

David W Eyre

List of Publications by Year in descending order

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Version: 2024-02-01

130
papers

13,188
citations

36691

53
h-index

35168

102
g-index

176
all docs

176
docs citations

176
times ranked

18671
citing authors

#	ARTICLE	IF	CITATIONS
1	Reduction in Chest CT Severity and Improved Hospital Outcomes in SARS-CoV-2 Omicron Compared with Delta Variant Infection. <i>Radiology</i> , 2023, 306, 261-269.	3.6	53
2	Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Infectivity by Viral Load, S Gene Variants and Demographic Factors, and the Utility of Lateral Flow Devices to Prevent Transmission. <i>Clinical Infectious Diseases</i> , 2022, 74, 407-415.	2.9	106
3	An Observational Cohort Study on the Incidence of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Infection and B.1.1.7 Variant Infection in Healthcare Workers by Antibody and Vaccination Status. <i>Clinical Infectious Diseases</i> , 2022, 74, 1208-1219.	2.9	64
4	Symptoms and Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Positivity in the General Population in the United Kingdom. <i>Clinical Infectious Diseases</i> , 2022, 75, e329-e337.	2.9	20
5	T-cell and antibody responses to first BNT162b2 vaccine dose in previously infected and SARS-CoV-2-naïve UK health-care workers: a multicentre prospective cohort study. <i>Lancet Microbe</i> , 2022, 3, e21-e31.	3.4	131
6	Time of Day of Vaccination Affects SARS-CoV-2 Antibody Responses in an Observational Study of Health Care Workers. <i>Journal of Biological Rhythms</i> , 2022, 37, 124-129.	1.4	42
7	Effect of Covid-19 Vaccination on Transmission of Alpha and Delta Variants. <i>New England Journal of Medicine</i> , 2022, 386, 744-756.	13.9	323
8	Infection prevention and control insights from a decade of pathogen whole-genome sequencing. <i>Journal of Hospital Infection</i> , 2022, 122, 180-186.	1.4	24
9	Antibody responses and correlates of protection in the general population after two doses of the ChAdOx1 or BNT162b2 vaccines. <i>Nature Medicine</i> , 2022, 28, 1072-1082.	15.2	147
10	Clinical Metagenomic Sequencing for Species Identification and Antimicrobial Resistance Prediction in Orthopedic Device Infection. <i>Journal of Clinical Microbiology</i> , 2022, 60, e0215621.	1.8	18
11	Divergent trajectories of antiviral memory after SARS-CoV-2 infection. <i>Nature Communications</i> , 2022, 13, 1251.	5.8	20
12	Real-world evaluation of rapid and laboratory-free COVID-19 triage for emergency care: external validation and pilot deployment of artificial intelligence driven screening. <i>The Lancet Digital Health</i> , 2022, 4, e266-e278.	5.9	28
13	K-mer based prediction of <i>Clostridioides difficile</i> relatedness and ribotypes. <i>Microbial Genomics</i> , 2022, 8, .	1.0	0
14	Combination therapy of infliximab and thiopurines, but not monotherapy with infliximab or vedolizumab, is associated with attenuated IgA and neutralisation responses to SARS-CoV-2 in inflammatory bowel disease. <i>Gut</i> , 2022, 71, 1919.2-1922.	6.1	3
15	Comparison of two T-cell assays to evaluate T-cell responses to SARS-CoV-2 following vaccination in naïve and convalescent healthcare workers. <i>Clinical and Experimental Immunology</i> , 2022, 209, 90-98.	1.1	5
16	Fatal COVID-19 outcomes are associated with an antibody response targeting epitopes shared with endemic coronaviruses. <i>JCI Insight</i> , 2022, 7, .	2.3	24
17	Whole genome sequencing reveals hidden transmission of carbapenemase-producing Enterobacterales. <i>Nature Communications</i> , 2022, 13, .	5.8	16
18	SARS-CoV-2 antibody trajectories after a single COVID-19 vaccination with and without prior infection. <i>Nature Communications</i> , 2022, 13, .	5.8	6

