Claire Jenkins

List of Publications by Year in descending order

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94433 138484 4,102 103 37 58 citations h-index g-index papers 105 105 105 3207 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Identification of <i>Salmonella</i> for public health surveillance using whole genome sequencing. PeerJ, 2016, 4, e1752.	2.0	236
2	Intercontinental dissemination of azithromycin-resistant shigellosis through sexual transmission: a cross-sectional study. Lancet Infectious Diseases, The, 2015, 15, 913-921.	9.1	204
3	Whole-Genome Sequencing for National Surveillance of Shiga Toxin–Producing∢i>Escherichia coli∢/i>O157. Clinical Infectious Diseases, 2015, 61, 305-312.	5.8	181
4	SnapperDB: a database solution for routine sequencing analysis of bacterial isolates. Bioinformatics, 2018, 34, 3028-3029.	4.1	164
5	Prediction of Phenotypic Antimicrobial Resistance Profiles From Whole Genome Sequences of Non-typhoidal Salmonella enterica. Frontiers in Microbiology, 2018, 9, 592.	3.5	139
6	Horizontal antimicrobial resistance transfer drives epidemics of multiple Shigella species. Nature Communications, 2018, 9, 1462.	12.8	121
7	Enterohemorrhagic Escherichia coli O26:H11/Hâ^': A New Virulent Clone Emerges in Europe. Clinical Infectious Diseases, 2013, 56, 1373-1381.	5.8	118
8	Pathogenicity assessment of Shiga toxinâ€producing Escherichia coli (STEC) and the public health risk posed by contamination of food with STEC. EFSA Journal, 2020, 18, e05967.	1.8	111
9	The epidemiology, microbiology and clinical impact of Shiga toxin-producing <i>Escherichia coli</i> in England, 2009–2012. Epidemiology and Infection, 2015, 143, 3475-3487.	2.1	110
10	Applying phylogenomics to understand the emergence of Shiga-toxin-producing Escherichia coli O157:H7 strains causing severe human disease in the UK. Microbial Genomics, 2015, 1, e000029.	2.0	105
11	Identification of Escherichia coli and Shigella Species from Whole-Genome Sequences. Journal of Clinical Microbiology, 2017, 55, 616-623.	3.9	103
12	Temporal Shedding Patterns and Virulence Factors of Escherichia coli Serogroups O26, O103, O111, O145, and O157 in a Cohort of Beef Calves and Their Dams. Applied and Environmental Microbiology, 2004, 70, 1708-1716.	3.1	85
13	Rifampicin Resistance in Tuberculosis Outbreak, London, England. Emerging Infectious Diseases, 2005, 11, 912-920.	4.3	83
14	Intensified shigellosis epidemic associated with sexual transmission in men who have sex with men - Shigella flexneri and S. sonnei in England, 2004 to end of February 2015. Eurosurveillance, 2015, 20, .	7.0	77
15	Public Health Investigation of Two Outbreaks of Shiga Toxin-Producing Escherichia coli O157 Associated with Consumption of Watercress. Applied and Environmental Microbiology, 2015, 81, 3946-3952.	3.1	68
16	Insight into Shiga toxin genes encoded by <i>Escherichia coli</i> O157 from whole genome sequencing. PeerJ, 2015, 3, e739.	2.0	66
17	Genomic epidemiology of Shigella in the United Kingdom shows transmission of pathogen sublineages and determinants of antimicrobial resistance. Scientific Reports, 2018, 8, 7389.	3.3	65
18	Shiga Toxin–Producing <i>Escherichia coli</i> O157, England and Wales, 1983–2012. Emerging Infectious Diseases, 2016, 22, 590-597.	4.3	61

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19	Comparison of phenotypic and WGS-derived antimicrobial resistance profiles of Shigella sonnei isolated from cases of diarrhoeal disease in England and Wales, 2015. Journal of Antimicrobial Chemotherapy, 2017, 72, 2496-2502.	3.0	61
20	Epidemiology and microbiology of Shiga toxin-producing Escherichia coli other than serogroup O157 in England, 2009–2013. Journal of Medical Microbiology, 2014, 63, 1181-1188.	1.8	59
21	Whole Genome Sequencing for Public Health Surveillance of Shiga Toxin-Producing Escherichia coli Other than Serogroup O157. Frontiers in Microbiology, 2016, 7, 258.	3.5	59
