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	Dynamics of the 2001 UK Foot and Mouth Epidemic: Stochastic Dispersal in a Heterogeneous Landscape. Science, 2001, 294, 813-817.	12.6	765
2	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
3	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
4	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
5	Super-shedding cattle and the transmission dynamics ofEscherichia coliO157. Epidemiology and Infection, 2006, 134, 131-142.	2.1	158
6	Low-coverage vaccination strategies for the conservation of endangered species. Nature, 2006, 443, 692-695.	27.8	157
7	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
8	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
9	Foot-and-mouth disease under control in the UK. Nature, 2001, 411, 258-259.	27.8	125
10	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
11	Epidemiological implications of the contact network structure for cattle farms and the 20–80 rule. Biology Letters, 2005, 1, 350-352.	2.3	90
12	Antimicrobial Use and Veterinary Care among Agro-Pastoralists in Northern Tanzania. PLoS ONE, 2017, 12, e0170328.	2.5	80
13	Antimicrobial resistant enteric bacteria are widely distributed amongst people, animals and the environment in Tanzania. Nature Communications, 2020, 11, 228.	12.8	69
14	New approaches to quantifying the spread of infection. Nature Reviews Microbiology, 2005, 3, 529-536.	28.6	66
15	Refugia and anthelmintic resistance: Concepts and challenges. International Journal for Parasitology: Drugs and Drug Resistance, 2019, 10, 51-57.	3.4	65
16	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
17	The control of sea lice in Atlantic salmon by selective breeding. Journal of the Royal Society Interface, 2015, 12, 20150574.	3.4	61
18	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

#	Article	IF	Citations
19	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
20	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
21	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
22	Topndash;down or bottomâ€"up regulation of intraâ€"host bloodâ€"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
23	Estimating the Potential Impact of Canine Distemper Virus on the Amur Tiger Population (Panthera) Tj ETQq1 1 0.784314 rgBT /Overlo	2.5	48
24	Canine distemper virus as a threat to wild tigers in Russia and across their range. Integrative Zoology, 2015, 10, 329-343.	2.6	47
25	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
26	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
27	Neighbourhood control policies and the spread of infectious diseases. Proceedings of the Royal Society B: Biological Sciences, 2003, 270, 1659-1666.	2.6	39
28	Pathogenic Potential to Humans of Bovine Escherichia coli O26, Scotland. Emerging Infectious Diseases, 2012, 18, 439-448.	4.3	38
29	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
30	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
31	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. coli O157 cases in Scotland between 1998-2000 and 2002-2004. BMC Microbiology, 2009, 9, 276.	3.3	37
32	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
33	A centuries-long epidemic of scrapie in British sheep?. Trends in Microbiology, 2001, 9, 67-70.	7.7	36
34	Identifying the seasonal origins of human campylobacteriosis. Epidemiology and Infection, 2013, 141, 1267-1275.	2.1	36
35	The distribution of the pathogenic nematode Nematodirus battus in lambs is zero-inflated. Parasitology, 2008, 135, 1225-1235.	1.5	34
36	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

#	Article	IF	Citations
37	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
38	Patchiness in plankton populations. Dynamical Systems, 1997, 12, 39-59.	0.7	32
39	Population dynamics of a scrapie outbreak. Archives of Virology, 2001, 146, 1173-1186.	2.1	32
40	Genetic dissection of MHC-associated susceptibility to Lepeophtheirus salmonis in Atlantic salmon. BMC Genetics, 2009, 10, 20.	2.7	30
41	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
42	Geographic determinants of reported human Campylobacter infections in Scotland. BMC Public Health, 2010, 10, 423.	2.9	27
43	Population dynamics of scrapie in a sheep flock. Philosophical Transactions of the Royal Society B: Biological Sciences, 1999, 354, 751-756.	4.0	26
44	Comparative epidemiology of scrapie outbreaks in individual sheep flocks. Epidemiology and Infection, 2002, 128, 513-521.	2.1	26
45	A mechanistic model of developing immunity to *Teladorsagia circumcincta* infection in lambs. Parasitology, 2011, 138, 322-332.	1.5	26
46	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
47	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
48	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
49	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
50	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
51	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
52	Exploiting strain diversity to expose transmission heterogeneities and predict the impact of targeting supershedding. Epidemics, 2009, 1, 221-229.	3.0	20
53	Implications of within-farm transmission for network dynamics: Consequences for the spread of avian influenza. Epidemics, 2013, 5, 67-76.	3.0	20
54	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

