Louise Matthews

List of Publications by Year
in descending order

90 papers	4,569 citations	117625 34 h-index	106344 65 g-index
91 all docs	91 docs citations	91 times ranked	5171 citing authors

#	Article	IF	Citations
1	Population genomics and geographic dispersal in Chagas disease vectors: Landscape drivers and evidence of possible adaptation to the domestic setting. PLoS Genetics, 2022, 18, e1010019.	3.5	4
2	How public health crises expose systemic, day-to-day health inequalities in low- and-middle income countries: an example from East Africa. Antimicrobial Resistance and Infection Control, 2022, 11, 34.	4.1	8
3	The hospital environment versus carriage: transmission pathways for third-generation cephalosporin-resistant bacteria in blood in neonates in a low-resource country healthcare setting. Scientific Reports, 2022, 12, 8347.	3.3	1
4	Existence of Multiple ESBL Genes among Phenotypically Confirmed ESBL Producing Klebsiella pneumoniae and Escherichia coli Concurrently Isolated from Clinical, Colonization and Contamination Samples from Neonatal Units at Bugando Medical Center, Mwanza, Tanzania. Antibiotics, 2021, 10, 476.	3.7	22
5	Developing practical clinical tools for predicting neonatal mortality at a neonatal intensive care unit in Tanzania. BMC Pediatrics, 2021, 21, 537.	1.7	2
6	Farm-Level Risk Factors of Increased Abortion and Mortality in Domestic Ruminants during the 2010 Rift Valley Fever Outbreak in Central South Africa. Pathogens, 2020, 9, 914.	2.8	2
7	Distemper, extinction, and vaccination of the Amur tiger. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 31954-31962.	7.1	33
8	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
9	Reply to Kloepfer and Gern: Independent studies suggest an arms race between influenza and rhinovirus: What next?. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 6988-6989.	7.1	0
10	Uptake of Diagnostic Tests by Livestock Farmers: A Stochastic Game Theory Approach. Frontiers in Veterinary Science, 2020, 7, 36.	2.2	7
11	Antimicrobial resistant enteric bacteria are widely distributed amongst people, animals and the environment in Tanzania. Nature Communications, 2020, 11, 228.	12.8	69
12	Analysing livestock network data for infectious disease control: an argument for routine data collection in emerging economies. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20180264.	4.0	49
13	Refugia and anthelmintic resistance: Concepts and challenges. International Journal for Parasitology: Drugs and Drug Resistance, 2019, 10, 51-57.	3.4	65
14	Divergent Allele Advantage Provides a Quantitative Model for Maintaining Alleles with a Wide Range of Intrinsic Merits. Genetics, 2019, 212, 553-564.	2.9	12
15	Virus–virus interactions impact the population dynamics of influenza and the common cold. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 27142-27150.	7.1	338
16	Estimation of temporal covariances in pathogen dynamics using Bayesian multivariate autoregressive models. PLoS Computational Biology, 2019, 15, e1007492.	3.2	9
17	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
18	Complex responses to movement-based disease control: when livestock trading helps. Journal of the Royal Society Interface, 2017, 14, 20160531.	3.4	2

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19	Antimicrobial Use and Veterinary Care among Agro-Pastoralists in Northern Tanzania. PLoS ONE, 2017, 12, e0170328.	2.5	80
20	Multistrain models predict sequential multidrug treatment strategies to result in less antimicrobial resistance than combination treatment. BMC Microbiology, 2016, 16, 118.	3.3	4
21	Modeling the growth dynamics of multiple Escherichia coli strains in the pig intestine following intramuscular ampicillin treatment. BMC Microbiology, 2016, 16, 205.	3.3	14
22	Detection of Rare Antimicrobial Resistance Profiles by Active and Passive Surveillance Approaches. PLoS ONE, 2016, 11, e0158515.	2.5	19
23	Support vector machine applied to predict the zoonotic potential of E. coli O157 cattle isolates. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 11312-11317.	7.1	55
24	Multitrait indices to predict worm length and number in sheep with natural, mixed predominantly Teladorsagia circumcincta infection. Parasitology, 2015, 142, 773-782.	1.5	5
25	A Bayesian generalized random regression model for estimating heritability using overdispersed count data. Genetics Selection Evolution, 2015, 47, 51.	3.0	10
26	Pharmacodynamic modelling of in vitro activity of tetracycline against a representative, naturally occurring population of porcine Escherichia coli. Acta Veterinaria Scandinavica, 2015, 57, 79.	1.6	17
27	Canine distemper virus as a threat to wild tigers in Russia and across their range. Integrative Zoology, 2015, 10, 329-343.	2.6	47
28	An analysis of cattle farmers' perceptions of drivers and barriers to on-farm control of Escherichia coli O157. Epidemiology and Infection, 2015, 143, 2355-2366.	2.1	20
29	Pharmacokinetic-Pharmacodynamic Model To Evaluate Intramuscular Tetracycline Treatment Protocols To Prevent Antimicrobial Resistance in Pigs. Antimicrobial Agents and Chemotherapy, 2015, 59, 1634-1642.	3.2	21
30	The control of sea lice in Atlantic salmon by selective breeding. Journal of the Royal Society Interface, 2015, 12, 20150574.	3.4	61
31	An explicit immunogenetic model of gastrointestinal nematode infection in sheep. Journal of the Royal Society Interface, 2014, 11, 20140416.	3.4	18
32	E. coli O157 on Scottish cattle farms: Evidence of local spread and persistence using repeat cross-sectional data. BMC Veterinary Research, 2014, 10, 95.	1.9	17
33	A metapopulation model for highly pathogenic avian influenza: implications for compartmentalization as a control measure. Epidemiology and Infection, 2014, 142, 1813-1825.	2.1	8
34	The transfer of IgA from mucus to plasma and the implications for diagnosis and control of nematode infections. Parasitology, 2014, 141, 875-879.	1.5	19
35	Estimating the Potential Impact of Canine Distemper Virus on the Amur Tiger Population (Panthera) Tj ETQq1 1 0.784314 rgBT /Overl	2.5	48
36	Implications of within-farm transmission for network dynamics: Consequences for the spread of avian influenza. Epidemics, 2013, 5, 67-76.	3.0	20

