

William P Hanage

List of Publications by Year in descending order

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Version: 2024-02-01

171
papers

21,688
citations

17405

63
h-index

11288

136
g-index

191
all docs

191
docs citations

191
times ranked

27254
citing authors

#	ARTICLE	IF	CITATIONS
1	The effect of human mobility and control measures on the COVID-19 epidemic in China. <i>Science</i> , 2020, 368, 493-497.	6.0	2,168
2	eBURST: Inferring Patterns of Evolutionary Descent among Clusters of Related Bacterial Genotypes from Multilocus Sequence Typing Data. <i>Journal of Bacteriology</i> , 2004, 186, 1518-1530.	1.0	1,697
3	Pandemic Potential of a Strain of Influenza A (H1N1): Early Findings. <i>Science</i> , 2009, 324, 1557-1561.	6.0	1,665
4	Persistence and Evolution of SARS-CoV-2 in an Immunocompromised Host. <i>New England Journal of Medicine</i> , 2020, 383, 2291-2293.	13.9	1,069
5	Rapid Pneumococcal Evolution in Response to Clinical Interventions. <i>Science</i> , 2011, 331, 430-434.	6.0	828
6	SARS-CoV-2 Titers in Wastewater Are Higher than Expected from Clinically Confirmed Cases. <i>MSystems</i> , 2020, 5, .	1.7	649
7	Assessing the age specificity of infection fatality rates for COVID-19: systematic review, meta-analysis, and public policy implications. <i>European Journal of Epidemiology</i> , 2020, 35, 1123-1138.	2.5	603
8	Recombination and the Nature of Bacterial Speciation. <i>Science</i> , 2007, 315, 476-480.	6.0	512
9	The Bacterial Species Challenge: Making Sense of Genetic and Ecological Diversity. <i>Science</i> , 2009, 323, 741-746.	6.0	381
10	Horizontal gene transfer and the evolution of bacterial and archaeal population structure. <i>Trends in Genetics</i> , 2013, 29, 170-175.	2.9	364
11	Population genomics of post-vaccine changes in pneumococcal epidemiology. <i>Nature Genetics</i> , 2013, 45, 656-663.	9.4	364
12	Variation in HIV-1 set-point viral load: Epidemiological analysis and an evolutionary hypothesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 17441-17446.	3.3	363
13	Making Sense of Mutation: What D614G Means for the COVID-19 Pandemic Remains Unclear. <i>Cell</i> , 2020, 182, 794-795.	13.5	353
14	Emergence of 19A as Virulent and Multidrug Resistant Pneumococcus in Massachusetts Following Universal Immunization of Infants With Pneumococcal Conjugate Vaccine. <i>Pediatric Infectious Disease Journal</i> , 2007, 26, 468-472.	1.1	320
15	Fuzzy species among recombinogenic bacteria. <i>BMC Biology</i> , 2005, 3, 6.	1.7	283
16	Genomic epidemiology of the <i>Escherichia coli</i> O104:H4 outbreaks in Europe, 2011. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 3065-3070.	3.3	262
17	Continued Impact of Pneumococcal Conjugate Vaccine on Carriage in Young Children. <i>Pediatrics</i> , 2009, 124, e1-e11.	1.0	258
18	An omics-based framework for assessing the health risk of antimicrobial resistance genes. <i>Nature Communications</i> , 2021, 12, 4765.	5.8	248