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19	Assessment of an institutional guideline for vancomycin dosing and identification of predictive factors associated with dose and drug trough levels. <i>Journal of Infection</i> , 2022, 85, 382-389.	1.7	1
20	Hospital Admission Location Prediction via Deep Interpretable Networks for the Year-Round Improvement of Emergency Patient Care. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021, 25, 289-300.	3.9	14
21	Possible contribution of shoes to <i>Clostridioides difficile</i> transmission within hospitals. <i>Clinical Microbiology and Infection</i> , 2021, 27, 797-799.	2.8	5
22	Antibody Status and Incidence of SARS-CoV-2 Infection in Health Care Workers. <i>New England Journal of Medicine</i> , 2021, 384, 533-540.	13.9	803
23	Community prevalence of SARS-CoV-2 in England from April to November, 2020: results from the ONS Coronavirus Infection Survey. <i>Lancet Public Health</i> , The, 2021, 6, e30-e38.	4.7	147
24	Probabilistic transmission models incorporating sequencing data for healthcare-associated <i>Clostridioides difficile</i> outperform heuristic rules and identify strain-specific differences in transmission. <i>PLoS Computational Biology</i> , 2021, 17, e1008417.	1.5	9
25	Stringent thresholds in SARS-CoV-2 IgG assays lead to under-detection of mild infections. <i>BMC Infectious Diseases</i> , 2021, 21, 187.	1.3	23
26	Home-based SARS-CoV-2 lateral flow antigen testing in hospital workers. <i>Journal of Infection</i> , 2021, 82, 282-327.	1.7	32
27	Rapid triage for COVID-19 using routine clinical data for patients attending hospital: development and prospective validation of an artificial intelligence screening test. <i>The Lancet Digital Health</i> , 2021, 3, e78-e87.	5.9	96
28	Utility of Whole Genome Sequencing in Assessing and Enhancing Partner Notification of <i>Neisseria gonorrhoeae</i> Infection. <i>Sexually Transmitted Diseases</i> , 2021, 48, 773-780.	0.8	2
29	SARS-CoV-2 within-host diversity and transmission. <i>Science</i> , 2021, 372, .	6.0	278
30	T cell assays differentiate clinical and subclinical SARS-CoV-2 infections from cross-reactive antiviral responses. <i>Nature Communications</i> , 2021, 12, 2055.	5.8	102
31	Major genetic discontinuity and novel toxigenic species in <i>Clostridioides difficile</i> taxonomy. <i>ELife</i> , 2021, 10, .	2.8	50
32	Use of lateral flow devices allows rapid triage of patients with SARS-CoV-2 on admission to hospital. <i>Journal of Infection</i> , 2021, 82, 276-316.	1.7	25
33	Quantitative SARS-CoV-2 anti-spike responses to Pfizerâ€™BioNTech and Oxfordâ€™AstraZeneca vaccines by previous infection status. <i>Clinical Microbiology and Infection</i> , 2021, 27, 1516.e7-1516.e14.	2.8	100
34	COVID-19: Rapid antigen detection for SARS-CoV-2 by lateral flow assay: A national systematic evaluation of sensitivity and specificity for mass-testing. <i>EClinicalMedicine</i> , 2021, 36, 100924.	3.2	162
35	Impact of vaccination on new SARS-CoV-2 infections in the United Kingdom. <i>Nature Medicine</i> , 2021, 27, 1370-1378.	15.2	260
36	Impaired antibody response to COVIDâ€™19 vaccination in patients with chronic myeloid neoplasms. <i>British Journal of Haematology</i> , 2021, 194, 1010-1015.	1.2	31

