## Bonnie L Quigley

List of Publications by Year in descending order

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218381 197535 2,590 59 26 49 citations h-index g-index papers 61 61 61 3214 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	A targeted approach to investigating immune genes of an iconic Australian marsupial. Molecular Ecology, 2022, 31, 3286-3303.	2.0	9
2	Phylogenetic and geographical analysis of a retrovirus during the early stages of endogenous adaptation and exogenous spread in a new host. Molecular Ecology, 2021, 30, 2626-2640.	2.0	16
3	The Koala Immune Response to Chlamydial Infection and Vaccine Development—Advancing Our Immunological Understanding. Animals, 2021, 11, 380.	1.0	8
4	The "Jack-of-all-Trades―Flagellum From Salmonella and E. coli Was Horizontally Acquired From an Ancestral β-Proteobacterium. Frontiers in Microbiology, 2021, 12, 643180.	1.5	6
5	Koala Retrovirus in Northern Australia Shows a Mixture of Stable Endogenization and Exogenous Lineage Diversification within Fragmented Koala Populations. Journal of Virology, 2021, 95, .	1.5	8
6	Capturing Complex Vaccine-Immune-Disease Relationships for Free-Ranging Koalas: Higher Chlamydial Loads Are Associated With Less IL17 Expression and More Chlamydial Disease. Frontiers in Veterinary Science, 2020, 7, 530686.	0.9	2
7	High-throughput immunogenetic typing of koalas suggests possible link between MHC alleles and cancers. Immunogenetics, 2020, 72, 499-506.	1.2	2
8	Koala immunogenetics and chlamydial strain type are more directly involved in chlamydial disease progression in koalas from two south east Queensland koala populations than koala retrovirus subtypes. Scientific Reports, 2020, 10, 15013.	1.6	15
9	Therapeutic vaccination of koalas harbouring endogenous koala retrovirus (KoRV) improves antibody responses and reduces circulating viral load. Npj Vaccines, 2020, 5, 60.	2.9	10
10	Koalas vaccinated against Koala retrovirus respond by producing increased levels of interferon-gamma. Virology Journal, 2020, 17, 168.	1.4	3
11	Helping koalas battle disease – Recent advances in <i>Chlamydia</i> and koala retrovirus (KoRV) disease understanding and treatment in koalas. FEMS Microbiology Reviews, 2020, 44, 583-605.	3.9	31
12	Vaccination of koalas during antibiotic treatment for Chlamydia-induced cystitis induces an improved antibody response to Chlamydia pecorum. Scientific Reports, 2020, 10, 10152.	1.6	8
13	Changes in Endogenous and Exogenous Koala Retrovirus Subtype Expression over Time Reflect Koala Health Outcomes. Journal of Virology, 2019, 93, .	1.5	21
14	Chlamydial infection and onâ€farm risk factors in dairy cattle herds in South East Queensland. Australian Veterinary Journal, 2019, 97, 505-508.	0.5	8
15	Antibody response against koala retrovirus (KoRV) in koalas harboring KoRV-A in the presence or absence of KoRV-B. Scientific Reports, 2019, 9, 12416.	1.6	11
16	Longitudinal study of wild koalas (Phascolarctos cinereus) reveals chlamydial disease progression in two thirds of infected animals. Scientific Reports, 2019, 9, 13194.	1.6	17
17	Antibiotic treatment of Chlamydia-induced cystitis in the koala is linked to expression of key inflammatory genes in reactive oxygen pathways. PLoS ONE, 2019, 14, e0221109.	1.1	5
18	Seventy Years of Chlamydia Vaccine Research – Limitations of the Past and Directions for the Future. Frontiers in Microbiology, 2019, 10, 70.	1.5	74