22	Disease severity of Shiga toxin-producing <i>E. coli </i> O157 and factors influencing the development of typical haemolytic uraemic syndrome: a retrospective cohort study, 2009–2012. BMJ Open, 2016, 6, e009933.	1.9	56
23	ESBL-Producing and Macrolide-Resistant <i>Shigella sonnei</i> li>Infections among Men Who Have Sex with Men, England, 2015. Emerging Infectious Diseases, 2016, 22, 1948-1952.	4.3	55
24	An outbreak of Shiga toxin-producing <i>Escherichia coli</i> O157:H7 associated with contaminated salad leaves: epidemiological, genomic and food trace back investigations. Epidemiology and Infection, 2018, 146, 187-196.	2.1	54
25	Assessment of a real-time PCR for the detection and characterization of verocytotoxigenic Escherichia coli. Journal of Medical Microbiology, 2012, 61, 1082-1085.	1.8	52
26	Antimicrobial resistance in Shiga toxin-producing <i>Escherichia coli</i> serogroups O157 and O26 isolated from human cases of diarrhoeal disease in England, 2015. Journal of Antimicrobial Chemotherapy, 2017, 72, 145-152.	3.0	51
27	Whole genome sequencing reveals an outbreak of Salmonella Enteritidis associated with reptile feeder mice in the United Kingdom, 2012-2015. Food Microbiology, 2018, 71, 32-38.	4.2	51
28	Whole genome sequencing improved case ascertainment in an outbreak of Shiga toxin-producing <i>Escherichia coli</i> O157 associated with raw drinking milk. Epidemiology and Infection, 2016, 144, 2812-2823.	2.1	49
29	Outbreaks of Shiga Toxin–Producing Escherichia coli Linked to Sprouted Seeds, Salad, and Leafy Greens: A Systematic Review. Journal of Food Protection, 2019, 82, 1950-1958.	1.7	46
30	Evolution of a zoonotic pathogen: investigating prophage diversity in enterohaemorrhagic Escherichia coli O157 by long-read sequencing. Microbial Genomics, 2016, 2, e000096.	2.0	46
31	Use of Whole-Genus Genome Sequence Data To Develop a Multilocus Sequence Typing Tool That Accurately Identifies Yersinia Isolates to the Species and Subspecies Levels. Journal of Clinical Microbiology, 2015, 53, 35-42.	3.9	45
32	Persistent Transmission of Shigellosis in England Is Associated with a Recently Emerged Multidrug-Resistant Strain of Shigella sonnei. Journal of Clinical Microbiology, 2020, 58, .	3.9	45
33	Use of whole-genome sequencing for the public health surveillance of Shigella sonnei in England and Wales, 2015. Journal of Medical Microbiology, 2016, 65, 882-884.	1.8	45
34	Short-term evolution of Shiga toxin-producing Escherichia coli O157:H7 between two food-borne outbreaks. Microbial Genomics, 2016, 2, e000084.	2.0	45
35	The serodiagnosis of infections caused by Verocytotoxinâ€producingEscherichia coli. Journal of Applied Microbiology, 1999, 86, 731-740.	3.1	43
36	Impact of whole genome sequencing on the investigation of food-borne outbreaks of Shiga toxin-producing Escherichia coli serogroup O157:H7, England, 2013 to 2017. Eurosurveillance, 2019, 24, .	7.0	43

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37	Comparison of single-nucleotide variants identified by Illumina and Oxford Nanopore technologies in the context of a potential outbreak of Shiga toxin–producing Escherichia coli. GigaScience, 2019, 8, .	6.4	42
38	Distribution of espl among clinical enterohaemorrhagic and enteropathogenic Escherichia coli isolates. Journal of Medical Microbiology, 2004, 53, 1145-1149.	1.8	41
39	Comparison of phenotypic and WGS-derived antimicrobial resistance profiles of enteroaggregative Escherichia coli isolated from cases of diarrhoeal disease in England, 2015–16. Journal of Antimicrobial Chemotherapy, 2017, 72, 3288-3297.	3.0	38
40	An assessment of the microbiological quality and safety of raw drinking milk on retail sale in England. Journal of Applied Microbiology, 2018, 124, 535-546.	3.1	37
