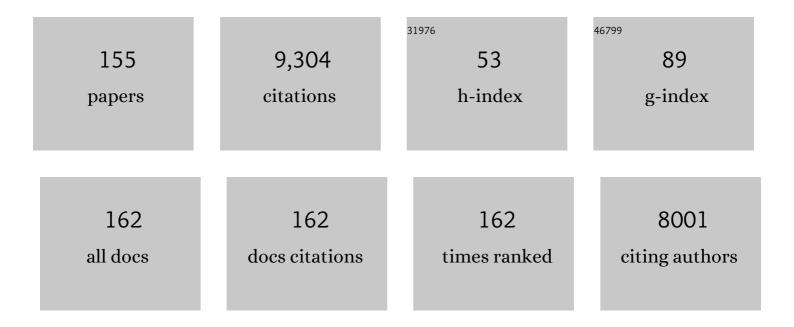
List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Genomic analysis of diversity, population structure, virulence, and antimicrobial resistance in <i>Klebsiella pneumoniae</i> , an urgent threat to public health. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E3574-81.	7.1	942
2	Invited Review: The Role of Cow, Pathogen, and Treatment Regimen in the Therapeutic Success of Bovine Staphylococcus aureus Mastitis. Journal of Dairy Science, 2006, 89, 1877-1895.	3.4	497
3	Molecular Epidemiology of Mastitis Pathogens of Dairy Cattle and Comparative Relevance to Humans. Journal of Mammary Gland Biology and Neoplasia, 2011, 16, 357-372.	2.7	323
4	Host-response patterns of intramammary infections in dairy cows. Veterinary Immunology and Immunopathology, 2011, 144, 270-289.	1.2	274
5	Listeria monocytogenes Isolates from Foods and Humans Form Distinct but Overlapping Populations. Applied and Environmental Microbiology, 2004, 70, 5833-5841.	3.1	229
6	Whole genome sequencing identifies zoonotic transmission of MRSA isolates with the novel <i>mecA</i> homologue <i>mecC</i> . EMBO Molecular Medicine, 2013, 5, 509-515.	6.9	192
7	Cow- and Quarter-Level Risk Factors for Streptococcus uberis and Staphylococcus aureus Mastitis. Journal of Dairy Science, 2001, 84, 2649-2663.	3.4	184
8	Some coagulase-negative Staphylococcus species affect udder health more than others. Journal of Dairy Science, 2011, 94, 2329-2340.	3.4	182
9	Human Streptococcus agalactiae strains in aquatic mammals and fish. BMC Microbiology, 2013, 13, 41.	3.3	174
10	Multilocus Sequence Typing of Intercontinental Bovine Staphylococcus aureus Isolates. Journal of Clinical Microbiology, 2005, 43, 4737-4743.	3.9	158
11	The newly described mecA homologue, mecALGA251, is present in methicillin-resistant Staphylococcus aureus isolates from a diverse range of host species. Journal of Antimicrobial Chemotherapy, 2012, 67, 2809-2813.	3.0	153
12	CNS mastitis: Nothing to worry about?. Veterinary Microbiology, 2009, 134, 9-14.	1.9	151
13	Invited review: The role of contagious disease in udder health. Journal of Dairy Science, 2009, 92, 4717-4729.	3.4	149
14	An update on environmental mastitis: Challenging perceptions. Transboundary and Emerging Diseases, 2018, 65, 166-185.	3.0	148
15	Methicillin Resistant S. aureus in Human and Bovine Mastitis. Journal of Mammary Gland Biology and Neoplasia, 2011, 16, 373-382.	2.7	137
16	Clinical, epidemiological and molecular characteristics of Streptococcus uberis infections in dairy herds. Epidemiology and Infection, 2003, 130, 335-349.	2.1	136
17	Comparison of Staphylococcus aureus Isolates from Bovine and Human Skin, Milking Equipment, and Bovine Milk by Phage Typing, Pulsed-Field Gel Electrophoresis, and Binary Typing. Journal of Clinical Microbiology, 2002, 40, 3894-3902.	3.9	129
18	Application of Pulsed-Field Gel Electrophoresis and Binary Typing as Tools in Veterinary Clinical Microbiology and Molecular Epidemiologic Analysis of Bovine and Human <i>Staphylococcus aureus</i> Isolates. Journal of Clinical Microbiology, 2000, 38, 1931-1939.	3.9	124

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19	Species identification of coagulase-negative staphylococci: Genotyping is superior to phenotyping. Veterinary Microbiology, 2009, 134, 20-28.	1.9	123
20	Occurrence of Mycobacterium avium subspecies paratuberculosis across host species and European countries with evidence for transmission between wildlife and domestic ruminants. BMC Microbiology, 2009, 9, 212.	3.3	114
21	Comparative genomics and the role of lateral gene transfer in the evolution of bovine adapted Streptococcus agalactiae. Infection, Genetics and Evolution, 2011, 11, 1263-1275.	2.3	99
