

Kate E Dingle

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3498334/publications.pdf>

Version: 2024-02-01

53
papers

5,771
citations

101384

36
h-index

182168

51
g-index

58
all docs

58
docs citations

58
times ranked

6682
citing authors

#	ARTICLE	IF	CITATIONS
1	Major genetic discontinuity and novel toxigenic species in <i>Clostridioides difficile</i> taxonomy. <i>ELife</i> , 2021, 10, .	2.8	50
2	DNA Thermo-Protection Facilitates Whole-Genome Sequencing of <i>Mycobacteria</i> Direct from Clinical Samples. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	14
3	Performance characteristics of five immunoassays for SARS-CoV-2: a head-to-head benchmark comparison. <i>Lancet Infectious Diseases</i> , The, 2020, 20, 1390-1400.	4.6	336
4	Antibody testing for COVID-19: A report from the National COVID Scientific Advisory Panel. Wellcome Open Research, 2020, 5, 139.	0.9	179
5	SARS-CoV-2 RNA detected in blood products from patients with COVID-19 is not associated with infectious virus. Wellcome Open Research, 2020, 5, 181.	0.9	81
6	SARS-CoV-2 RNA detected in blood products from patients with COVID-19 is not associated with infectious virus. Wellcome Open Research, 2020, 5, 181.	0.9	122
7	SARS-CoV-2 antibody prevalence, titres and neutralising activity in an antenatal cohort, United Kingdom, 14 April to 15 June 2020. <i>Eurosurveillance</i> , 2020, 25, .	3.9	17
8	Comparative genomics of <i>Clostridioides difficile</i> toxinotypes identifies module-based toxin gene evolution. <i>Microbial Genomics</i> , 2020, 6, .	1.0	8
9	<i>Clostridium difficile</i> trehalose metabolism variants are common and not associated with adverse patient outcomes when variably present in the same lineage. <i>EBioMedicine</i> , 2019, 43, 347-355.	2.7	35
10	A Role for Tetracycline Selection in Recent Evolution of Agriculture-Associated <i>Clostridium difficile</i> PCR Ribotype 078. <i>MBio</i> , 2019, 10, .	1.8	46
11	Two Distinct Patterns of <i>Clostridium difficile</i> Diversity Across Europe Indicating Contrasting Routes of Spread. <i>Clinical Infectious Diseases</i> , 2018, 67, 1035-1044.	2.9	60
12	Effects of control interventions on <i>Clostridium difficile</i> infection in England: an observational study. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 411-421.	4.6	269
13	<i>Clostridium difficile</i> in England: can we stop washing our hands? Authors' reply. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 478-479.	4.6	1
14	Epidemiology of <i>Clostridium difficile</i> in infants in Oxfordshire, UK: Risk factors for colonization and carriage, and genetic overlap with regional <i>C. difficile</i> infection strains. <i>PLoS ONE</i> , 2017, 12, e0182307.	1.1	82
15	Detection of a <i>cfr</i> (B) Variant in German <i>Enterococcus faecium</i> Clinical Isolates and the Impact on Linezolid Resistance in <i>Enterococcus</i> spp.. <i>PLoS ONE</i> , 2016, 11, e0167042.	1.1	46
16	Wild birds-associated <i>Campylobacter jejuni</i> isolates are a consistent source of human disease, in Oxfordshire, United Kingdom. <i>Environmental Microbiology Reports</i> , 2015, 7, 782-788.	1.0	61
17	The Complexity and Diversity of the Pathogenicity Locus in <i>Clostridium difficile</i> Clade 5. <i>Genome Biology and Evolution</i> , 2014, 6, 3159-3170.	1.1	31
18	Evolutionary History of the <i>Clostridium difficile</i> Pathogenicity Locus. <i>Genome Biology and Evolution</i> , 2014, 6, 36-52.	1.1	190