41	The utility and public health implications of PCR and whole genome sequencing for the detection and investigation of an outbreak of Shiga toxin-producingEscherichia coliserogroup O26:H11. Epidemiology and Infection, 2015, 143, 1672-1680.	2.1	34
42	Association between Shiga Toxin–Producing <i>Escherichia coli</i> O157:H7 <i>stx</i> Gene Subtype and Disease Severity, England, 2009–2019. Emerging Infectious Diseases, 2020, 26, 2394-2400.	4.3	34
43	Identification of verocytotoxin-producing Escherichia coli O117:H7 in men who have sex with men, England, November 2013 to August 2014. Eurosurveillance, 2014, 19, .	7.0	33
44	Escherichia coli serogroup O26 ? a new look at an old adversary. Journal of Applied Microbiology, 2007, 104, 070717025310002-???.	3.1	32
45	Highly Pathogenic Clone of Shiga Toxin–Producing <i>Escherichia coli</i> O157:H7, England and Wales. Emerging Infectious Diseases, 2018, 24, 2303-2308.	4.3	32
46	A paradigm for the molecular identification of Mycobacterium species in a routine diagnostic laboratory. Journal of Medical Microbiology, 2007, 56, 598-602.	1.8	31
47	Outbreak of Shiga toxin-producing Escherichia coli O157:H7 linked to raw drinking milk resolved by rapid application of advanced pathogen characterisation methods, England, August to October 2017. Eurosurveillance, 2019, 24, .	7.0	30
48	Whole-Genome Sequencing for National Surveillance of Shigella flexneri. Frontiers in Microbiology, 2017, 8, 1700.	3.5	29
49	Association of putative pathogenicity genes with adherence characteristics and fimbrial genotypes in typical enteroaggregative Escherichia coli from patients with and without diarrhoea in the United Kingdom. European Journal of Clinical Microbiology and Infectious Diseases, 2007, 26, 901-906.	2.9	28
50	Farm-to-fork investigation of an outbreak of Shiga toxin-producing Escherichia coli O157. Microbial Genomics, 2018, 4, .	2.0	27
51	Outbreak of Shiga toxin-producing E. coli O157 associated with consumption of watercress, United Kingdom, August to September 2013. Eurosurveillance, 2013, 18, .	7.0	26
52	Evaluation of Whole-Genome Sequencing for Identification and Typing of Vibrio cholerae. Journal of Clinical Microbiology, 2018, 56, .	3.9	25
53	Comparison of Shiga toxin-encoding bacteriophages in highly pathogenic strains of Shiga toxin-producing Escherichia coli O157:H7 in the UK. Microbial Genomics, 2020, 6, .	2.0	25
54	Evolutionary Context of Non–Sorbitol-Fermenting Shiga Toxin–Producing∢i>Escherichia coli∢/i>O55:H7. Emerging Infectious Diseases, 2017, 23, 1966-1973.	4.3	24

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55	Investigation of a national outbreak of STEC <i>Escherichia coli</i> O157 using online consumer panel control methods: Great Britain, October 2014. Epidemiology and Infection, 2017, 145, 864-871.	2.1	23
56	An outbreak of Shiga toxin-producing <i>Escherichia coli</i> serogroup O157 linked to a lamb-feeding event. Epidemiology and Infection, 2016, 144, 2494-2500.	2.1	21
57	Recurrent seasonal outbreak of an emerging serotype of Shiga toxin-producing Escherichia coli (STEC) Tj ETQq1	1 0.78431 7.0	4 rgBT /Ove
58	Serotypes, intimin subtypes, and antimicrobial resistance patterns of atypical enteropathogenic Escherichia coli isolated in England from 1993 to 1996. European Journal of Clinical Microbiology and Infectious Diseases, 2006, 25, 19-24.	2.9	20
59	Whole Genome Sequencing of an Unusual Serotype of Shiga Toxin–producingEscherichia coli. Emerging Infectious Diseases, 2013, 19, 1302-1304.	4.3	20
60	Epidemiological and Microbiological Investigation of an Outbreak of Severe Disease from Shiga Toxin–Producing Escherichia coli O157 Infection Associated with Consumption of a Slaw Garnish. Journal of Food Protection, 2016, 79, 1161-1168.	1.7	20
61	The emerging importance of Shiga toxin-producing Escherichia coli other than serogroup O157 in England. Journal of Medical Microbiology, 2021, 70, .	1.8	20
