

# Birgitta Duim

## List of Publications by Year in descending order

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80  
papers

4,075  
citations

87888

38  
h-index

123424

61  
g-index

82  
all docs

82  
docs citations

82  
times ranked

3917  
citing authors

#	ARTICLE	IF	CITATIONS
1	Canine <i>Staphylococcus argenteus</i> : Case Report from The Netherlands. <i>Pathogens</i> , 2022, 11, 153.	2.8	4
2	Genomic Investigation of Two <i>Acinetobacter baumannii</i> Outbreaks in a Veterinary Intensive Care Unit in The Netherlands. <i>Pathogens</i> , 2022, 11, 123.	2.8	7
3	Sources and transmission routes of campylobacteriosis: A combined analysis of genome and exposure data. <i>Journal of Infection</i> , 2021, 82, 216-226.	3.3	42
4	Complete Genome Sequence of a Clinical <i>Campylobacter</i> Isolate Identical to a Novel <i>Campylobacter</i> Species. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	2
5	Absence of Host-Specific Genes in Canine and Human <i>Staphylococcus pseudintermedius</i> as Inferred from Comparative Genomics. <i>Antibiotics</i> , 2021, 10, 854.	3.7	8
6	Differential Analysis of Longitudinal Methicillin-Resistant <i>Staphylococcus aureus</i> Colonization in Relation to Microbial Shifts in the Nasal Microbiome of Neonatal Piglets. <i>MSystems</i> , 2021, 6, e0015221.	3.8	4
7	Specific staphylococcal cassette chromosome <i>mecA</i> ( <i>SCC<sub>mecA</sub></i> ) types and clonal complexes are associated with low-level amoxicillin/clavulanic acid and cefalotin resistance in methicillin-resistant <i>Staphylococcus pseudintermedius</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 508-511.	3.0	8
8	Tracing the animal sources of surface water contamination with <i>Campylobacter jejuni</i> and <i>Campylobacter coli</i> . <i>Water Research</i> , 2020, 187, 116421.	11.3	34
9	A Case of Persistent Diarrhea in a Man with the Molecular Detection of Various <i>Campylobacter</i> species and the First Isolation of <i>Campylobacter infantis</i> . <i>Pathogens</i> , 2020, 9, 1003.	2.8	6
10	After the bite: bacterial transmission from grey seals ( <i>Halichoerus grypus</i> ) to harbour porpoises ( <i>Phocoena phocaena</i> ). <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 116421.	2.4	5
11	Fecal Carriage of Extended-Spectrum-β-Lactamase/AmpC-Producing <i>Escherichia coli</i> in Horses. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	9
12	Living in Cold Blood: <i>Arcobacter</i> , <i>Campylobacter</i> , and <i>Helicobacter</i> in Reptiles. <i>Frontiers in Microbiology</i> , 2019, 10, 1086.	3.5	18
13	Zoonotic Endocarditis in a Man, the Netherlands. <i>Emerging Infectious Diseases</i> , 2019, 25, 180-182.	4.3	3
14	Homologous Recombination between Genetically Divergent <i>Campylobacter fetus</i> Lineages Supports Host-Associated Speciation. <i>Genome Biology and Evolution</i> , 2018, 10, 716-722.	2.5	16
15	Methicillin-resistant <i>Staphylococcus pseudintermedius</i> among dogs in the description of novel <i>SCC<sub>mecA</sub></i> variants. <i>Veterinary Microbiology</i> , 2018, 213, 136-141.	1.9	12
16	Comparative genomics of phenotypic antimicrobial resistances in methicillin-resistant <i>Staphylococcus pseudintermedius</i> of canine origin. <i>Veterinary Microbiology</i> , 2018, 225, 125-131.	1.9	32
17	High Production of LukMF <sup>TM</sup> in <i>Staphylococcus aureus</i> Field Strains Is Associated with Clinical Bovine Mastitis. <i>Toxins</i> , 2018, 10, 200.	3.4	29
18	<i>Campylobacter blaseri</i> sp. nov., isolated from common seals ( <i>Phoca vitulina</i> ). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 1787-1794.	1.7	22