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19	Therapeutic effect of a Chlamydia pecorum recombinant major outer membrane protein vaccine on ocular disease in koalas (Phascolarctos cinereus). PLoS ONE, 2019, 14, e0210245.	1.1	14
20	Evolution of higher torque in Campylobacter-type bacterial flagellar motors. Scientific Reports, 2018, 8, 97.	1.6	70
21	Molecular Dynamics and Mode of Transmission of Koala Retrovirus as It Invades and Spreads through a Wild Queensland Koala Population. Journal of Virology, 2018, 92, .	1.5	38
22	The relative contribution of causal factors in the transition from infection to clinical chlamydial disease. Scientific Reports, 2018, 8, 8893.	1.6	18
23	The vaginal microbiome of pregnant women is less rich and diverse, with lower prevalence of Mollicutes, compared to non-pregnant women. Scientific Reports, 2017, 7, 9212.	1.6	136
24	Distinct Campylobacter fetus lineages adapted as livestock pathogens and human pathobionts in the intestinal microbiota. Nature Communications, 2017, 8, 1367.	5.8	56
25	Epidemiology of chlamydial infection and disease in a free-ranging koala (Phascolarctos cinereus) population. PLoS ONE, 2017, 12, e0190114.	1.1	39
26	Comparative Genomics of cpn60-Defined Enterococcus hirae Ecotypes and Relationship of Gene Content Differences to Competitive Fitness. Microbial Ecology, 2016, 72, 917-930.	1.4	7
27	Effect of sample pooling and transport conditions on the clinical sensitivity of a real-time polymerase chain reaction assay for Campylobacter fetus subsp. venerealis in preputial samples from bulls. Canadian Journal of Veterinary Research, 2016, 80, 32-9.	0.2	4
28	A Study of the Vaginal Microbiome in Healthy Canadian Women Utilizing cpn60-Based Molecular Profiling Reveals Distinct Gardnerella Subgroup Community State Types. PLoS ONE, 2015, 10, e0135620.	1.1	93
29	Optimizing a PCR protocol for cpn60-based microbiome profiling of samples variously contaminated with host genomic DNA. BMC Research Notes, 2015, 8, 253.	0.6	16
30	The flagellum in bacterial pathogens: For motility and a whole lot more. Seminars in Cell and Developmental Biology, 2015, 46, 91-103.	2.3	275
31	Characterization of the Fecal Microbiota of Pigs before and after Inoculation with "Brachyspira hampsonii― PLoS ONE, 2014, 9, e106399.	1.1	38
32	Prevalence and Diversity of Campylobacter Species in Saskatchewan Retail Ground Beef. Journal of Food Protection, 2014, 77, 2106-2110.	0.8	9
33	Comparison of Baseline Bacterial Levels in Retail Ground Beef Originating from Different Regulatory, Processing, and Packaging Environments. Journal of Food Protection, 2014, 77, 404-411.	0.8	2
34	Clinical sensitivity and specificity of a real-time PCR assay for Campylobacter fetus subsp venerealis in preputial samples from bulls. American Journal of Veterinary Research, 2014, 75, 851-860.	0.3	14
35	Characterization of the vaginal microbiota of healthy Canadian women through the menstrual cycle. Microbiome, 2014, 2, 23.	4.9	198
36	Detection and Identification of <i>Pectinatus</i> Brewery Contaminants Based on the Gene for the Major Outer Membrane Protein. Journal of the American Society of Brewing Chemists, 2014, 72, 169-174.	0.8	4