22	Extensive Capsule Locus Variation and Large-Scale Genomic Recombination within the Klebsiella pneumoniae Clonal Group 258. Genome Biology and Evolution, 2015, 7, 1267-1279.	2.5	99
23	Streptococcus agalactiae in the environment of bovine dairy herds – rewriting the textbooks?. Veterinary Microbiology, 2016, 184, 64-72.	1.9	98
24	Prevalence of Campylobacter and Salmonella in African food animals and meat: A systematic review and meta-analysis. International Journal of Food Microbiology, 2020, 315, 108382.	4.7	97
25	Biofilm production by Staphylococcus aureus associated with intramammary infection. Veterinary Microbiology, 2005, 107, 295-299.	1.9	95
26	A Partial Budget Model to Estimate Economic Benefits of Lactational Treatment of Subclinical Staphylococcus aureus Mastitis. Journal of Dairy Science, 2005, 88, 4273-4287.	3.4	91
27	Molecular Epidemiology of Two <i>Klebsiella pneumoniae</i> Mastitis Outbreaks on a Dairy Farm in New York State. Journal of Clinical Microbiology, 2007, 45, 3964-3971.	3.9	90
28	Using whole genome sequencing to investigate transmission in a multi-host system: bovine tuberculosis in New Zealand. BMC Genomics, 2017, 18, 180.	2.8	86
29	Analysis of an Outbreak of Streptococcus uberis Mastitis. Journal of Dairy Science, 2001, 84, 590-599.	3.4	82
30	The "Other―Gram-Negative Bacteria in Mastitis. Veterinary Clinics of North America - Food Animal Practice, 2012, 28, 239-256.	1.2	81
31	Performance of API Staph ID 32 and Staph-Zym for identification of coagulase-negative staphylococci isolated from bovine milk samples. Veterinary Microbiology, 2009, 136, 300-305.	1.9	79
32	Randomized clinical trial to evaluate the efficacy of a 5-day ceftiofur hydrochloride intramammary treatment on nonsevere gram-negative clinical mastitis. Journal of Dairy Science, 2011, 94, 6203-6215.	3.4	78
33	Development of Molecular Typing Methods for Bacillus spp. and Paenibacillus spp. Isolated from Fluid Milk Products. Journal of Food Science, 2006, 71, M50.	3.1	74
34	Changing trends in mastitis. Irish Veterinary Journal, 2009, 62, S59-70.	2.1	74
35	Molecular Ecology of <i>Listeria monocytogenes</i> : Evidence for a Reservoir in Milking Equipment on a Dairy Farm. Applied and Environmental Microbiology, 2009, 75, 1315-1323.	3.1	73
36	A novel hybrid SCCmec-mecC region in Staphylococcus sciuri. Journal of Antimicrobial Chemotherapy, 2014, 69, 911-918.	3.0	73

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37	A mathematical model of Staphylococcus aureus control in dairy herds. Epidemiology and Infection, 2002, 129, 397-416.	2.1	72
38	Limitations of variable number of tandem repeat typing identified through whole genome sequencing of Mycobacterium avium subsp. paratuberculosis on a national and herd level. BMC Genomics, 2015, 16, 161.	2.8	71
39	Antimicrobial susceptibility of coagulase-negative staphylococci isolated from bovine milk samples. Veterinary Microbiology, 2011, 150, 173-179.	1.9	70
40	Prevalence of non-aureus staphylococci species causing intramammary infections in Canadian dairy herds. Journal of Dairy Science, 2017, 100, 5592-5612.	3.4	70
41	Confirmation of triclabendazole resistance in liver fluke in the UK. Veterinary Record, 2012, 171, 159-160.	0.3	67
42	A Staphylococcus xylosus Isolate with a New <i>mecC</i> Allotype. Antimicrobial Agents and Chemotherapy, 2013, 57, 1524-1528.	3.2	67
43	Bovine milk microbiome: a more complex issue than expected. Veterinary Research, 2019, 50, 44.	3.0	67
44	Strain-specific pathogenicity of putative host-adapted and nonadapted strains of Streptococcus uberis in dairy cattle. Journal of Dairy Science, 2013, 96, 5129-5145.	3.4	66
45	Prevalence and properties of mecC methicillin-resistant Staphylococcus aureus (MRSA) in bovine bulk tank milk in Great Britain. Journal of Antimicrobial Chemotherapy, 2014, 69, 598-602.	3.0	66