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37	Predicting the public health benefit of vaccinating cattle against *Escherichia* *coli* O157. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 16265-16270.	7.1	106
38	Identifying the seasonal origins of human campylobacteriosis. Epidemiology and Infection, 2013, 141, 1267-1275.	2.1	36
39	Do antibiotic residues in soils play a role in amplification and transmission of antibiotic resistant bacteria in cattle populations?. Frontiers in Microbiology, 2013, 4, 193.	3.5	37
40	The diversity of antimicrobial resistance is different in *Salmonella* Typhimurium DT104 from co-located animals and humans. Proceedings of the Royal Society B: Biological Sciences, 2012, 279, 2924-2925.	2.6	2
41	An ecological approach to assessing the epidemiology of antimicrobial resistance in animal and human populations. Proceedings of the Royal Society B: Biological Sciences, 2012, 279, 1630-1639.	2.6	60
42	Using sequence data to identify alternative routes and risk of infection: a case-study of campylobacter in Scotland. BMC Infectious Diseases, 2012, 12, 80.	2.9	24
43	Pathogenic Potential to Humans of Bovine *Escherichia coli* O26, Scotland. Emerging Infectious Diseases, 2012, 18, 439-448.	4.3	38
44	Quantifying the sources of variability in equine faecal egg counts: Implications for improving the utility of the method. Veterinary Parasitology, 2012, 188, 120-126.	1.8	41
45	Selective forces shaping diversity in the class I region of the major histocompatibility complex in dairy cattle. Animal Genetics, 2012, 43, 239-249.	1.7	29
46	An evolutionary perspective on gastrointestinal nematodes of sheep. Journal of Helminthology, 2011, 85, 113-120.	1.0	19
47	A mechanistic model of developing immunity to *Teladorsagia circumcincta* infection in lambs. Parasitology, 2011, 138, 322-332.	1.5	26
48	Generating social network data using partially described networks: an example informing avian influenza control in the British poultry industry. BMC Veterinary Research, 2011, 7, 66.	1.9	11
49	From phenotype to genotype: a Bayesian solution. Proceedings of the Royal Society B: Biological Sciences, 2011, 278, 1434-1440.	2.6	4
50	The Prevalences of Salmonella Genomic Island 1 Variants in Human and Animal Salmonella Typhimurium DT104 Are Distinguishable Using a Bayesian Approach. PLoS ONE, 2011, 6, e27220.	2.5	12
51	Putative household outbreaks of campylobacteriosis typically comprise single MLST genotypes. Epidemiology and Infection, 2010, 138, 1744-1747.	2.1	13
52	Comparison of three alternative methods for analysis of equine Faecal Egg Count Reduction Test data. Preventive Veterinary Medicine, 2010, 93, 316-323.	1.9	34
53	Geographic determinants of reported human Campylobacter infections in Scotland. BMC Public Health, 2010, 10, 423.	2.9	27
54	On the generality of stability–complexity relationships in Lotka–Volterra ecosystems. Journal of Theoretical Biology, 2010, 267, 243-251.	1.7	13