62	Identification and typing of Yersinia enterocolitica and Yersinia pseudotuberculosis isolated from human clinical specimens in England between 2004 and 2018. Journal of Medical Microbiology, 2019, 68, 538-548.	1.8	20
63	Evaluation of chromogenic selective agar (CHROMagar STEC) for the direct detection of Shiga toxin-producing Escherichia coli from faecal specimens. Journal of Medical Microbiology, 2020, 69, 487-491.	1.8	20
64	Evidence for re-infection and persistent carriage of Shigella species in adult males reporting domestically acquired infection in England. Clinical Microbiology and Infection, 2021, 27, 126.e7-126.e13.	6.0	18
65	Enhanced heterogeneity of rpoB in Mycobacterium tuberculosis found at low pH. Journal of Antimicrobial Chemotherapy, 2009, 63, 1118-1120.	3.0	16
66	Use of whole-genome sequencing to identify clusters of Shigella flexneri associated with sexual transmission in men who have sex with men in England: a validation study using linked behavioural data. Microbial Genomics, 2019, 5, .	2.0	16
67	A spatial and temporal analysis of risk factors associated with sporadic Shiga toxin-producing <i>Escherichia coli</i> O157 infection in England between 2009 and 2015. Epidemiology and Infection, 2018, 146, 1928-1939.	2.1	15
68	The epidemiology of Shiga toxin-producing Escherichia coli infections in the South East of England: November 2013–March 2017 and significance for clinical and public health. Journal of Medical Microbiology, 2019, 68, 930-939.	1.8	15
69	Shiga toxin-producing Escherichia coli haemolytic uraemic syndrome (STEC-HUS): diagnosis, surveillance and public-health management in England. Journal of Medical Microbiology, 2020, 69, 1034-1036.	1.8	15
70	Phylogenetic structure of Shiga toxin-producing Escherichia coli O157:H7 from sub-lineage to SNPs. Microbial Genomics, 2021, 7, .	2.0	14
71	First use of whole-genome sequencing to investigate a cluster of Yersinia enterocolitica, Liverpool, United Kingdom, 2017. Journal of Medical Microbiology, 2018, 67, 1747-1752.	1.8	14
72	Antimicrobial resistance in Shiga toxin-producing Escherichia coli other than serotype O157 : H7 in England, 2014–2016. Journal of Medical Microbiology, 2020, 69, 379-386.	1.8	14

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73	Emergence of novel strains of Shigella flexneri associated with sexual transmission in adult men in England, 2019–2020. Journal of Medical Microbiology, 2021, 70, .	1.8	14
74	Antimicrobial resistance profiles of diarrhoeagenic Escherichia coli isolated from travellers returning to the UK, 2015–2017. Journal of Medical Microbiology, 2020, 69, 932-943.	1.8	13
75	The epidemiology of Shiga toxin-producing <i>Escherichia coli</i> serogroup O157 in England, 2009–2019. Epidemiology and Infection, 2022, 150, e52.	2.1	13
76	Investigation into a national outbreak of STEC O157:H7 associated with frozen beef burgers, UK, 2017. Epidemiology and Infection, 2020, 148, e215.	2.1	12
77	Rifampicin resistance in tuberculosis outbreak, London, England. Emerging Infectious Diseases, 2005, 11, 931-4.	4.3	12
78	Large outbreak of multiple gastrointestinal pathogens associated with fresh curry leaves in North East England, 2013. Epidemiology and Infection, 2018, 146, 1940-1947.	2.1	10
79	Yersinia canariae sp. nov., isolated from a human yersiniosis case. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2382-2387.	1.7	10
80	Introduction of PCR testing reveals a previously unrecognized burden of yersiniosis in Hampshire, UK. Journal of Medical Microbiology, 2020, 69, 419-426.	1.8	10
81	Epidemiology and genomic analysis of Shiga toxin-producing Escherichia coli clonal complex 165 in the UK. Journal of Medical Microbiology, 2021, 70, .	1.8	10
82	Analysis of a small outbreak of Shiga toxin-producing Escherichia coli O157:H7 using long-read sequencing. Microbial Genomics, 2021, 7, .	2.0	9