#	Article	IF	Citations
55	An evolutionary perspective on gastrointestinal nematodes of sheep. Journal of Helminthology, 2011, 85, 113-120.	1.0	19
56	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
57	Detection of Rare Antimicrobial Resistance Profiles by Active and Passive Surveillance Approaches. PLoS ONE, 2016, 11, e0158515.	2.5	19
58	An explicit immunogenetic model of gastrointestinal nematode infection in sheep. Journal of the Royal Society Interface, 2014, 11, 20140416.	3.4	18
59	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
60	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
61	Introduction. Cross-scale influences on epidemiological dynamics: from genes to ecosystems. Journal of the Royal Society Interface, 2007, 4, 763-765.	3.4	15
62	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
63	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
64	Metapopulation dynamics of Escherichia coli O157 in cattle: an exploratory model. Journal of the Royal Society Interface, 2007, 4, 917-924.	3.4	13
65	Putative household outbreaks of campylobacteriosis typically comprise single MLST genotypes. Epidemiology and Infection, 2010, 138, 1744-1747.	2.1	13
66	On the generality of stability–complexity relationships in Lotka–Volterra ecosystems. Journal of Theoretical Biology, 2010, 267, 243-251.	1.7	13
67	Associations between the Presence of Virulence Determinants and the Epidemiology and Ecology of Zoonotic <i>Escherichia coli</i>. Applied and Environmental Microbiology, 2010, 76, 8110-8116.	3.1	13
68	Modelling the epidemiology of Verocytotoxin-producing Escherichia coli serogroups in young calves. Epidemiology and Infection, 2005, 133, 449-458.	2.1	12
69	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
70	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
71	Can parasites drive population cycles in mountain hares?. Proceedings of the Royal Society B: Biological Sciences, 2009, 276, 1611-1617.	2.6	11
72	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

#	Article	IF	Citations
73	A Bayesian generalized random regression model for estimating heritability using overdispersed count data. Genetics Selection Evolution, 2015, 47, 51.	3.0	10
74	Estimation of temporal covariances in pathogen dynamics using Bayesian multivariate autoregressive models. PLoS Computational Biology, 2019, 15, e1007492.	3.2	9
75	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
76	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
77	Modelling the epidemiology and transmission of Verocytotoxin-producing Escherichia coli serogroups O26 and O103 in two different calf cohorts. Epidemiology and Infection, 2007, 135, 1316-1323.	2.1	7
78	Uptake of Diagnostic Tests by Livestock Farmers: A Stochastic Game Theory Approach. Frontiers in Veterinary Science, 2020, 7, 36.	2.2	7
79	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
80	From phenotype to genotype: a Bayesian solution. Proceedings of the Royal Society B: Biological Sciences, 2011, 278, 1434-1440.	2.6	4
81	Multistrain models predict sequential multidrug treatment strategies to result in less antimicrobial resistance than combination treatment. BMC Microbiology, 2016, 16, 118.	3.3	4
82	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
83	Competitive suppression in mixed-clone parasite cultures. Biology Letters, 2005, 1, 108-111.	2.3	3
84	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
85	Complex responses to movement-based disease control: when livestock trading helps. Journal of the Royal Society Interface, 2017, 14, 20160531.	3.4	2
86	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
87	Developing practical clinical tools for predicting neonatal mortality at a neonatal intensive care unit in Tanzania. BMC Pediatrics, 2021, 21, 537.	1.7	2
88	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
89	Genetic disorders and the quest for candidate genes: Hypotheses worth testing. Veterinary Journal, 2007, 174, 217-218.	1.7	0
90	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