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19	Phylogenetic analysis of SARS-CoV-2 in Boston highlights the impact of superspreading events. <i>Science</i> , 2021, 371, .	6.0	226
20	Horizontal gene transfer and adaptive evolution in bacteria. <i>Nature Reviews Microbiology</i> , 2022, 20, 206-218.	13.6	214
21	Comprehensive Identification of Single Nucleotide Polymorphisms Associated with Beta-lactam Resistance within Pneumococcal Mosaic Genes. <i>PLoS Genetics</i> , 2014, 10, e1004547.	1.5	205
22	Functional Characterization of Bacteria Isolated from Ancient Arctic Soil Exposes Diverse Resistance Mechanisms to Modern Antibiotics. <i>PLoS ONE</i> , 2015, 10, e0069533.	1.1	202
23	Genomic epidemiology of <i>Neisseria gonorrhoeae</i> with reduced susceptibility to cefixime in the USA: a retrospective observational study. <i>Lancet Infectious Diseases</i> , The, 2014, 14, 220-226.	4.6	193
24	SARS-CoV-2 RNA concentrations in wastewater foreshadow dynamics and clinical presentation of new COVID-19 cases. <i>Science of the Total Environment</i> , 2022, 805, 150121.	3.9	192
25	Scientific consensus on the COVID-19 pandemic: we need to act now. <i>Lancet</i> , The, 2020, 396, e71-e72.	6.3	189
26	Origin and Proliferation of Multiple-Drug Resistance in Bacterial Pathogens. <i>Microbiology and Molecular Biology Reviews</i> , 2015, 79, 101-116.	2.9	183
27	Whole-Genome Sequencing for National Surveillance of Shiga Toxin-Producing <i>Escherichia coli</i> O157. <i>Clinical Infectious Diseases</i> , 2015, 61, 305-312.	2.9	181
28	Displaying the relatedness among isolates of bacterial species “the eBURST approach. <i>FEMS Microbiology Letters</i> , 2004, 241, 129-134.	0.7	179
29	Detection of recombination events in bacterial genomes from large population samples. <i>Nucleic Acids Research</i> , 2012, 40, e6-e6.	6.5	179
30	Restricted Gene Flow among Hospital Subpopulations of <i>Enterococcus faecium</i> . <i>MBio</i> , 2012, 3, e00151-12.	1.8	177
31	Population biology of Gram-positive pathogens: high-risk clones for dissemination of antibiotic resistance. <i>FEMS Microbiology Reviews</i> , 2011, 35, 872-900.	3.9	173
32	Diversification of bacterial genome content through distinct mechanisms over different timescales. <i>Nature Communications</i> , 2014, 5, 5471.	5.8	173
33	Microbiology: Microbiome science needs a healthy dose of scepticism. <i>Nature</i> , 2014, 512, 247-248.	13.7	172
34	Efficient Inference of Recent and Ancestral Recombination within Bacterial Populations. <i>Molecular Biology and Evolution</i> , 2017, 34, 1167-1182.	3.5	168
35	Sequences, sequence clusters and bacterial species. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 1917-1927.	1.8	167
36	Conjugative plasmids interact with insertion sequences to shape the horizontal transfer of antimicrobial resistance genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	161

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37	Multi-institute analysis of carbapenem resistance reveals remarkable diversity, unexplained mechanisms, and limited clonal outbreaks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1135-1140.	3.3	158
38	Within-Host Bacterial Diversity Hinders Accurate Reconstruction of Transmission Networks from Genomic Distance Data. <i>PLoS Computational Biology</i> , 2014, 10, e1003549.	1.5	148
39	Neutral microepidemic evolution of bacterial pathogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 1968-1973.	3.3	141
40	Invasiveness of Serotypes and Clones of <i>Streptococcus pneumoniae</i> among Children in Finland. <i>Infection and Immunity</i> , 2005, 73, 431-435.	1.0	137
41	Cryptic ecology among host generalist <i>Campylobacter jejuni</i> in domestic animals. <i>Molecular Ecology</i> , 2014, 23, 2442-2451.	2.0	131
42	No coexistence for free: Neutral null models for multistrain pathogens. <i>Epidemics</i> , 2009, 1, 2-13.	1.5	130
43	Ecological Overlap and Horizontal Gene Transfer in <i>Staphylococcus aureus</i> and <i>Staphylococcus epidermidis</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 1313-1328.	1.1	130
44	Evidence that pneumococcal serotype replacement in Massachusetts following conjugate vaccination is now complete. <i>Epidemics</i> , 2010, 2, 80-84.	1.5	128
45	Diversity and Antibiotic Resistance among Nonvaccine Serotypes of <i>Streptococcus pneumoniae</i> Carriage Isolates in the Post-Heptavalent Conjugate Vaccine Era. <i>Journal of Infectious Diseases</i> , 2007, 195, 347-352.	1.9	127
46	Frequency-dependent selection in vaccine-associated pneumococcal population dynamics. <i>Nature Ecology and Evolution</i> , 2017, 1, 1950-1960.	3.4	121
47	Wastewater surveillance of SARS-CoV-2 across 40 U.S. states from February to June 2020. <i>Water Research</i> , 2021, 202, 117400.	5.3	119
48	An early warning approach to monitor COVID-19 activity with multiple digital traces in near real time. <i>Science Advances</i> , 2021, 7, .	4.7	114
49	Identifying Currents in the Gene Pool for Bacterial Populations Using an Integrative Approach. <i>PLoS Computational Biology</i> , 2009, 5, e1000455.	1.5	112
50	Serotype specific invasive capacity and persistent reduction in invasive pneumococcal disease. <i>Vaccine</i> , 2010, 29, 283-288.	1.7	112
51	Evidence for Soft Selective Sweeps in the Evolution of Pneumococcal Multidrug Resistance and Vaccine Escape. <i>Genome Biology and Evolution</i> , 2014, 6, 1589-1602.	1.1	112
52	The impact of homologous recombination on the generation of diversity in bacteria. <i>Journal of Theoretical Biology</i> , 2006, 239, 210-219.	0.8	106
53	Using Multilocus Sequence Data To Define the Pneumococcus. <i>Journal of Bacteriology</i> , 2005, 187, 6223-6230.	1.0	104
54	Making sense of differences in pneumococcal serotype replacement. <i>Lancet Infectious Diseases</i> , The, 2019, 19, e213-e220.	4.6	100