#	ARTICLE	IF	CITATIONS
19	Can rapid integrated polymerase chain reaction-based diagnostics for gastrointestinal pathogens improve routine hospital infection control practice? A diagnostic study. <i>Health Technology Assessment</i> , 2014, 18, 1-167.	1.3	19
20	Recombinational Switching of the <i>Clostridium difficile</i> S-Layer and a Novel Glycosylation Gene Cluster Revealed by Large-Scale Whole-Genome Sequencing. <i>Journal of Infectious Diseases</i> , 2013, 207, 675-686.	1.9	93
21	Whole genome sequencing and de novo assembly identifies Sydney-like variant noroviruses and recombinants during the winter 2012/2013 outbreak in England. <i>Virology Journal</i> , 2013, 10, 335.	1.4	37
22	Diverse Sources of <i>C. difficile</i> Infection Identified on Whole-Genome Sequencing. <i>New England Journal of Medicine</i> , 2013, 369, 1195-1205.	13.9	595
23	Relationship Between Bacterial Strain Type, Host Biomarkers, and Mortality in <i>Clostridium difficile</i> Infection. <i>Clinical Infectious Diseases</i> , 2013, 56, 1589-1600.	2.9	191
24	Real-Time Genomic Epidemiological Evaluation of Human <i>Campylobacter</i> Isolates by Use of Whole-Genome Multilocus Sequence Typing. <i>Journal of Clinical Microbiology</i> , 2013, 51, 2526-2534.	1.8	124
25	A Modified RNA-Seq Approach for Whole Genome Sequencing of RNA Viruses from Faecal and Blood Samples. <i>PLoS ONE</i> , 2013, 8, e66129.	1.1	62
26	Surveillance of Infection Severity: A Registry Study of Laboratory Diagnosed <i>Clostridium difficile</i> . <i>PLoS Medicine</i> , 2012, 9, e1001279.	3.9	8
27	Predictors of First Recurrence of <i>Clostridium difficile</i> Infection: Implications for Initial Management. <i>Clinical Infectious Diseases</i> , 2012, 55, S77-S87.	2.9	180
28	<i>Clostridium difficile</i> Mixed Infection and Reinfection. <i>Journal of Clinical Microbiology</i> , 2012, 50, 142-144.	1.8	55
29	A Longitudinal 6-Year Study of the Molecular Epidemiology of Clinical <i>Campylobacter</i> Isolates in Oxfordshire, United Kingdom. <i>Journal of Clinical Microbiology</i> , 2012, 50, 3193-3201.	1.8	79
30	Microevolutionary analysis of <i>Clostridium difficile</i> genomes to investigate transmission. <i>Genome Biology</i> , 2012, 13, R118.	13.9	199
31	Macro and Micro Diversity of <i>Clostridium difficile</i> Isolates from Diverse Sources and Geographical Locations. <i>PLoS ONE</i> , 2012, 7, e31559.	1.1	114
32	Characterisation of <i>Clostridium difficile</i> Hospital Ward-Based Transmission Using Extensive Epidemiological Data and Molecular Typing. <i>PLoS Medicine</i> , 2012, 9, e1001172.	3.9	202
33	Clinical <i>Clostridium difficile</i> : Clonality and Pathogenicity Locus Diversity. <i>PLoS ONE</i> , 2011, 6, e19993.	1.1	150
34	Molecular Epidemiology of <i>Clostridium difficile</i> Strains in Children Compared with That of Strains Circulating in Adults with <i>Clostridium difficile</i> -Associated Infection : Fig. 1.. <i>Journal of Clinical Microbiology</i> , 2011, 49, 3994-3996.	1.8	32
35	Genetic Relationships among Reptilian and Mammalian <i>Campylobacter fetus</i> Strains Determined by Multilocus Sequence Typing. <i>Journal of Clinical Microbiology</i> , 2010, 48, 977-980.	1.8	24
36	Ciprofloxacin-resistant campylobacteriosis in the UK. <i>Lancet</i> , The, 2010, 376, 1987.	6.3	39

#	ARTICLE	IF	CITATIONS
37	Multilocus Sequence Typing of <i>Clostridium difficile</i> . Journal of Clinical Microbiology, 2010, 48, 770-778.	1.8	399
38	<i>Campylobacter</i> infection of broiler chickens in a free-range environment. Environmental Microbiology, 2008, 10, 2042-2050.	1.8	89
39	Extended Sequence Typing of <i>Campylobacter</i> spp., United Kingdom. Emerging Infectious Diseases, 2008, 14, 1620-1622.	2.0	73
40	Host-associated Genetic Import in <i>Campylobacter jejuni</i> . Emerging Infectious Diseases, 2007, 13, 267-272.	2.0	134
41	Sequence Typing and Comparison of Population Biology of <i>Campylobacter coli</i> and <i>Campylobacter jejuni</i> . Journal of Clinical Microbiology, 2005, 43, 340-347.	1.8	183
42	Clonal Nature of <i>Campylobacter fetus</i> as Defined by Multilocus Sequence Typing. Journal of Clinical Microbiology, 2005, 43, 5888-5898.	1.8	79
43	Stable and Noncompetitive RNA Internal Control for Routine Clinical Diagnostic Reverse Transcription-PCR. Journal of Clinical Microbiology, 2004, 42, 1003-1011.	1.8	43
44	Mutation in a Lordsdale Norovirus Epidemic Strain as a Potential Indicator of Transmission Routes. Journal of Clinical Microbiology, 2004, 42, 3950-3957.	1.8	70
45	Comparative Genotyping of <i>Campylobacter jejuni</i> by Amplified Fragment Length Polymorphism, Multilocus Sequence Typing, and Short Repeat Sequencing: Strain Diversity, Host Range, and Recombination. Journal of Clinical Microbiology, 2003, 41, 15-26.	1.8	242
46	Molecular Evidence for Dissemination of Unique <i>Campylobacter jejuni</i> Clones in Curaçao, Netherlands Antilles. Journal of Clinical Microbiology, 2003, 41, 5593-5597.	1.8	61
47	Molecular Characterization of <i>Campylobacter jejuni</i> Clones: A Basis for Epidemiologic Investigation. Emerging Infectious Diseases, 2002, 8, 949-955.	2.0	211
48	Molecular Characterization of <i>Campylobacter jejuni</i> Clones: A Basis for Epidemiologic Investigation. Emerging Infectious Diseases, 2002, 8, 949-955.	2.0	192
49	Interactions between Hepatitis Delta Virus Proteins. Journal of Virology, 2000, 74, 5509-5515.	1.5	17
50	Electrophoretic analysis of the ribonucleoproteins of hepatitis delta virus. Journal of Virological Methods, 1998, 75, 199-204.	1.0	11
51	Initiation of Hepatitis Delta Virus Genome Replication. Journal of Virology, 1998, 72, 4783-4788.	1.5	34
52	Isolation, Identification, Subspecies Differentiation, and Typing of <i>Campylobacter fetus</i> . , 0, , 213-225.		5
53	Population Biology of <i>Campylobacter jejuni</i> and Related Organisms. , 0, , 27-40.		8