83	Gastrointestinal infections caused by consumption of raw drinking milk in England & Wales, 1992–2017. Epidemiology and Infection, 2019, 147, e281.	2.1	8
84	Outbreak of Shiga toxin-producing Escherichia coli O157 linked with consumption of a fast-food product containing imported cucumbers, United Kingdom, August 2020. International Journal of Infectious Diseases, 2021, 110, S62-S68.	3.3	8
85	Influence of socio-economic status on Shiga toxin-producing <i>Escherichia coli</i> infection incidence, risk factors and clinical features. Epidemiology and Infection, 2019, 147, e215.	2.1	7
86	Identification of domestic reservoirs and common exposures in an emerging lineage of Shiga toxin-producing Escherichia coli O157:H7 in England: a genomic epidemiological analysis. Lancet Microbe, The, 2022, 3, e606-e615.	7.3	7
87	An outbreak of Shiga toxinâ€producing <i>Escherichia coli</i> O157:H7 linked to a mudâ€based obstacle course, England, August 2018. Zoonoses and Public Health, 2020, 67, 467-473.	2.2	6
88	Epidemiological investigation of recurrent outbreaks of haemolytic uraemic syndrome caused by Shiga toxin-producing ⟨i⟩Escherichia coli ⟨/i⟩serotype O55:H7 in England, 2014–2018. Epidemiology and Infection, 2021, 149, e108.	2.1	6
89	A cluster of Shiga Toxin-producing <i>Escherichia coli</i> O157:H7 highlights raw pet food as an emerging potential source of infection in humans. Epidemiology and Infection, 2021, 149, e124.	2.1	6
90	Epidemiological investigations identified an outbreak of Shiga toxin-producing <i>Escherichia coli</i> serotype O26:H11 associated with pre-packed sandwiches. Epidemiology and Infection, 2021, 149, e178.	2.1	6

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91	Utility of whole-genome sequencing during an investigation of multiple foodborne outbreaks of <i>Shigella sonnei</i> . Epidemiology and Infection, 2021, 149, e71.	2.1	6
92	Outbreak of STEC O157:H7 linked to a milk pasteurisation failure at a dairy farm in England, 2019. Epidemiology and Infection, 2022, 150, 1-22.	2.1	6
93	Analysis Shiga Toxin-Encoding Bacteriophage in a Rare Strain of Shiga Toxin-Producing Escherichia coli O157:H7 stx2a/stx2c. Frontiers in Microbiology, 2020, 11, 577658.	3.5	5
94	Phylogenetic context of Shiga toxin-producing Escherichia coli serotype O26:H11 in England. Microbial Genomics, 2021, 7, .	2.0	5
95	Use of Nanopore Sequencing to Characterise the Genomic Architecture of Mobile Genetic Elements Encoding blaCTX-M-15 in Escherichia coli Causing Travellers' Diarrhoea. Frontiers in Microbiology, 2022, 13, 862234.	3.5	4
96	Application of kernel smoothing to estimate the spatio-temporal variation in risk of STEC O157 in England. Spatial and Spatio-temporal Epidemiology, 2020, 32, 100305.	1.7	3
97	Shiga toxin-producing <i>Escherichia coli</i> diagnosed by Stx PCR: assessing the public health risk of non-O157 strains. European Journal of Public Health, 2021, 31, 576-582.	0.3	3
98	Evidence of on-going transmission of Shiga toxin-producing <i>Escherichia coli</i> O157:H7 following a foodborne outbreak. Epidemiology and Infection, 2021, 149, e147.	2.1	3
99	Escherichia coli and Shigella spp , 0, , 347-365.		3
100	A Shiga Toxin-Encoding Prophage Recombination Event Confounds the Phylogenetic Relationship Between Two Isolates of Escherichia coli O157:H7 From the Same Patient. Frontiers in Microbiology, 2020, 11, 588769.	3.5	3
101	Salmonella spp , 2006, , 367-376.		1
102	Comparison of genome-derived and phenotypic antimicrobial resistance profiles of Shigella species isolated from patients with symptoms of gastrointestinal disease in England, 2015-2020. Access Microbiology, 2022, 4, .	0.5	0
103	Use of long read sequencing to characterise the genomic architecture of mobile genetic elements encoding blaCTX-M-15 in Escherichia coli causing travellers' diarrhoea. Access Microbiology, 2022, 4, .	0.5	О