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19	Sustained fecal-oral human-to-human transmission following a zoonotic event. <i>Current Opinion in Virology</i> , 2017, 22, 1-6.	5.4	46
20	Whole genome-based phylogeny of reptile-associated <i>Helicobacter</i> indicates independent niche adaptation followed by diversification in a poikilothermic host. <i>Scientific Reports</i> , 2017, 7, 8387.	3.3	19
21	<i>Staphylococcus aureus</i> Nasal Colonization Differs among Pig Lineages and Is Associated with the Presence of Other Staphylococcal Species. <i>Frontiers in Veterinary Science</i> , 2017, 4, 97.	2.2	12
22	Development of a real-time PCR for detection of <i>Staphylococcus pseudintermedius</i> using a novel automated comparison of whole-genome sequences. <i>PLoS ONE</i> , 2017, 12, e0183925.	2.5	20
23	Raw pet food as a risk factor for shedding of extended-spectrum beta-lactamase-producing Enterobacteriaceae in household cats. <i>PLoS ONE</i> , 2017, 12, e0187239.	2.5	50
24	Simultaneous Quantification and Differentiation of <i>Streptococcus suis</i> Serotypes 2 and 9 by Quantitative Real-Time PCR, Evaluated in Tonsillar and Nasal Samples of Pigs. <i>Pathogens</i> , 2016, 5, 46.	2.8	10
25	The Effectiveness of Bacteriophages against Methicillin-Resistant <i>Staphylococcus aureus</i> ST398 Nasal Colonization in Pigs. <i>PLoS ONE</i> , 2016, 11, e0160242.	2.5	31
26	Comparative Genomics of <i>Campylobacter fetus</i> from Reptiles and Mammals Reveals Divergent Evolution in Host-Associated Lineages. <i>Genome Biology and Evolution</i> , 2016, 8, 2006-2019.	2.5	25
27	Comparative Genomics of <i>Campylobacter iguaniorum</i> to Unravel Genetic Regions Associated with Reptilian Hosts. <i>Genome Biology and Evolution</i> , 2016, 8, 3022-3029.	2.5	8
28	Whole genome sequence analysis indicates recent diversification of mammal-associated <i>Campylobacter fetus</i> and implicates a genetic factor associated with H <sub>2</sub> S production. <i>BMC Genomics</i> , 2016, 17, 713.	2.8	18
29	Quantifying potential sources of surface water contamination with <i>Campylobacter jejuni</i> and <i>Campylobacter coli</i> . <i>Water Research</i> , 2016, 101, 36-45.	11.3	56
30	Transmission through air as a possible route of exposure for MRSA. <i>Journal of Exposure Science and Environmental Epidemiology</i> , 2016, 26, 263-269.	3.9	85
31	Changes in the Population of Methicillin-Resistant <i>Staphylococcus pseudintermedius</i> and Dissemination of Antimicrobial-Resistant Phenotypes in the Netherlands. <i>Journal of Clinical Microbiology</i> , 2016, 54, 283-288.	3.9	56
32	<i>Campylobacter fetus</i> Subspecies Contain Conserved Type IV Secretion Systems on Multiple Genomic Islands and Plasmids. <i>PLoS ONE</i> , 2016, 11, e0152832.	2.5	30
33	<i>Campylobacter iguaniorum</i> sp. nov., isolated from reptiles. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 975-982.	1.7	32
34	Longitudinal Study of Extended-Spectrum-β-Lactamase- and AmpC-Producing Enterobacteriaceae in Household Dogs. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 3117-3124.	3.2	50
35	Occurrence, Diversity, and Host Association of Intestinal <i>Campylobacter</i> , <i>Arcobacter</i> , and <i>Helicobacter</i> in Reptiles. <i>PLoS ONE</i> , 2014, 9, e101599.	2.5	43
36	<i>Staphylococcus aureus</i> ST398 gene expression profiling during ex vivo colonization of porcine nasal epithelium. <i>BMC Genomics</i> , 2014, 15, 915.	2.8	7