46	<i>Streptococcus agalactiae</i> Serotype IV in Humans and Cattle, Northern Europe1. Emerging Infectious Diseases, 2016, 22, 2097-2103.	4.3	65
47	Further evidence for the existence of environmental and host-associated species of coagulase-negative staphylococci in dairy cattle. Veterinary Microbiology, 2014, 172, 466-474.	1.9	64
48	Sources of Klebsiella and Raoultella species on dairy farms: Be careful where you walk. Journal of Dairy Science, 2011, 94, 1045-1051.	3.4	63
49	Combining genomics and epidemiology to analyse bi-directional transmission of Mycobacterium bovis in a multi-host system. ELife, 2019, 8, .	6.0	63
50	Prevalence and characterization of human mecC methicillin-resistant Staphylococcus aureus isolates in England. Journal of Antimicrobial Chemotherapy, 2014, 69, 907-910.	3.0	62
51	Multilocus sequence typing of a global collection of Pasteurella multocida isolates from cattle and other host species demonstrates niche association. BMC Microbiology, 2011, 11, 115.	3.3	59
52	Molecular Subtyping and Characterization of Bovine and Human Streptococcus agalactiae Isolates. Journal of Clinical Microbiology, 2005, 43, 1177-1186.	3.9	58
53	Pilus distribution among lineages of group b streptococcus: an evolutionary and clinical perspective. BMC Microbiology, 2014, 14, 159.	3.3	58
54	Multilocus Sequence Typing of Streptococcus uberis Provides Sensitive and Epidemiologically Relevant Subtype Information and Reveals Positive Selection in the Virulence Gene pauA. Journal of Clinical Microbiology, 2005, 43, 2407-2417.	3.9	56

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55	Fecal Shedding of Klebsiella pneumoniae by Dairy Cows. Journal of Dairy Science, 2006, 89, 3425-3430.	3.4	54
56	Ribotyping of Streptococcus uberis from a dairy's environment, bovine feces and milk. Veterinary Microbiology, 2005, 109, 257-265.	1.9	53
57	Mastitis-Causing Streptococci Are Important Contributors to Bacterial Counts in Raw Bulk Tank Milk. Journal of Food Protection, 2004, 67, 2644-2650.	1.7	51
58	One hypervirulent clone, sequence type 283, accounts for a large proportion of invasive Streptococcus agalactiae isolated from humans and diseased tilapia in Southeast Asia. PLoS Neglected Tropical Diseases, 2019, 13, e0007421.	3.0	51
59	Use of Molecular Epidemiology in Veterinary Practice. Veterinary Clinics of North America - Food Animal Practice, 2006, 22, 229-261.	1.2	49
60	HumanStreptococcus suisMeningitis in the United States. New England Journal of Medicine, 2006, 354, 1325-1325.	27.0	49
61	Bovine and ovine rumen fluke in Ireland—Prevalence, risk factors and species identity based on passive veterinary surveillance and abattoir findings. Veterinary Parasitology, 2015, 212, 168-174.	1.8	49
62	Association between genotypic diversity and biofilm production in group B Streptococcus. BMC Microbiology, 2016, 16, 86.	3.3	49
63	Genomic analysis of the multi-host pathogen Erysipelothrix rhusiopathiae reveals extensive recombination as well as the existence of three generalist clades with wide geographic distribution. BMC Genomics, 2016, 17, 461.	2.8	49
64	Short communication: Methicillin-resistant Staphylococcus aureus detection in US bulk tank milk. Journal of Dairy Science, 2009, 92, 4988-4991.	3.4	48
65	Mastitomics, the integrated omics of bovine milk in an experimental model of Streptococcus uberis mastitis: 1. High abundance proteins, acute phase proteins and peptidomics. Molecular BioSystems, 2016, 12, 2735-2747.	2.9	47
66	Identification of LukPQ, a novel, equid-adapted leukocidin of Staphylococcus aureus. Scientific Reports, 2017, 7, 40660.	3.3	47
67	Identification of risk factors associated with carriage of resistant Escherichia coli in three culturally diverse ethnic groups in Tanzania: a biological and socioeconomic analysis. Lancet Planetary Health, The, 2018, 2, e489-e497.	11.4	47