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55	Associations between the Presence of Virulence Determinants and the Epidemiology and Ecology of Zoonotic *Escherichia coli*. Applied and Environmental Microbiology, 2010, 76, 8110-8116.	3.1	13
56	Sequence-Based Prediction for Vaccine Strain Selection and Identification of Antigenic Variability in Foot-and-Mouth Disease Virus. PLoS Computational Biology, 2010, 6, e1001027.	3.2	63
57	Effect of the initial dose of foot-and-mouth disease virus on the early viral dynamics within pigs. Journal of the Royal Society Interface, 2009, 6, 835-847.	3.4	23
58	Temporal and spatial patterns of bovine Escherichia coli O157 prevalence and comparison of temporal changes in the patterns of phage types associated with bovine shedding and human E. coliO157 cases in Scotland between 1998-2000 and 2002-2004. BMC Microbiology, 2009, 9, 276.	3.3	37
59	Genetic dissection of MHC-associated susceptibility to Lepeophtheirus salmonis in Atlantic salmon. BMC Genetics, 2009, 10, 20.	2.7	30
60	Exploiting strain diversity to expose transmission heterogeneities and predict the impact of targeting supershedding. Epidemics, 2009, 1, 221-229.	3.0	20
61	Can parasites drive population cycles in mountain hares?. Proceedings of the Royal Society B: Biological Sciences, 2009, 276, 1611-1617.	2.6	11
62	Super-shedding and the link between human infection and livestock carriage of Escherichia coli O157. Nature Reviews Microbiology, 2008, 6, 904-912.	28.6	300
63	The distribution of the pathogenic nematode *Nematodirus battus* in lambs is zero-inflated. Parasitology, 2008, 135, 1225-1235.	1.5	34
64	Risk Factors for the Presence of High-Level Shedders of Escherichia coli O157 on Scottish Farms. Journal of Clinical Microbiology, 2007, 45, 1594-1603.	3.9	137
65	Modelling the epidemiology and transmission of Verocytotoxin-producingEscherichia coliserogroups O26 and O103 in two different calf cohorts. Epidemiology and Infection, 2007, 135, 1316-1323.	2.1	7
66	Introduction. Cross-scale influences on epidemiological dynamics: from genes to ecosystems. Journal of the Royal Society Interface, 2007, 4, 763-765.	3.4	15
67	The dynamic influence of genetic variation on the susceptibility of sheep to gastrointestinal nematode infection. Journal of the Royal Society Interface, 2007, 4, 767-776.	3.4	37
68	Metapopulation dynamics of Escherichia coli O157 in cattle: an exploratory model. Journal of the Royal Society Interface, 2007, 4, 917-924.	3.4	13
69	Genetic disorders and the quest for candidate genes: Hypotheses worth testing. Veterinary Journal, 2007, 174, 217-218.	1.7	0
70	Geographic risk factors for inter-river dispersal of Gyrodactylus salaris in fjord systems in Norway. Diseases of Aquatic Organisms, 2007, 74, 139-149.	1.0	22
71	Super-shedding cattle and the transmission dynamics ofEscherichia coliO157. Epidemiology and Infection, 2006, 134, 131-142.	2.1	158
72	Comparative evidence for a link between Peyer's patch development and susceptibility to transmissible spongiform encephalopathies. BMC Infectious Diseases, 2006, 6, 5.	2.9	49

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73	Low-coverage vaccination strategies for the conservation of endangered species. Nature, 2006, 443, 692-695.	27.8	157
74	Modelling the spread of scrapie in a sheep flock: evidence for increased transmission during lambing seasons. Archives of Virology, 2006, 151, 735-751.	2.1	37
75	Heterogeneous shedding of Escherichia coli O157 in cattle and its implications for control. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 547-552.	7.1	235
76	Modelling the epidemiology of Verocytotoxin-producing Escherichia coli serogroups in young calves. Epidemiology and Infection, 2005, 133, 449-458.	2.1	12
77	New approaches to quantifying the spread of infection. Nature Reviews Microbiology, 2005, 3, 529-536.	28.6	66
78	Competitive suppression in mixed-clone parasite cultures. Biology Letters, 2005, 1, 108-111.	2.3	3
79	Epidemiological implications of the contact network structure for cattle farms and the 20–80 rule. Biology Letters, 2005, 1, 350-352.	2.3	90
80	Genotype-level variation in lifetime breeding success, litter size and survival of sheep in scrapie-affected flocks. Journal of General Virology, 2005, 86, 1229-1238.	2.9	15
81	Topndash;down or bottom–up regulation of intra–host blood–stage malaria: do malaria parasites most resemble the dynamics of prey or predator?. Proceedings of the Royal Society B: Biological Sciences, 2003, 270, 289-298.	2.6	48
82	Neighbourhood control policies and the spread of infectious diseases. Proceedings of the Royal Society B: Biological Sciences, 2003, 270, 1659-1666.	2.6	39
83	The construction and analysis of epidemic trees with reference to the 2001 UK foot–and–mouth outbreak. Proceedings of the Royal Society B: Biological Sciences, 2003, 270, 121-127.	2.6	146
84	Comparative epidemiology of scrapie outbreaks in individual sheep flocks. Epidemiology and Infection, 2002, 128, 513-521.	2.1	26
85	A centuries-long epidemic of scrapie in British sheep?. Trends in Microbiology, 2001, 9, 67-70.	7.7	36
86	Population dynamics of a scrapie outbreak. Archives of Virology, 2001, 146, 1173-1186.	2.1	32
87	Foot-and-mouth disease under control in the UK. Nature, 2001, 411, 258-259.	27.8	125
88	Dynamics of the 2001 UK Foot and Mouth Epidemic: Stochastic Dispersal in a Heterogeneous Landscape. Science, 2001, 294, 813-817.	12.6	765
89	Population dynamics of scrapie in a sheep flock. Philosophical Transactions of the Royal Society B: Biological Sciences, 1999, 354, 751-756.	4.0	26
90	Patchiness in plankton populations. Dynamical Systems, 1997, 12, 39-59.	0.7	32