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37	First Closed Genome Sequence of <i>Campylobacter fetus</i> subsp. <i>venerealis</i> bv. <i>intermedius</i> . <i>Genome Announcements</i> , 2014, 2, .	0.8	9
38	Experimental nasal colonization of piglets with methicillin-susceptible and methicillin-resistant <i>Staphylococcus aureus</i> . <i>Veterinary Microbiology</i> , 2014, 174, 483-488.	1.9	7
39	Inconsistency of Phenotypic and Genomic Characteristics of <i>Campylobacter fetus</i> Subspecies Requires Reevaluation of Current Diagnostics. <i>Journal of Clinical Microbiology</i> , 2014, 52, 4183-4188.	3.9	45
40	<i>Campylobacter fetus</i> subsp. <i>testudinum</i> subsp. nov., isolated from humans and reptiles. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 2944-2948.	1.7	78
41	Complete Genome Sequence of <i>Campylobacter iguaniorum</i> Strain 1485E T, Isolated from a Bearded Dragon ( <i>Pogona vitticeps</i> ). <i>Genome Announcements</i> , 2014, 2, .	0.8	10
42	Evaluation of molecular assays for identification <i>Campylobacter fetus</i> species and subspecies and development of a <i>C. fetus</i> specific real-time PCR assay. <i>Journal of Microbiological Methods</i> , 2013, 95, 93-97.	1.6	42
43	Propidium monoazide does not fully inhibit the detection of dead <i>Campylobacter</i> on broiler chicken carcasses by qPCR. <i>Journal of Microbiological Methods</i> , 2013, 95, 32-38.	1.6	49
44	Complete Genome Sequence of <i>Campylobacter fetus</i> subsp. <i>testudinum</i> Strain 03-427 <sup>T</sup>. <i>Genome Announcements</i> , 2013, 1, .	0.8	10
45	High prevalence of fecal carriage of extended spectrum $\beta$ -lactamase/AmpC-producing Enterobacteriaceae in cats and dogs. <i>Frontiers in Microbiology</i> , 2013, 4, 242.	3.5	186
46	An Ex Vivo Porcine Nasal Mucosa Explants Model to Study MRSA Colonization. <i>PLoS ONE</i> , 2013, 8, e53783.	2.5	10
47	Methicillin-Resistant Coagulase-Negative Staphylococci on Pig Farms as a Reservoir of Heterogeneous Staphylococcal Cassette Chromosome <i>mec</i> Elements. <i>Applied and Environmental Microbiology</i> , 2012, 78, 299-304.	3.1	74
48	Livestock-associated MRSA ST398 carriage in pig slaughterhouse workers related to quantitative environmental exposure. <i>Occupational and Environmental Medicine</i> , 2012, 69, 472-478.	2.8	48
49	Differences in the Population Structure of Invasive <i>Streptococcus suis</i> Strains Isolated from Pigs and from Humans in the Netherlands. <i>PLoS ONE</i> , 2012, 7, e33854.	2.5	82
50	<i>In vitro</i> antimicrobial activity of miconazole and polymyxin B against canine methicillin-resistant <i>Staphylococcus aureus</i> and methicillin-resistant <i>Staphylococcus pseudintermedius</i> isolates. <i>Veterinary Dermatology</i> , 2012, 23, 381.	1.2	24
51	Livestock-associated methicillin-resistant <i>Staphylococcus aureus</i> in animals and humans. <i>International Journal of Medical Microbiology</i> , 2011, 301, 630-634.	3.6	263
52	Longitudinal Study on Methicillin-Resistant <i>Staphylococcus pseudintermedius</i> in Households. <i>PLoS ONE</i> , 2011, 6, e27788.	2.5	76
53	Suspected Horse-to-Human Transmission of MRSA ST398. <i>Emerging Infectious Diseases</i> , 2011, 17, 1137-1139.	4.3	40
54	Clonal spread of methicillin-resistant <i>Staphylococcus pseudintermedius</i> in Europe and North America: an international multicentre study. <i>Journal of Antimicrobial Chemotherapy</i> , 2010, 65, 1145-1154.	3.0	391

