Claire Jenkins

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1725328/publications.pdf

Version: 2024-02-01

103	4,102	94433	138484
papers	citations	37 h-index	58 g-index

105	105	105	3207
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The epidemiology of Shiga toxin-producing Escherichia coli serogroup O157 in England, 2009â€“2019. Epidemiology and Infection, 2022, 150, e52.	2.1	13
2	Use of Nanopore Sequencing to Characterise the Genomic Architecture of Mobile Genetic Elements Encoding blaCTX-M-15 in Escherichia coli Causing Travellersâ€™ Diarrhoea. Frontiers in Microbiology, 2022, 13, 862234.	3.5	4
3	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
4	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
5	Use of long read sequencing to characterise the genomic architecture of mobile genetic elements encoding blaCTX-M-15 in Escherichia coli causing travellersâ€™ diarrhoea. Access Microbiology, 2022, 4, .	0.5	0
6	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
7	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
8	Shiga toxin-producing Escherichia coli 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
9	Evidence of on-going transmission of Shiga toxin-producing Escherichia coli O157:H7 following a foodborne outbreak. Epidemiology and Infection, 2021, 149, e147.	2.1	3
10	Epidemiological investigation of recurrent outbreaks of haemolytic uraemic syndrome caused by Shiga toxin-producingEscherichia coliserotype O55:H7 in England, 2014â€“2018. Epidemiology and Infection, 2021, 149, e108.	2.1	6
11	A cluster of Shiga Toxin-producing Escherichia coli O157:H7 highlights raw pet food as an emerging potential source of infection in humans. Epidemiology and Infection, 2021, 149, e124.	2.1	6
12	Epidemiological investigations identified an outbreak of Shiga toxin-producing Escherichia coli serotype O26:H11 associated with pre-packed sandwiches. Epidemiology and Infection, 2021, 149, e178.	2.1	6
13	Analysis of a small outbreak of Shiga toxin-producing Escherichia coli O157:H7 using long-read sequencing. Microbial Genomics, 2021, 7, .	2.0	9
14	Phylogenetic structure of Shiga toxin-producing Escherichia coli O157:H7 from sub-lineage to SNPs. Microbial Genomics, 2021, 7, .	2.0	14
15	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
16	The emerging importance of Shiga toxin-producing Escherichia coli other than serogroup O157 in England. Journal of Medical Microbiology, 2021, 70, .	1.8	20
17	Utility of whole-genome sequencing during an investigation of multiple foodborne outbreaks of Shigella sonnei. Epidemiology and Infection, 2021, 149, e71.	2.1	6
18	Phylogenetic context of Shiga toxin-producing Escherichia coli serotype O26:H11 in England. Microbial Genomics, 2021, 7, .	2.0	5

#	Article	IF	Citations
19	Emergence of novel strains of Shigella flexneri associated with sexual transmission in adult men in England, 2019â€“2020. Journal of Medical Microbiology, 2021, 70, .	1.8	14
20	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
21	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
22	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
23	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
24	Association between Shiga Toxinâ€“Producing Escherichia coli O157:H7 stx Gene Subtype and Disease Severity, England, 2009â€“2019. Emerging Infectious Diseases, 2020, 26, 2394-2400.	4.3	34
25	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
26	An outbreak of Shiga toxinâ€producing Escherichia coli O157:H7 linked to a mudâ€based obstacle course, England, August 2018. Zoonoses and Public Health, 2020, 67, 467-473.	2.2	6
27	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
28	Yersinia canariae sp. nov., isolated from a human yersiniosis case. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2382-2387.	1.7	10
29	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
30	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
31	Antimicrobial resistance in Shiga toxin-producing Escherichia coli other than serotype O157â€Š:â€ŠH7 in England, 2014â€“2016. Journal of Medical Microbiology, 2020, 69, 379-386.	1.8	14
32	Antimicrobial resistance profiles of diarrhoeagenic Escherichia coli isolated from travellers returning to the UK, 2015â€“2017. Journal of Medical Microbiology, 2020, 69, 932-943.	1.8	13
33	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
34	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
35	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
36	Comparison of single-nucleotide variants identified by Illumina and Oxford Nanopore technologies in the context of a potential outbreak of Shiga toxinâ€“producing Escherichia coli. GigaScience, 2019, 8, .	6.4	42