68	Genome characterization and population genetic structure of the zoonotic pathogen, Streptococcus canis. BMC Microbiology, 2012, 12, 293.	3.3	45
69	Mastitomics, the integrated omics of bovine milk in an experimental model of Streptococcus uberis mastitis: 2. Label-free relative quantitative proteomics. Molecular BioSystems, 2016, 12, 2748-2761.	2.9	45
70	Use of partial budgeting to determine the economic benefits of antibiotic treatment of chronic subclinical mastitis caused by Streptococcus uberis or Streptococcus dysgalactiae. Journal of Dairy Research, 2005, 72, 75-85.	1.4	44
71	Bacterial Genomics Reveal the Complex Epidemiology of an Emerging Pathogen in Arctic and Boreal Ungulates. Frontiers in Microbiology, 2016, 7, 1759.	3.5	44
72	Technical note: Use of transfer RNA-intergenic spacer PCR combined with capillary electrophoresis to identify coagulase-negative Staphylococcus species originating from bovine milk and teat apices. Journal of Dairy Science, 2009, 92, 3204-3210.	3.4	43

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73	Genomic comparison of virulent and nonâ€virulent <i> <scp>S</scp>treptococcus agalactiae</i> in fish. Journal of Fish Diseases, 2016, 39, 13-29.	1.9	42
74	Molecular Diagnostics Applied to Mastitis Problems on Dairy Farms. Veterinary Clinics of North America - Food Animal Practice, 2012, 28, 565-576.	1.2	40
75	Assessing Genetic Heterogeneity within Bacterial Species Isolated from Gastrointestinal and Environmental Samples: How Many Isolates Does It Take?. Applied and Environmental Microbiology, 2008, 74, 3490-3496.	3.1	39
76	Effect of penethamate hydriodide treatment on bacteriological cure, somatic cell count and milk production of cows and quarters with chronic subclinical Streptococcus uberis or Streptococcus dysgalactiae infection. Journal of Dairy Research, 2003, 70, 387-394.	1.4	37
77	Effect of lactation therapy on Staphylococcus aureus transmission dynamics in two commercial dairy herds. BMC Veterinary Research, 2013, 9, 28.	1.9	36
78	Population Gene Introgression and High Genome Plasticity for the Zoonotic Pathogen Streptococcus agalactiae. Molecular Biology and Evolution, 2019, 36, 2572-2590.	8.9	36
79	Somatic Cell Count During and Between Milkings. Journal of Dairy Science, 2007, 90, 3733-3741.	3.4	35
80	A mathematical model demonstrating indirect and overall effects of lactation therapy targeting subclinical mastitis in dairy herds. Preventive Veterinary Medicine, 2009, 90, 31-42.	1.9	35
81	Host adaptation of bovine Staphylococcus aureus seems associated with bacteriological cure after lactational antimicrobial treatment. Journal of Dairy Science, 2010, 93, 2550-2558.	3.4	35
82	Mastitomics, the integrated omics of bovine milk in an experimental model of Streptococcus uberis mastitis: 3. Untargeted metabolomics. Molecular BioSystems, 2016, 12, 2762-2769.	2.9	35
83	Epidemiological investigation of Streptococcus equi subspecies zooepidemicus involved in clinical mastitis in dairy goats. Journal of Dairy Science, 2009, 92, 943-951.	3.4	32
84	Old Drugs To Treat Resistant Bugs: Methicillin-Resistant Staphylococcus aureus Isolates with <i>mecC</i> Are Susceptible to a Combination of Penicillin and Clavulanic Acid. Antimicrobial Agents and Chemotherapy, 2015, 59, 7396-7404.	3.2	32
85	Cleanliness Scores as Indicator of Klebsiella Exposure in Dairy Cows. Journal of Dairy Science, 2008, 91, 3908-3916.	3.4	31
86	Genotypic and Phenotypic Detection of Macrolide and Lincosamide Resistance in Streptococcus uberis. Journal of Dairy Science, 2007, 90, 5089-5096.	3.4	29
87	Prevalence of <i>Pasteurella multocida</i> and other respiratory pathogens in the nasal tract of Scottish calves. Veterinary Record, 2010, 167, 555-560.	0.3	29