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37	Ct threshold values, a proxy for viral load in community SARS-CoV-2 cases, demonstrate wide variation across populations and over time. <i>ELife</i> , 2021, 10, .	2.8	91
38	Antibody responses to SARS-CoV-2 vaccines in 45,965 adults from the general population of the United Kingdom. <i>Nature Microbiology</i> , 2021, 6, 1140-1149.	5.9	254
39	Metagenomic Sequencing as a Pathogen-Agnostic Clinical Diagnostic Tool for Infectious Diseases: a Systematic Review and Meta-analysis of Diagnostic Test Accuracy Studies. <i>Journal of Clinical Microbiology</i> , 2021, 59, e0291620.	1.8	50
40	Human and Porcine Transmission of <i>Clostridioides difficile</i> Ribotype 078, Europe. <i>Emerging Infectious Diseases</i> , 2021, 27, 2294-2300.	2.0	12
41	Epidemiology of <i>Mycobacterium abscessus</i> in England: an observational study. <i>Lancet Microbe</i> , The, 2021, 2, e498-e507.	3.4	20
42	Daily testing for contacts of individuals with SARS-CoV-2 infection and attendance and SARS-CoV-2 transmission in English secondary schools and colleges: an open-label, cluster-randomised trial. <i>Lancet</i> , The, 2021, 398, 1217-1229.	6.3	87
43	Epidemiological data and genome sequencing reveals that nosocomial transmission of SARS-CoV-2 is underestimated and mostly mediated by a small number of highly infectious individuals. <i>Journal of Infection</i> , 2021, 83, 473-482.	1.7	55
44	The Duration, Dynamics, and Determinants of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Antibody Responses in Individual Healthcare Workers. <i>Clinical Infectious Diseases</i> , 2021, 73, e699-e709.	2.9	235
45	Transmission of community- and hospital-acquired SARS-CoV-2 in hospital settings in the UK: A cohort study. <i>PLoS Medicine</i> , 2021, 18, e1003816.	3.9	35
46	Immunogenicity of standard and extended dosing intervals of BNT162b2 mRNA vaccine. <i>Cell</i> , 2021, 184, 5699-5714.e11.	13.5	262
47	Effect of Delta variant on viral burden and vaccine effectiveness against new SARS-CoV-2 infections in the UK. <i>Nature Medicine</i> , 2021, 27, 2127-2135.	15.2	450
48	Anti-spike antibody response to natural SARS-CoV-2 infection in the general population. <i>Nature Communications</i> , 2021, 12, 6250.	5.8	88
49	Probabilistic modelling of effects of antibiotics and calendar time on transmission of healthcare-associated infection. <i>Scientific Reports</i> , 2021, 11, 21417.	1.6	2
50	Equations To Predict Antimicrobial MICs in <i>Neisseria gonorrhoeae</i> Using Molecular Antimicrobial Resistance Determinants. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	37
51	Should modern molecular testing be routinely available for the diagnosis of musculoskeletal infection?. <i>Bone and Joint Journal</i> , 2020, 102-B, 1274-1276.	1.9	6
52	In vitro activity of eravacycline against common ribotypes of <i>Clostridioides difficile</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 2879-2884.	1.3	7
53	High precision <i>Neisseria gonorrhoeae</i> variant and antimicrobial resistance calling from metagenomic Nanopore sequencing. <i>Genome Research</i> , 2020, 30, 1354-1363.	2.4	27
54	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

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55	Ethnically diverse urban transmission networks of <i>Neisseria gonorrhoeae</i> without evidence of HIV serosorting. <i>Sexually Transmitted Infections</i> , 2020, 96, 106-109.	0.8	3
56	Genetic Heterogeneity of Australian <i>Candida auris</i> Isolates: Insights From a Nonoutbreak Setting Using Whole-Genome Sequencing. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa158.	0.4	12
57	<i>In Vitro</i> Activity of Omadacycline, a New Tetracycline Analog, and Comparators against <i>Clostridioides difficile</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	14
58	Genomic diversity affects the accuracy of bacterial single-nucleotide polymorphism calling pipelines. <i>GigaScience</i> , 2020, 9, .	3.3	92
59	Optimizing DNA Extraction Methods for Nanopore Sequencing of <i>Neisseria gonorrhoeae</i> Directly from Urine Samples. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	33
60	Antibody testing for COVID-19: A report from the National COVID Scientific Advisory Panel. Wellcome Open Research, 2020, 5, 139.	0.9	179
61	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
62	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
63	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
64	RNA polymerase mutations cause cephalosporin resistance in clinical <i>Neisseria gonorrhoeae</i> isolates. <i>ELife</i> , 2020, 9, .	2.8	31
65	Differential occupational risks to healthcare workers from SARS-CoV-2 observed during a prospective observational study. <i>ELife</i> , 2020, 9, .	2.8	196
66	<i>Clostridium difficile</i> : Investigating Transmission Patterns Between Infected and Colonized Patients Using Whole Genome Sequencing. <i>Clinical Infectious Diseases</i> , 2019, 68, 204-209.	2.9	55
67	Antimicrobial Resistance in <i>Neisseria gonorrhoeae</i> and Treatment of Gonorrhoea. <i>Methods in Molecular Biology</i> , 2019, 1997, 37-58.	0.4	71
68	Prediction of Minimum Inhibitory Concentrations of Antimicrobials for <i>Neisseria gonorrhoeae</i> Using Whole-Genome Sequencing. <i>Methods in Molecular Biology</i> , 2019, 1997, 59-76.	0.4	8
69	The global challenge of <i>Candida auris</i> in the intensive care unit. <i>Critical Care</i> , 2019, 23, 150.	2.5	26
70	<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
71	Male gender is an independent predictor for worse survival and relapse in a large, consecutive cohort of elderly DLBCL patients treated with CHOP. <i>British Journal of Haematology</i> , 2019, 186, e94-e98.	1.2	10
72	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