#	Article	IF	Citations
37	Influence of socio-economic status on Shiga toxin-producing Escherichia coli (STEC) infection incidence, risk factors and clinical features. Epidemiology and Infection, 2019, 147, e215.	2.1	7
38	Outbreaks of Shiga Toxinâ€“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
39	Gastrointestinal infections caused by consumption of raw drinking milk in England & Wales, 1992â€“2017. Epidemiology and Infection, 2019, 147, e281.	2.1	8
40	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
41	The epidemiology of Shiga toxin-producing Escherichia coli infections in the South East of England: November 2013â€“March 2017 and significance for clinical and public health. Journal of Medical Microbiology, 2019, 68, 930-939.	1.8	15
42	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
43	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
44	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
45	Horizontal antimicrobial resistance transfer drives epidemics of multiple Shigella species. Nature Communications, 2018, 9, 1462.	12.8	121
46	SnapperDB: a database solution for routine sequencing analysis of bacterial isolates. Bioinformatics, 2018, 34, 3028-3029.	4.1	164
47	An outbreak of Shiga toxin-producing Escherichia coli O157:H7 associated with contaminated salad leaves: epidemiological, genomic and food trace back investigations. Epidemiology and Infection, 2018, 146, 187-196.	2.1	54
48	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
49	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
50	Farm-to-fork investigation of an outbreak of Shiga toxin-producing Escherichia coli O157. Microbial Genomics, 2018, 4, .	2.0	27
51	Highly Pathogenic Clone of Shiga Toxinâ€“ProducingEscherichia coliO157:H7, England and Wales. Emerging Infectious Diseases, 2018, 24, 2303-2308.	4.3	32
52	A spatial and temporal analysis of risk factors associated with sporadic Shiga toxin-producingEscherichia coliO157 infection in England between 2009 and 2015. Epidemiology and Infection, 2018, 146, 1928-1939.	2.1	15
53	Prediction of Phenotypic Antimicrobial Resistance Profiles From Whole Genome Sequences of Non-typhoidal Salmonella enterica. Frontiers in Microbiology, 2018, 9, 592.	3.5	139
54	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

#	Article	IF	Citations
55	Evaluation of Whole-Genome Sequencing for Identification and Typing of Vibrio cholerae. Journal of Clinical Microbiology, 2018, 56, .	3.9	25
56	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
57	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
58	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
59	Identification of Escherichia coli and Shigella Species from Whole-Genome Sequences. Journal of Clinical Microbiology, 2017, 55, 616-623.	3.9	103
60	Investigation of a national outbreak of STEC Escherichia coli O157 using online consumer panel control methods: Great Britain, October 2014. Epidemiology and Infection, 2017, 145, 864-871.	2.1	23
61	Antimicrobial resistance in Shiga toxin-producingEscherichia coliserogroups O157 and O26 isolated from human cases of diarrhoeal disease in England, 2015. Journal of Antimicrobial Chemotherapy, 2017, 72, 145-152.	3.0	51
62	Comparison of phenotypic and WGS-derived antimicrobial resistance profiles of enteroaggregative Escherichia coli isolated from cases of diarrhoeal disease in England, 2015â€“16. Journal of Antimicrobial Chemotherapy, 2017, 72, 3288-3297.	3.0	38
63	Whole-Genome Sequencing for National Surveillance of Shigella flexneri. Frontiers in Microbiology, 2017, 8, 1700.	3.5	29
64	Evolutionary Context of Nonâ€“Sorbitol-Fermenting Shiga Toxinâ€“ProducingEscherichia coliO55:H7. Emerging Infectious Diseases, 2017, 23, 1966-1973.	4.3	24
65	Recurrent seasonal outbreak of an emerging serotype of Shiga toxin-producing Escherichia coli (STEC) Tj ETQq1 1 0.784314 rgBT /Ov	7.0	21
66	Shiga Toxinâ€“ProducingEscherichia coliO157, England and Wales, 1983â€“2012. Emerging Infectious Diseases, 2016, 22, 590-597.	4.3	61
67	ESBL-Producing and Macrolide-ResistantShigella sonneiInfections among Men Who Have Sex with Men, England, 2015. Emerging Infectious Diseases, 2016, 22, 1948-1952.	4.3	55
68	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
69	Whole genome sequencing improved case ascertainment in an outbreak of Shiga toxin-producing Escherichia coli O157 associated with raw drinking milk. Epidemiology and Infection, 2016, 144, 2812-2823.	2.1	49
70	Epidemiological and Microbiological Investigation of an Outbreak of Severe Disease from Shiga Toxinâ€“Producing Escherichia coli O157 Infection Associated with Consumption of a Slaw Garnish. Journal of Food Protection, 2016, 79, 1161-1168.	1.7	20
71	An outbreak of Shiga toxin-producing Escherichia coli serogroup O157 linked to a lamb-feeding event. Epidemiology and Infection, 2016, 144, 2494-2500.	2.1	21
72	Disease severity of Shiga toxin-producingE. coliO157 and factors influencing the development of typical haemolytic uraemic syndrome: a retrospective cohort study, 2009â€“2012. BMJ Open, 2016, 6, e009933.	1.9	56