88	Staphylococcus devriesei sp. nov., isolated from teat apices and milk of dairy cows. International Journal of Systematic and Evolutionary Microbiology, 2010, 60, 2739-2744.	1.7	29
89	Macrolide and lincosamide resistance genes of environmental streptococci from bovine milk. Veterinary Microbiology, 2005, 111, 133-138.	1.9	28
90	Incidence and Characterisation of Methicillin-Resistant Staphylococcus aureus (MRSA) from Nasal Colonisation in Participants Attending a Cattle Veterinary Conference in the UK. PLoS ONE, 2013, 8, e68463.	2.5	28

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91	Correlation of hypothetical virulence traits of two Streptococcus uberis strains with the clinical manifestation of bovine mastitis. Veterinary Research, 2015, 46, 123.	3.0	27
92	Prevalence of Liver Fluke (Fasciola hepatica) in Wild Red Deer (Cervus elaphus): Coproantigen ELISA Is a Practicable Alternative to Faecal Egg Counting for Surveillance in Remote Populations. PLoS ONE, 2016, 11, e0162420.	2.5	25
93	Bacteremia in critical care units at Bugando Medical Centre, Mwanza, Tanzania: the role of colonization and contaminated cots and mothers' hands in cross-transmission of multidrug resistant Gram-negative bacteria. Antimicrobial Resistance and Infection Control, 2020, 9, 58.	4.1	25
94	Cross-Infection Between Cats and Cows: Origin and Control of Streptococcus canis Mastitis in a Dairy Herd. Journal of Dairy Science, 2005, 88, 2707-2713.	3.4	24
95	Genome-Wide Diversity and Phylogeography of Mycobacterium avium subsp. paratuberculosis in Canadian Dairy Cattle. PLoS ONE, 2016, 11, e0149017.	2.5	24
96	Gene content differences across strains of Streptococcus uberis identified using oligonucleotide microarray comparative genomic hybridization. Infection, Genetics and Evolution, 2009, 9, 179-188.	2.3	23
97	The integration of molecular tools into veterinary and spatial epidemiology. Spatial and Spatio-temporal Epidemiology, 2011, 2, 159-171.	1.7	23
98	Early host response in the mammary gland after experimental Streptococcus uberis challenge in heifers. Journal of Dairy Science, 2013, 96, 3723-3736.	3.4	23
99	Molecular epidemiology and strain-specific characteristics of Streptococcus agalactiae at the herd and cow level. Journal of Dairy Science, 2015, 98, 6913-6924.	3.4	23
100	Investigating the Meat Pathway as a Source of Human Nontyphoidal <i>Salmonella</i> Bloodstream Infections and Diarrhea in East Africa. Clinical Infectious Diseases, 2021, 73, e1570-e1578.	5.8	23
101	Effect of strain and enviromental conditions on the virulence of Streptococcus agalactiae (Group B) Tj ETQq1 1 G).784314 r 3.5	gBT /Overloc
102	Short Communication: Patterns of Fecal Shedding of Klebsiella by Dairy Cows. Journal of Dairy Science, 2007, 90, 1220-1224.	3.4	22
103	Molecular epidemiology of Pasteurella multocida in dairy and beef calves. Veterinary Microbiology, 2011, 151, 329-335.	1.9	22
104	Streptococcus agalactiae is not always an obligate intramammary pathogen: Molecular epidemiology of GBS from milk, feces and environment in Colombian dairy herds. PLoS ONE, 2018, 13, e0208990.	2.5	22
105	Antibiotic dry cow therapy: where next?. Veterinary Record, 2016, 178, 93-94.	0.3	21
106	Potential group B Streptococcus interspecies transmission between cattle and people in Colombian dairy farms. Scientific Reports, 2019, 9, 14025.	3.3	21
107	Point-of-care tests for bovine clinical mastitis: what do we have and what do we need?. Journal of Dairy Research, 2020, 87, 60-66.	1.4	20
108	Short communication: Molecular epidemiology of Streptococcus agalactiae differs between countries. Journal of Dairy Science, 2017, 100, 9294-9297.	3.4	18

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109	<i>Galleria mellonella</i> as an infection model for the multi-host pathogen <i>Streptococcus agalactiae</i> reflects hypervirulence of strains associated with human invasive disease. Virulence, 2019, 10, 600-609.	4.4	18