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73	O03.5â€¦Utility of real-time whole genome sequencing in partner notification and control of neisseria gonorrhoeae infection. , 2019, , .		0
74	P675â€¦Two recent cases of extensively drug-resistant (XDR) gonorrhoea in the united kingdom linked to a european party destination. , 2019, , .		1
75	Hash-Based Core Genome Multilocus Sequence Typing for Clostridium difficile. Journal of Clinical Microbiology, 2019, 58, .	1.8	16
76	WGS to determine the extent of <i>Clostridioides difficile</i> transmission in a high incidence setting in North Wales in 2015. Journal of Antimicrobial Chemotherapy, 2019, 74, 1092-1100.	1.3	6
77	Detection in the United Kingdom of the Neisseria gonorrhoeae FC428 clone, with ceftriaxone resistance and intermediate resistance to azithromycin, October to December 2018. Eurosurveillance, 2019, 24, .	3.9	107
78	Genetic relatedness of ceftriaxone-resistant and high-level azithromycin resistant Neisseria gonorrhoeae cases, United Kingdom and Australia, February to April 2018. Eurosurveillance, 2019, 24, .	3.9	77
79	Two Distinct Patterns of Clostridium difficile Diversity Across Europe Indicating Contrasting Routes of Spread. Clinical Infectious Diseases, 2018, 67, 1035-1044.	2.9	60
80	Patient and Strain Characteristics Associated With Clostridium difficile Transmission and Adverse Outcomes. Clinical Infectious Diseases, 2018, 67, 1379-1387.	2.9	24
81	Results of a multicentre <sc>UK</sc>-wide compassionate use programme evaluating the efficacy of idelalisib monotherapy in relapsed, refractory follicular lymphoma. British Journal of Haematology, 2018, 181, 555-559.	1.2	13
82	Whole genome sequencing of <i>Neisseria gonorrhoeae</i> reveals transmission clusters involving patients of mixed HIV serostatus. Sexually Transmitted Infections, 2018, 94, 138-143.	0.8	19
83	Gonorrhoea treatment failure caused by a Neisseria gonorrhoeae strain with combined ceftriaxone and high-level azithromycin resistance, England, February 2018. Eurosurveillance, 2018, 23, .	3.9	255
84	PTU-047â€¦High prevalence of clostridium difficile ribotype 078 in IBD outpatients. , 2018, , .		0
85	Real-time analysis of nanopore-based metagenomic sequencing from infected orthopaedic devices. BMC Genomics, 2018, 19, 714.	1.2	128
86	A <i>Candida auris</i> Outbreak and Its Control in an Intensive Care Setting. New England Journal of Medicine, 2018, 379, 1322-1331.	13.9	318
87	Impact of Intended and Relative Dose Intensity of RCHOP in a Large, Consecutive Cohort of Elderly DLBCL Patients: No Difference in DFS for 70-80 Years Versus >80 Years and Idi Independently Predicts Survival. Blood, 2018, 132, 573-573.	0.6	1
88	Effects of control interventions on Clostridium difficile infection in England: an observational study. Lancet Infectious Diseases, The, 2017, 17, 411-421.	4.6	269
89	Molecular Diagnosis of Orthopedic-Device-Related Infection Directly from Sonication Fluid by Metagenomic Sequencing. Journal of Clinical Microbiology, 2017, 55, 2334-2347.	1.8	174
90	Clostridium difficile in England: can we stop washing our hands? â€œ Authors' reply. Lancet Infectious Diseases, The, 2017, 17, 478-479.	4.6	1