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37	Isolation rates of Campylobacter fetus subsp venerealis from bovine preputial samples via passive filtration on nonselective medium versus selective medium, with and without transport medium. American Journal of Veterinary Research, 2013, 74, 1066-1069.	0.3	22
38	mPUMA: a computational approach to microbiota analysis by de novo assembly of operational taxonomic units based on protein-coding barcode sequences. Microbiome, 2013, 1, 23.	4.9	29
39	CRISPRs of Enterococcus faecalis and E. hirae Isolates from Pig Feces Have Species-Specific Repeats But Share Some Common Spacer Sequences. Microbial Ecology, 2013, 66, 182-188.	1.4	8
40	Characterization of the Upper Respiratory Tract Microbiomes of Patients with Pandemic H1N1 Influenza. PLoS ONE, 2013, 8, e69559.	1.1	67
41	A â€~universal' type II chaperonin PCR detection system for the investigation of Archaea in complex microbial communities. ISME Journal, 2012, 6, 430-439.	4.4	27
42	A Molecular Enrichment Strategy Based on cpn60 for Detection of Epsilon-Proteobacteria in the Dog Fecal Microbiome. Microbial Ecology, 2012, 63, 348-357.	1.4	32
43	Evaluation of a Campylobacter fetus subspecies venerealis real-time quantitative polymerase chain reaction for direct analysis of bovine preputial samples. Canadian Journal of Veterinary Research, 2012, 76, 166-73.	0.2	9
44	Detection and quantification of 14 Campylobacter species in pet dogs reveals an increase in species richness in feces of diarrheic animals. BMC Microbiology, 2010, 10, 73.	1.3	119
45	Multiple Zoonotic Pathogens Identified in Canine Feces Collected from a Remote Canadian Indigenous Community. American Journal of Tropical Medicine and Hygiene, 2010, 83, 338-341.	0.6	48
46	AglC and AglK Are Involved in Biosynthesis and Attachment of Diacetylated Glucuronic Acid to the N-Glycan in Methanococcus voltae. Journal of Bacteriology, 2009, 191, 187-195.	1.0	46
47	Different Minimal Signal Peptide Lengths Recognized by the Archaeal Prepilin-Like Peptidases FlaK and PibD. Journal of Bacteriology, 2009, 191, 6732-6740.	1.0	27
48	Development of <i>cpn60</i> -Based Real-Time Quantitative PCR Assays for the Detection of 14 <i>Campylobacter</i> Species and Application to Screening of Canine Fecal Samples. Applied and Environmental Microbiology, 2009, 75, 3055-3061.	1.4	75
49	Sweet to the extreme: protein glycosylation in Archaea. Molecular Microbiology, 2008, 68, 1079-1084.	1.2	65
50	Identification of a Putative Acetyltransferase Gene, MMP0350, Which Affects Proper Assembly of both Flagella and Pili in the Archaeon <i>Methanococcus maripaludis</i> . Journal of Bacteriology, 2008, 190, 5300-5307.	1.0	40
51	Identification of the Archaeal <i>alg7</i> Gene Homolog (Encoding <i>N</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock Complementation in <i>Saccharomyces cerevisiae</i> . Journal of Bacteriology, 2008, 190, 2217-2220.	₹ 10 Tf 50 1.0	) 187 Td (- <mark>A</mark> d 34
52	Archaeal signal peptidases. Microbiology (United Kingdom), 2007, 153, 305-314.	0.7	46
53	Systematic deletion analyses of the <i>fla</i> genes in the flagella operon identify several genes essential for proper assembly and function of flagella in the archaeon, <i>Methanococcus maripaludis</i> . Molecular Microbiology, 2007, 66, 596-609.	1.2	100
54	Archaeal Flagella, Bacterial Flagella and Type IV Pili: A Comparison of Genes and Posttranslational Modifications. Journal of Molecular Microbiology and Biotechnology, 2006, 11, 167-191.	1.0	110

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55	Archaeal habitats $\hat{a} \in \text{``from the extreme to the ordinary. Canadian Journal of Microbiology, 2006, 52, 73-116.}$	0.8	214
56	Identification of genes involved in the biosynthesis and attachment ofMethanococcus voltae N-linked glycans: insight intoN-linked glycosylation pathways in Archaea. Molecular Microbiology, 2006, 61, 259-268.	1.2	138
57	The flagellin gene and protein from the brewing spoilage bacteria Pectinatus cerevisiiphilus and Pectinatus frisingensis. Canadian Journal of Microbiology, 2005, 51, 863-874.	0.8	11
58	Lactobacillus casei, Lactobacillus rhamnosus, and Lactobacillus zeae isolates identified by sequence signature and immunoblot phenotype. Canadian Journal of Microbiology, 2004, 50, 482-488.	0.8	26
59	Immunoblotting Used for Identification of Beer Spoilage Pediococci, Including the New Species <i>Pediococcus Claussenii </i> Journal of the American Society of Brewing Chemists, 2002, 60, 170-175.	0.8	12