110	Draft Genome Sequence of a Nonhemolytic Fish-Pathogenic Streptococcus agalactiae Strain. Journal of Bacteriology, 2012, 194, 6341-6342.	2.2	15
111	Use of on-farm data to guide treatment and control mastitis caused by Streptococcus uberis. Journal of Dairy Science, 2016, 99, 7690-7699.	3.4	15
112	Practical and effective diagnosis of animal anthrax in endemic low-resource settings. PLoS Neglected Tropical Diseases, 2020, 14, e0008655.	3.0	15
113	Composite <i>Fasciola hepatica</i> faecal egg sedimentation test for cattle. Veterinary Record, 2019, 184, 589-589.	0.3	15
114	High-resolution melt analysis for species identification of coagulase-negative staphylococci derived from bovine milk. Diagnostic Microbiology and Infectious Disease, 2013, 75, 227-234.	1.8	14
115	Development and Application of a Prophage Integrase Typing Scheme for Group B Streptococcus. Frontiers in Microbiology, 2020, 11, 1993.	3.5	14
116	A Universal Approach to Molecular Identification of Rumen Fluke Species Across Hosts, Continents, and Sample Types. Frontiers in Veterinary Science, 2020, 7, 605259.	2.2	14
117	Herd level approach to high bulk milk somatic cell count problems in dairy cattle. Veterinary Quarterly, 2013, 33, 82-93.	6.7	13
118	Direct RT-PCR from serum enables fast and cost-effective phylogenetic analysis of bovine viral diarrhoea virus. Journal of Virological Methods, 2013, 190, 1-3.	2.1	13
119	Comparative molecular analysis of ovine and bovine Streptococcus uberis isolates. Journal of Dairy Science, 2013, 96, 962-970.	3.4	12
120	The fall and rise of group B Streptococcus in dairy cattle: reintroduction due to human-to-cattle host jumps?. Microbial Genomics, 2021, 7, .	2.0	12
121	Streptococcus bovimastitidis sp. nov., isolated from a dairy cow with mastitis. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 21-27.	1.7	12
122	One Health Research in Northern Tanzania – Challenges and Progress. The East African Health Research Journal, 2017, 1, 8-18.	0.4	11
123	Comparison of bacteriological culture and PCR for detection of bacteria in ovine milk—Sheep are not small cows. Journal of Dairy Science, 2014, 97, 6326-6333.	3.4	10
124	Experimental infection of rabbits with bovine viral diarrhoea virus by a natural route of exposure. Veterinary Research, 2014, 45, 34.	3.0	10
125	Analysis of bovine viral diarrhoea virus: Biobank and sequence database to support eradication in Scotland. Veterinary Record, 2017, 180, 447-447.	0.3	10
126	Evaluation of PCR primers targeting thegroELgene for the specific detection ofStreptococcus agalactiaein the context of aquaculture. Journal of Applied Microbiology, 2018, 125, 666-674.	3.1	10

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127	Meat Safety in Northern Tanzania: Inspectors' and Slaughter Workers' Risk Perceptions and Management. Frontiers in Veterinary Science, 2020, 7, 309.	2.2	9
128	Meat Safety in Tanzania's Value Chain: Experiences, Explanations and Expectations in Butcheries and Eateries. International Journal of Environmental Research and Public Health, 2020, 17, 2833.	2.6	9
129	Evaluation of molecular methods for the field study of the natural history of Dicrocoelium dendriticum. Veterinary Parasitology, 2017, 235, 100-105.	1.8	8
130	Development and evaluation of a quantitative polymerase chain reaction for aquatic <i>Streptococcus agalactiae</i> based on the <i>groEL</i> gene. Journal of Applied Microbiology, 2020, 129, 63-74.	3.1	8
131	Antimicrobial resistance in ovine bacteria: A sheep in wolf's clothing?. PLoS ONE, 2020, 15, e0238708.	2.5	8
132	Heifer and CNS mastitis. Veterinary Microbiology, 2009, 134, 1-2.	1.9	7
133	Short communication: Comparison of virulence factors in Klebsiella pneumoniae strains associated with multiple or single cases of mastitis. Journal of Dairy Science, 2014, 97, 2213-2218.	3.4	7