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91	Contribution to Clostridium Difficile Transmission of Symptomatic Patients With Toxigenic Strains Who Are Fecal Toxin Negative. Clinical Infectious Diseases, 2017, 64, 1163-1170.	2.9	45
92	Genomic analysis of urogenital and rectal <i>Neisseria meningitidis</i> isolates reveals encapsulated hyperinvasive meningococci and coincident multidrug-resistant gonococci. Sexually Transmitted Infections, 2017, 93, 445-451.	0.8	26
93	WGS to predict antibiotic MICs for Neisseria gonorrhoeae. Journal of Antimicrobial Chemotherapy, 2017, 72, 1937-1947.	1.3	169
94	Results of a multicentre UK-wide retrospective study evaluating the efficacy of brentuximab vedotin in relapsed, refractory classical Hodgkin lymphoma in the transplant naive setting. British Journal of Haematology, 2017, 179, 471-479.	1.2	20
95	Covert dissemination of carbapenemase-producing Klebsiella pneumoniae (KPC) in a successfully controlled outbreak: long- and short-read whole-genome sequencing demonstrate multiple genetic modes of transmission. Journal of Antimicrobial Chemotherapy, 2017, 72, 3025-3034.	1.3	73
96	Transmission of Staphylococcus aureus between health-care workers, the environment, and patients in an intensive care unit: a longitudinal cohort study based on whole-genome sequencing. Lancet Infectious Diseases, The, 2017, 17, 207-214.	4.6	155
97	Clostridium difficile: Investigating Transmission Patterns Between Symptomatic and Asymptomatic Patients Using Whole Genome Sequencing. Open Forum Infectious Diseases, 2017, 4, S1-S1.	0.4	1
98	BugMat and FindNeighbour: command line and server applications for investigating bacterial relatedness. BMC Bioinformatics, 2017, 18, 477.	1.2	16
99	Comparison of Control of Clostridium difficile Infection in Six English Hospitals Using Whole-Genome Sequencing. Clinical Infectious Diseases, 2017, 65, 433-441.	2.9	40
100	Epidemiology of Clostridium difficile in infants in Oxfordshire, UK: Risk factors for colonization and carriage, and genetic overlap with regional C. difficile infection strains. PLoS ONE, 2017, 12, e0182307.	1.1	82
101	Lack of Evidence for Toxin Immunoassay-Negative Patients as a Significant Source of Clostridium difficile Transmission at an Academic Medical Center. Open Forum Infectious Diseases, 2016, 3, .	0.4	0
102	Comparison of Pulsed-Field Gel Electrophoresis and Whole Genome Sequencing in Clostridium difficile Typing. Open Forum Infectious Diseases, 2016, 3, .	0.4	1
103	Whole-genome sequencing to determine transmission of Neisseria gonorrhoeae : an observational study. Lancet Infectious Diseases, The, 2016, 16, 1295-1303.	4.6	149
104	Results of a multicentre UK-wide retrospective study evaluating the efficacy of pixantrone in relapsed, refractory diffuse large B cell lymphoma. British Journal of Haematology, 2016, 173, 896-904.	1.2	19
105	Results of a large retrospective analysis of the effect of intended dose intensity of R-CHOP on outcome in a cohort of consecutive, unselected elderly patients with <i>de novo</i> diffuse large B cell lymphoma. British Journal of Haematology, 2016, 173, 487-491.	1.2	38
106	Whole-genome sequencing for prediction of Mycobacterium tuberculosis drug susceptibility and resistance: a retrospective cohort study. Lancet Infectious Diseases, The, 2015, 15, 1193-1202.	4.6	553
107	Two cases of Clostridium difficile infection in unrelated oncology patients attributable to a single clone of C. difficile PCR ribotype 126. JMM Case Reports, 2015, 2, .	1.3	7
108	Emergence and spread of predominantly community-onset Clostridium difficile PCR ribotype 244 infection in Australia, 2010 to 2012. Eurosurveillance, 2015, 20, 21059.	3.9	55