#	Article	IF	Citations
73	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
74	Short-term evolution of Shiga toxin-producing Escherichia coli O157:H7 between two food-borne outbreaks. Microbial Genomics, 2016, 2, e000084.	2.0	45
75	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
76	Identification ofSalmonellafor public health surveillance using whole genome sequencing. PeerJ, 2016, 4, e1752.	2.0	236
77	The epidemiology, microbiology and clinical impact of Shiga toxin-producingEscherichia coliin England, 2009â€“2012. Epidemiology and Infection, 2015, 143, 3475-3487.	2.1	110
78	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
79	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
80	Intercontinental dissemination of azithromycin-resistant shigellosis through sexual transmission: a cross-sectional study. Lancet Infectious Diseases, The, 2015, 15, 913-921.	9.1	204
81	Whole-Genome Sequencing for National Surveillance of Shiga Toxinâ€“ProducingEscherichia coliO157. Clinical Infectious Diseases, 2015, 61, 305-312.	5.8	181
82	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
83	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
84	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
85	Insight into Shiga toxin genes encoded byEscherichia coliO157 from whole genome sequencing. PeerJ, 2015, 3, e739.	2.0	66
86	Epidemiology and microbiology of Shiga toxin-producing Escherichia coli other than serogroup O157 in England, 2009â€“2013. Journal of Medical Microbiology, 2014, 63, 1181-1188.	1.8	59
87	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
88	Enterohemorrhagic Escherichia coli O26:H11/Hâ^': A New Virulent Clone Emerges in Europe. Clinical Infectious Diseases, 2013, 56, 1373-1381.	5.8	118
89	Whole Genome Sequencing of an Unusual Serotype of Shiga Toxinâ€“producingEscherichia coli. Emerging Infectious Diseases, 2013, 19, 1302-1304.	4.3	20
90	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

#	Article	IF	Citations
91	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
92	Enhanced heterogeneity of rpoB in Mycobacterium tuberculosis found at low pH. Journal of Antimicrobial Chemotherapy, 2009, 63, 1118-1120.	3.0	16
93	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
94	Escherichia coli serogroup O26 ? a new look at an old adversary. Journal of Applied Microbiology, 2007, 104, 070717025310002-???.	3.1	32
95	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
96	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
97	Salmonella spp.. , 2006, , 367-376.		1
98	Rifampicin Resistance in Tuberculosis Outbreak, London, England. Emerging Infectious Diseases, 2005, 11, 912-920.	4.3	83
99	Rifampicin resistance in tuberculosis outbreak, London, England. Emerging Infectious Diseases, 2005, 11, 931-4.	4.3	12
100	Distribution of espI among clinical enterohaemorrhagic and enteropathogenic Escherichia coli isolates. Journal of Medical Microbiology, 2004, 53, 1145-1149.	1.8	41
101	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
102	The serodiagnosis of infections caused by Verocytotoxinâ€producingEscherichia coli. Journal of Applied Microbiology, 1999, 86, 731-740.	3.1	43
103	Escherichia coli and Shigella spp.. , 0, , 347-365.		3