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55	Molecular analysis of methicillin-resistant <i>Staphylococcus pseudintermedius</i> of feline origin from different European countries and North America. <i>Journal of Antimicrobial Chemotherapy</i> , 2010, 65, 1826-1828.	3.0	67
56	Strain variation within <i>Campylobacter</i> species in fecal samples from dogs and cats. <i>Veterinary Microbiology</i> , 2009, 133, 199-205.	1.9	19
57	Evaluation of a <i>Chlamydomphila psittaci</i> Infection Diagnostic Platform for Zoonotic Risk Assessment. <i>Journal of Clinical Microbiology</i> , 2008, 46, 281-285.	3.9	52
58	Emergence of multidrug-resistant Gram-negative bacteria during selective decontamination of the digestive tract on an intensive care unit—authors' response. <i>Journal of Antimicrobial Chemotherapy</i> , 2007, 60, 446-446.	3.0	0
59	Genotyping of <i>Chlamydomphila psittaci</i> in Human Samples. <i>Emerging Infectious Diseases</i> , 2006, 12, 1989-1990.	4.3	63
60	Application of Minimal Sequence Quality Values Prevents Misidentification of the blaSHV Type in Single Bacterial Isolates Carrying Different SHV Extended-Spectrum $\beta$ -Lactamase Genes. <i>Journal of Clinical Microbiology</i> , 2006, 44, 1896-1898.	3.9	9
61	Emergence of multidrug-resistant Gram-negative bacteria during selective decontamination of the digestive tract on an intensive care unit. <i>Journal of Antimicrobial Chemotherapy</i> , 2006, 58, 853-856.	3.0	47
62	A CTX-M extended-spectrum $\beta$ -lactamase in <i>Pseudomonas aeruginosa</i> and <i>Stenotrophomonas maltophilia</i> . <i>Journal of Medical Microbiology</i> , 2006, 55, 1607-1608.	1.8	64
63	An outbreak of psittacosis due to <i>Chlamydomphila psittaci</i> genotype A in a veterinary teaching hospital. <i>Journal of Medical Microbiology</i> , 2006, 55, 1571-1575.	1.8	68
64	Widespread Transfer of Resistance Genes between Bacterial Species in an Intensive Care Unit: Implications for Hospital Epidemiology. <i>Journal of Clinical Microbiology</i> , 2005, 43, 4862-4864.	3.9	97
65	Identification of Distinct <i>Campylobacter lari</i> Genogroups by Amplified Fragment Length Polymorphism and Protein Electrophoretic Profiles. <i>Applied and Environmental Microbiology</i> , 2004, 70, 18-24.	3.1	30
66	Multiplex-endonuclease genotyping approach (mega): a tool for the fine-scale detection of unlinked polymorphic DNA markers. <i>Chromosoma</i> , 2003, 111, 518-524.	2.2	13
67	Comparative Genotyping of <i>Campylobacter jejuni</i> by Amplified Fragment Length Polymorphism, Multilocus Sequence Typing, and Short Repeat Sequencing: Strain Diversity, Host Range, and Recombination. <i>Journal of Clinical Microbiology</i> , 2003, 41, 15-26.	3.9	242
68	Molecular Evidence for Dissemination of Unique <i>Campylobacter jejuni</i> Clones in Curaciao, Netherlands Antilles. <i>Journal of Clinical Microbiology</i> , 2003, 41, 5593-5597.	3.9	61
69	Generation of <i>Campylobacter jejuni</i> genetic diversity in vivo. <i>Molecular Microbiology</i> , 2002, 44, 351-359.	2.5	150
70	Homonucleotide stretches in chromosomal DNA of <i>Campylobacter jejuni</i> display high frequency polymorphism as detected by direct PCR analysis. <i>FEMS Microbiology Letters</i> , 2002, 212, 77-85.	1.8	49
71	Molecular Characterization of <i>Campylobacter jejuni</i> Clones: A Basis for Epidemiologic Investigation. <i>Emerging Infectious Diseases</i> , 2002, 8, 949-955.	4.3	192
72	Comparative Study Using Amplified Fragment Length Polymorphism Fingerprinting, PCR Genotyping, and Phenotyping To Differentiate <i>Campylobacter fetus</i> Strains Isolated from Animals. <i>Journal of Clinical Microbiology</i> , 2001, 39, 2283-2286.	3.9	50

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73	Genomic Relatedness within Five Common Finnish <i>Campylobacter jejuni</i> Pulsed-Field Gel Electrophoresis Genotypes Studied by Amplified Fragment Length Polymorphism Analysis, Ribotyping, and Serotyping. <i>Applied and Environmental Microbiology</i> , 2001, 67, 1581-1586.	3.1	44
74	Amplified Fragment Length Polymorphism Analysis of <i>Campylobacter jejuni</i> Strains Isolated from Chickens and from Patients with Gastroenteritis or Guillain-Barré or Miller Fisher Syndrome. <i>Applied and Environmental Microbiology</i> , 2000, 66, 3917-3923.	3.1	58
75	Computer-Assisted Analysis and Epidemiological Value of Genotyping Methods for <i>Campylobacter jejuni</i> and <i>Campylobacter coli</i> . <i>Journal of Clinical Microbiology</i> , 2000, 38, 1940-1946.	3.9	92
76	Molecular Characterization of <i>Campylobacter jejuni</i> from Patients with Guillain-Barre and Miller Fisher Syndromes. <i>Journal of Clinical Microbiology</i> , 2000, 38, 2297-2301.	3.9	10
77	High-Resolution Genotyping of <i>Campylobacter</i> Strains Isolated from Poultry and Humans with Amplified Fragment Length Polymorphism Fingerprinting. <i>Applied and Environmental Microbiology</i> , 1999, 65, 2369-2375.	3.1	158
78	Sequence variation in the hpd gene of nonencapsulated <i>Haemophilus influenzae</i> isolated from patients with chronic bronchitis. <i>Gene</i> , 1997, 191, 57-60.	2.2	8
79	Antigenic drift of non-encapsulated <i>Haemophilus influenzae</i> major outer membrane protein P2 in patients with chronic bronchitis is caused by point mutations. <i>Molecular Microbiology</i> , 1994, 11, 1181-1189.	2.5	78
80	Genetic analysis of the diversity in outer membrane protein P2 of non-encapsulated <i>Haemophilus influenzae</i> . <i>Microbial Pathogenesis</i> , 1993, 14, 451-462.	2.9	49