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109	Whole-Genome Sequencing Demonstrates That Fidaxomicin Is Superior to Vancomycin for Preventing Reinfection and Relapse of Infection With <i>Clostridium difficile</i> . <i>Journal of Infectious Diseases</i> , 2014, 209, 1446-1451.	1.9	54
110	Evolutionary History of the <i>Clostridium difficile</i> Pathogenicity Locus. <i>Genome Biology and Evolution</i> , 2014, 6, 36-52.	1.1	190
111	Diverse Sources of <i>C. difficile</i> Infection. <i>New England Journal of Medicine</i> , 2014, 370, 182-184.	13.9	12
112	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
113	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
114	Whole-genome sequencing to delineate <i>Mycobacterium tuberculosis</i> outbreaks: a retrospective observational study. <i>Lancet Infectious Diseases</i> , The, 2013, 13, 137-146.	4.6	786
115	Predicting antimicrobial susceptibilities for <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> isolates using whole genomic sequence data. <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 2234-2244.	1.3	314
116	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
117	Comparison of Multilocus Variable-Number Tandem-Repeat Analysis and Whole-Genome Sequencing for Investigation of <i>Clostridium difficile</i> Transmission. <i>Journal of Clinical Microbiology</i> , 2013, 51, 4141-4149.	1.8	69
118	Detection of Mixed Infection from Bacterial Whole Genome Sequence Data Allows Assessment of Its Role in <i>Clostridium difficile</i> Transmission. <i>PLoS Computational Biology</i> , 2013, 9, e1003059.	1.5	75
119	Regarding "Clostridium Difficile Ribotype Does Not Predict Severe Infection". <i>Clinical Infectious Diseases</i> , 2013, 56, 1845-1846.	2.9	8
120	HIV-associated late seminal vesicle <i>BCGosis</i> ™ following intravesical bacille Calmette-Guérin therapy. <i>Journal of Clinical Urology</i> , 2013, 6, 20-21.	0.1	1
121	Risk Factors for <i>Clostridium difficile</i> Acquisition in Infants: Importance of Study Design. <i>Clinical Infectious Diseases</i> , 2013, 56, 1680-1681.	2.9	5
122	<i>Clostridium difficile</i> surveillance: harnessing new technologies to control transmission. <i>Expert Review of Anti-Infective Therapy</i> , 2013, 11, 1193-1205.	2.0	22
123	Short-Term Genome Stability of Serial <i>Clostridium difficile</i> Ribotype 027 Isolates in an Experimental Gut Model and Recurrent Human Disease. <i>PLoS ONE</i> , 2013, 8, e63540.	1.1	16
124	Asymptomatic <i>Clostridium difficile</i> Colonisation and Onward Transmission. <i>PLoS ONE</i> , 2013, 8, e78445.	1.1	113
125	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
126	<i>Clostridium difficile</i> Mixed Infection and Reinfection. <i>Journal of Clinical Microbiology</i> , 2012, 50, 142-144.	1.8	55

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127	A pilot study of rapid benchtop sequencing of <i>Staphylococcus aureus</i> and <i>Clostridium difficile</i> for outbreak detection and surveillance. <i>BMJ Open</i> , 2012, 2, e001124.	0.8	228
128	Microevolutionary analysis of <i>Clostridium difficile</i> genomes to investigate transmission. <i>Genome Biology</i> , 2012, 13, R118.	13.9	199
129	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
130	Mortality risks associated with empirical antibiotic activity in <i>Escherichia coli</i> bacteraemia: an analysis of electronic health records. <i>Journal of Antimicrobial Chemotherapy</i> , 0, , .	1.3	3