

Birgitta Duim

List of Publications by Year in descending order

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80
papers

4,075
citations

87888

38
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123424

61
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82
all docs

82
docs citations

82
times ranked

3917
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | 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 |
| 2 | 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 |
| 3 | 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 |
| 4 | 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 |
| 5 | High prevalence of fecal carriage of extended spectrum β -lactamase/AmpC-producing Enterobacteriaceae in cats and dogs. <i>Frontiers in Microbiology</i> , 2013, 4, 242. | 3.5 | 186 |
| 6 | 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 |
| 7 | Generation of <i>Campylobacter jejuni</i> genetic diversity in vivo. <i>Molecular Microbiology</i> , 2002, 44, 351-359. | 2.5 | 150 |
| 8 | 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 |
| 9 | 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 |
| 10 | 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 |
| 11 | 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 |
| 12 | 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 |
| 13 | <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 |
| 14 | Longitudinal Study on Methicillin-Resistant <i>Staphylococcus pseudintermedius</i> in Households. <i>PLoS ONE</i> , 2011, 6, e27788. | 2.5 | 76 |
| 15 | Methicillin-Resistant Coagulase-Negative <i>Staphylococci</i> on Pig Farms as a Reservoir of Heterogeneous <i>Staphylococcal</i> Cassette Chromosome <i>mec</i> Elements. <i>Applied and Environmental Microbiology</i> , 2012, 78, 299-304. | 3.1 | 74 |
| 16 | An outbreak of psittacosis due to <i>Chlamydia psittaci</i> genotype A in a veterinary teaching hospital. <i>Journal of Medical Microbiology</i> , 2006, 55, 1571-1575. | 1.8 | 68 |
| 17 | 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 |
| 18 | A CTX-M extended-spectrum β -lactamase in <i>Pseudomonas aeruginosa</i> and <i>Stenotrophomonas maltophilia</i> . <i>Journal of Medical Microbiology</i> , 2006, 55, 1607-1608. | 1.8 | 64 |

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|----|--|------|-----------|
| 19 | Genotyping of <i>Chlamydomphila psittaci</i> in Human Samples. <i>Emerging Infectious Diseases</i> , 2006, 12, 1989-1990. | 4.3 | 63 |
| 20 | Molecular Evidence for Dissemination of Unique <i>Campylobacter jejuni</i> Clones in Curaçao, Netherlands Antilles. <i>Journal of Clinical Microbiology</i> , 2003, 41, 5593-5597. | 3.9 | 61 |
| 21 | 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 |
| 22 | 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 |
| 23 | 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 |
| 24 | 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 |
| 25 | 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 |
| 26 | 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 |
| 27 | 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 |
| 28 | 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 |
| 29 | 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 |
| 30 | 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 |
| 31 | 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 |
| 32 | 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 |
| 33 | Sustained fecal-oral human-to-human transmission following a zoonotic event. <i>Current Opinion in Virology</i> , 2017, 22, 1-6. | 5.4 | 46 |
| 34 | 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 |
| 35 | 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 |
| 36 | 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 |

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|----|--|------|-----------|
| 37 | 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 |
| 38 | 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 |
| 39 | Suspected Horse-to-Human Transmission of MRSA ST398. <i>Emerging Infectious Diseases</i> , 2011, 17, 1137-1139. | 4.3 | 40 |
| 40 | 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 |
| 41 | <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 |
| 42 | 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 |
| 43 | 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 |
| 44 | 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 |
| 45 | <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 |
| 46 | High Production of LukMF [™] in <i>Staphylococcus aureus</i> Field Strains Is Associated with Clinical Bovine Mastitis. <i>Toxins</i> , 2018, 10, 200. | 3.4 | 29 |
| 47 | 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 |
| 48 | <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 |
| 49 | <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 |
| 50 | 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 |
| 51 | 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 |
| 52 | 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 |
| 53 | Whole genome sequence analysis indicates recent diversification of mammal-associated <i>Campylobacter fetus</i> and implicates a genetic factor associated with H ₂ S production. <i>BMC Genomics</i> , 2016, 17, 713. | 2.8 | 18 |
| 54 | 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 |

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|----|--|-----|-----------|
| 55 | 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 |
| 56 | 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 |
| 57 | <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 |
| 58 | Methicillin-resistant <i>Staphylococcus pseudintermedius</i> among dogs in the description of novel SCCmec variants. <i>Veterinary Microbiology</i> , 2018, 213, 136-141. | 1.9 | 12 |
| 59 | Complete Genome Sequence of <i>Campylobacter fetus</i> subsp. <i>testudinum</i> Strain 03-427. <i>Genome Announcements</i> , 2013, 1, . | 0.8 | 10 |
| 60 | 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 |
| 61 | 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 |
| 62 | An Ex Vivo Porcine Nasal Mucosa Explants Model to Study MRSA Colonization. <i>PLoS ONE</i> , 2013, 8, e53783. | 2.5 | 10 |
| 63 | 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 |
| 64 | Application of Minimal Sequence Quality Values Prevents Misidentification of the blaSHV Type in Single Bacterial Isolates Carrying Different SHV Extended-Spectrum β -Lactamase Genes. <i>Journal of Clinical Microbiology</i> , 2006, 44, 1896-1898. | 3.9 | 9 |
| 65 | 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 |
| 66 | 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 |
| 67 | 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 |
| 68 | 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 |
| 69 | Specific staphylococcal cassette chromosome <i>mec</i> (SCC <i>mec</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 |
| 70 | 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 |
| 71 | <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 |
| 72 | 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 |

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| 73 | 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 |
| 74 | 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 infans</i> . <i>Pathogens</i> , 2020, 9, 1003. | 2.8 | 6 |
| 75 | 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> , 2021, 66, 1000-1005. | 2.4 | 5 |
| 76 | 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 |
| 77 | Canine <i>Staphylococcus argenteus</i> : Case Report from The Netherlands. <i>Pathogens</i> , 2022, 11, 153. | 2.8 | 4 |
| 78 | Zoonotic Endocarditis in a Man, the Netherlands. <i>Emerging Infectious Diseases</i> , 2019, 25, 180-182. | 4.3 | 3 |
| 79 | 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 |
| 80 | 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 |