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55	Interim results of an ecological experiment – Conjugate vaccination against the pneumococcus and serotype replacement. <i>Human Vaccines and Immunotherapeutics</i> , 2016, 12, 358-374.	1.4	93
56	Modelling bacterial speciation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 2039-2044.	1.8	88
57	HIV-1 Transmitting Couples Have Similar Viral Load Set-Points in Rakai, Uganda. <i>PLoS Pathogens</i> , 2010, 6, e1000876.	2.1	88
58	Heterogeneity in the Frequency and Characteristics of Homologous Recombination in Pneumococcal Evolution. <i>PLoS Genetics</i> , 2014, 10, e1004300.	1.5	84
59	Shared Genomic Variants: Identification of Transmission Routes Using Pathogen Deep-Sequence Data. <i>American Journal of Epidemiology</i> , 2017, 186, 1209-1216.	1.6	84
60	Ability of Pneumococcal Serotypes and Clones To Cause Acute Otitis Media: Implications for the Prevention of Otitis Media by Conjugate Vaccines. <i>Infection and Immunity</i> , 2004, 72, 76-81.	1.0	83
61	What is the mechanism for persistent coexistence of drug-susceptible and drug-resistant strains of <i>Streptococcus pneumoniae</i> ?. <i>Journal of the Royal Society Interface</i> , 2010, 7, 905-919.	1.5	83
62	Impact of 13-Valent Pneumococcal Conjugate Vaccination on <i>Streptococcus pneumoniae</i> Carriage in Young Children in Massachusetts. <i>Journal of the Pediatric Infectious Diseases Society</i> , 2014, 3, 23-32.	0.6	78
63	Selective and Genetic Constraints on Pneumococcal Serotype Switching. <i>PLoS Genetics</i> , 2015, 11, e1005095.	1.5	78
64	Variable recombination dynamics during the emergence, transmission and –disarming– of a multidrug-resistant pneumococcal clone. <i>BMC Biology</i> , 2014, 12, 49.	1.7	75
65	Global emergence and population dynamics of divergent serotype 3 CC180 pneumococci. <i>PLoS Pathogens</i> , 2018, 14, e1007438.	2.1	74
66	Rapid inference of antibiotic resistance and susceptibility by genomic neighbour typing. <i>Nature Microbiology</i> , 2020, 5, 455-464.	5.9	74
67	Population impact of SARS-CoV-2 variants with enhanced transmissibility and/or partial immune escape. <i>Cell</i> , 2021, 184, 6229-6242.e18.	13.5	72
68	Pneumococcal Carriage and Antibiotic Resistance in Young Children Before 13-valent Conjugate Vaccine. <i>Pediatric Infectious Disease Journal</i> , 2012, 31, 249-254.	1.1	71
69	Comparative Genomics of Recent Shiga Toxin-Producing <i>Escherichia coli</i> O104:H4: Short-Term Evolution of an Emerging Pathogen. <i>MBio</i> , 2013, 4, e00452-12.	1.8	68
70	Diverse evolutionary patterns of pneumococcal antigens identified by pangenome-wide immunological screening. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E357-E366.	3.3	68
71	Metrics to relate COVID-19 wastewater data to clinical testing dynamics. <i>Water Research</i> , 2022, 212, 118070.	5.3	68
72	Population genomic datasets describing the post-vaccine evolutionary epidemiology of <i>Streptococcus pneumoniae</i> . <i>Scientific Data</i> , 2015, 2, 150058.	2.4	67

