2016**, 17, 713	4.5	13
32	Complete Genome Sequences of Campylobacter hyointestinalis subsp. hyointestinalis Strain LMG 9260 and C. hyointestinalis subsp. lawsonii Strain LMG 15993. *Genome Announcements*, **2016**, 4,		10
31	Discriminative power of Campylobacter phenotypic and genotypic typing methods. *Journal of Microbiological Methods*, **2016**, 125, 33-9	2.8	15
30	Campylobacter fetus Subspecies Contain Conserved Type IV Secretion Systems on Multiple Genomic Islands and Plasmids. *PLoS ONE*, **2016**, 11, e0152832	3.7	15
29	Complete Genome Sequence of Campylobacter iguaniorum Strain RM11343, Isolated from an Alpaca. *Genome Announcements*, **2016**, 4,		5

28	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. *Genome Announcements*, **2016**, 4,		10
27	Comparative Genomics of Campylobacter fetus from Reptiles and Mammals Reveals Divergent Evolution in Host-Associated Lineages. *Genome Biology and Evolution*, **2016**, 8, 2006-19	3.9	21
26	Complete Genome Sequence of Campylobacter gracilis ATCC 33236T. *Genome Announcements*, **2015**, 3,		9
25	Complete Genome Sequences of Two Outbreak Strains of Salmonella enterica subsp. enterica Serovar Thompson Associated with Cilantro. *Genome Announcements*, **2015**, 3,		1
24	Complete Genome Sequence of the Campylobacter ureolyticus Clinical Isolate RIGS 9880. *Genome Announcements*, **2015**, 3,		4
23	Complete Genome Sequences of Campylobacter jejuni Strains RM3196 (233.94) and RM3197 (308.95) Isolated from Patients with Guillain-Barr Syndrome. *Genome Announcements*, **2015**, 3,		3
22	Campylobacter iguaniorum sp. nov., isolated from reptiles. *International Journal of Systematic and Evolutionary Microbiology*, **2015**, 65, 975-982	2.2	22
21	Campylobacter fetus subsp. testudinum subsp. nov., isolated from humans and reptiles. *International Journal of Systematic and Evolutionary Microbiology*, **2014**, 64, 2944-2948	2.2	52
20	Molecular Epidemiology of Campylobacter Species **2014**, 191-211		8
19	Complete Genome Sequence of Campylobacter iguaniorum Strain 1485ET, Isolated from a Bearded Dragon (Pogona vitticeps). *Genome Announcements*, **2014**, 2,		7
18	Biological roles of the O-methyl phosphoramidate capsule modification in Campylobacter jejuni. *PLoS ONE*, **2014**, 9, e87051	3.7	41
17	Complete Genome Sequence and Annotation of a Campylobacter jejuni Strain, MTVDSCj20, Isolated from a Naturally Colonized Farm-Raised Chicken. *Genome Announcements*, **2014**, 2,		2
16	Inconsistency of phenotypic and genomic characteristics of Campylobacter fetus subspecies requires reevaluation of current diagnostics. *Journal of Clinical Microbiology*, **2014**, 52, 4183-8	9.7	29
15	Comparative genomics of the Campylobacter lari group. *Genome Biology and Evolution*, **2014**, 6, 3252-66	3.9	44
14	Divergent distribution of the sensor kinase CosS in non-thermotolerant campylobacter species and its functional incompatibility with the response regulator CosR of Campylobacter jejuni. *PLoS ONE*, **2014**, 9, e89774	3.7	4
13	Progressive genome-wide introgression in agricultural Campylobacter coli. *Molecular Ecology*, **2013**, 22, 1051-64	5.7	98
12	Multilocus sequence typing methods for the emerging Campylobacter Species C. hyointestinalis, C. lanienae, C. sputorum, C. concisus, and C. curvus. *Frontiers in Cellular and Infection Microbiology*, **2012**, 2, 45	5.9	42
11	First multi-locus sequence typing scheme for Arcobacter spp. *BMC Microbiology*, **2009**, 9, 196	4.5	48

10	The complete genome sequence and analysis of the human pathogen Campylobacter lari. *Foodborne Pathogens and Disease*, **2008**, 5, 371-86	3.8	34
9	The complete genome sequence and analysis of the epsilonproteobacterium Arcobacter butzleri. *PLoS ONE*, **2007**, 2, e1358	3.7	155
8	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. *BMC Microbiology*, **2007**, 7, 11	4.5	25
7	Cryptic plasmids isolated from Campylobacter strains represent multiple, novel incompatibility groups. *Plasmid*, **2007**, 57, 108-17	3.3	8
6	Identification of host-associated alleles by multilocus sequence typing of Campylobacter coli strains from food animals. *Microbiology (United Kingdom)*, **2006**, 152, 245-255	2.9	110
5	Extended multilocus sequence typing system for Campylobacter coli, C. lari, C. upsaliensis, and C. helveticus. *Journal of Clinical Microbiology*, **2005**, 43, 2315-29	9.7	172
4	Diversity within the Campylobacter jejuni type I restriction-modification loci. *Microbiology (United Kingdom)*, **2005**, 151, 337-351	2.9	49
3	Comparative Genomics of Campylobacter Species Other than Campylobacter jejuni73-95		5
2	Arcobacter: an Opportunistic Human Food-Borne Pathogen?185-212		8
1	Campylobacter and Arcobacter49-65		3