134	Pilot study into milk haptoglobin as an indicator of udder health in heifers after calving. Research in Veterinary Science, 2018, 116, 83-87.	1.9	7
135	Uptake of Diagnostic Tests by Livestock Farmers: A Stochastic Game Theory Approach. Frontiers in Veterinary Science, 2020, 7, 36.	2.2	7
136	Prevalence and Sequence-Based Identity of Rumen Fluke in Cattle and Deer in New Caledonia. PLoS ONE, 2016, 11, e0152603.	2.5	7
137	Laboratory-based evaluation of a simplified point-of-care test intended to support treatment decisions in non-severe bovine clinical mastitis. Journal of Dairy Research, 2021, 88, 170-175.	1.4	6
138	Bovine viral diarrhoea virus loses quasispecies diversity rapidly in culture. Microbial Genomics, 2020, 6, .	2.0	6
139	Assessment of the rabbit as a wildlife reservoir of bovine viral diarrhea virus: serological analysis and generation of trans-placentally infected offspring. Frontiers in Microbiology, 2015, 6, 1000.	3.5	5
140	Habitat and host factors associated with liver fluke (Fasciola hepatica) diagnoses in wild red deer (Cervus elaphus) in the Scottish Highlands. Parasites and Vectors, 2019, 12, 535.	2.5	5
141	Food Safety, Health Management, and Biosecurity Characteristics of Poultry Farms in Arusha City, Northern Tanzania, Along a Gradient of Intensification. The East African Health Research Journal, 2018, 2, 168-180.	0.4	5
142	Investigation of extramammary sources of Group B Streptococcus reveals its unusual ecology and epidemiology in camels. PLoS ONE, 2021, 16, e0252973.	2.5	5
143	Population genomics of Bacillus anthracis from an anthrax hyperendemic area reveals transmission processes across spatial scales and unexpected within-host diversity. Microbial Genomics, 2022, 8, .	2.0	5
144	Circulation of <i>Streptococcus agalactiae</i> ST103 in a Free Stall Italian Dairy Farm. Applied and Environmental Microbiology, 2022, 88, e0038322.	3.1	5

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#	Article	IF	CITATIONS
145	Genomic analysis of group B Streptococcus from milk demonstrates the need for improved biosecurity: a cross-sectional study of pastoralist camels in Kenya. BMC Microbiology, 2021, 21, 217.	3.3	3
146	Assessing potential routes of Streptococcus agalactiae transmission between dairy herds using national surveillance, animal movement and molecular typing data. Preventive Veterinary Medicine, 2021, 197, 105501.	1.9	3
147	Wild deer in the United Kingdom are a potential reservoir for the livestock parasite Babesia divergens. Current Research in Parasitology and Vector-borne Diseases, 2021, 1, 100019.	1.9	3
148	Spread of Nontyphoidal <i>Salmonella</i> in the Beef Supply Chain in Northern Tanzania: Sensitivity in a Probabilistic Model Integrating Microbiological Data and Data from Stakeholder Interviews. Risk Analysis, 2022, 42, 989-1006.	2.7	2
149	Routine antibiotic dry cow therapy. Veterinary Record, 2016, 178, 174-174.	0.3	1
150	Food Safety, Health Management, and Biosecurity Characteristics of Poultry Farms in Arusha City, Northern Tanzania, Along a Gradient of Intensification. The East African Health Research Journal, 2018, 2, 168-180.	0.4	1
151	Participatory mapping identifies risk areas and environmental predictors of endemic anthrax in rural Africa. Scientific Reports, 2022, 12, .	3.3	1
152	Practical and effective diagnosis of animal anthrax in endemic low-resource settings. , 2020, 14, e0008655.		0
153	Practical and effective diagnosis of animal anthrax in endemic low-resource settings. , 2020, 14, e0008655.		0
154	Practical and effective diagnosis of animal anthrax in endemic low-resource settings. , 2020, 14, e0008655.		0
155	Practical and effective diagnosis of animal anthrax in endemic low-resource settings. , 2020, 14, e0008655.		0