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73	Serotype-specific problems associated with pneumococcal conjugate vaccination. <i>Future Microbiology</i> , 2008, 3, 23-30.	1.0	64
74	Phylogenetic interpretation during outbreaks requires caution. <i>Nature Microbiology</i> , 2020, 5, 876-877.	5.9	64
75	Global Phylogenomic Analysis of Nonencapsulated <i>Streptococcus pneumoniae</i> Reveals a Deep-Branching Classic Lineage That Is Distinct from Multiple Sporadic Lineages. <i>Genome Biology and Evolution</i> , 2014, 6, 3281-3294.	1.1	63
76	Mechanisms of genome evolution of <i>Streptococcus</i> . <i>Infection, Genetics and Evolution</i> , 2015, 33, 334-342.	1.0	63
77	Re-emergence of the type 1 pilus among <i>Streptococcus pneumoniae</i> isolates in Massachusetts, USA. <i>Vaccine</i> , 2010, 28, 4842-4846.	1.7	60
78	Carried Pneumococci in Massachusetts Children. <i>Pediatric Infectious Disease Journal</i> , 2011, 30, 302-308.	1.1	55
79	Historical Zoonoses and Other Changes in Host Tropism of <i>Staphylococcus aureus</i> , Identified by Phylogenetic Analysis of a Population Dataset. <i>PLoS ONE</i> , 2013, 8, e62369.	1.1	55
80	Modelling infectious disease – time to think outside the box?. <i>Nature Reviews Microbiology</i> , 2006, 4, 307-312.	13.6	54
81	Navigating the future of bacterial molecular epidemiology. <i>Current Opinion in Microbiology</i> , 2010, 13, 640-645.	2.3	54
82	Low Effective Dispersal of Asexual Genotypes in Heterogeneous Landscapes by the Endemic Pathogen <i>Penicillium marneffei</i> . <i>PLoS Pathogens</i> , 2005, 1, e20.	2.1	52
83	Weak Epistasis May Drive Adaptation in Recombining Bacteria. <i>Genetics</i> , 2018, 208, 1247-1260.	1.2	51
84	Not So Simple After All: Bacteria, Their Population Genetics, and Recombination. <i>Cold Spring Harbor Perspectives in Biology</i> , 2016, 8, a018069.	2.3	50
85	Recombination in <i>Streptococcus pneumoniae</i> Lineages Increase with Carriage Duration and Size of the Polysaccharide Capsule. <i>MBio</i> , 2016, 7, .	1.8	50
86	Estimating the hospitalization burden associated with influenza and respiratory syncytial virus in New York City, 2003–2011. <i>Influenza and Other Respiratory Viruses</i> , 2015, 9, 225-233.	1.5	46
87	Genomic Epidemiology of Penicillin-Nonsusceptible Pneumococci with Nonvaccine Serotypes Causing Invasive Disease in the United States. <i>Journal of Clinical Microbiology</i> , 2017, 55, 1104-1115.	1.8	44
88	US racial and ethnic data for COVID-19 cases: still missing in action. <i>Lancet</i> , The, 2020, 396, e81.	6.3	44
89	The Distribution of Pairwise Genetic Distances: A Tool for Investigating Disease Transmission. <i>Genetics</i> , 2014, 198, 1395-1404.	1.2	43
90	Leveraging Africa's preparedness towards the next phase of the COVID-19 pandemic. <i>The Lancet Global Health</i> , 2020, 8, e884-e885.	2.9	42

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91	COVID-19: US federal accountability for entry, spread, and inequities—lessons for the future. <i>European Journal of Epidemiology</i> , 2020, 35, 995-1006.	2.5	38
92	Coronavirus Disease 2019 Vaccine Impact on Rates of Severe Acute Respiratory Syndrome Coronavirus 2 Cases and Postvaccination Strain Sequences Among Health Care Workers at an Urban Academic Medical Center: A Prospective Cohort Study. <i>Open Forum Infectious Diseases</i> , 2021, 8, ofab465.	0.4	38
93	Previously undetected super-spreading of <i>Mycobacterium tuberculosis</i> revealed by deep sequencing. <i>ELife</i> , 2020, 9, .	2.8	38
94	Transmission from vaccinated individuals in a large SARS-CoV-2 Delta variant outbreak. <i>Cell</i> , 2022, 185, 485-492.e10.	13.5	38
95	A Pluralistic Account of Homology: Adapting the Models to the Data. <i>Molecular Biology and Evolution</i> , 2014, 31, 501-516.	3.5	37
96	Evolution via recombination: Cell-to-cell contact facilitates larger recombination events in <i>Streptococcus pneumoniae</i> . <i>PLoS Genetics</i> , 2018, 14, e1007410.	1.5	37
97	Recombination produces coherent bacterial species clusters in both core and accessory genomes. <i>Microbial Genomics</i> , 2015, 1, e000038.	1.0	37
98	Population structure in the <i>Neisseria</i> , and the biological significance of fuzzy species. <i>Journal of the Royal Society Interface</i> , 2012, 9, 1208-1215.	1.5	33
99	Immunization, Antibiotic Use, and Pneumococcal Colonization Over a 15-Year Period. <i>Pediatrics</i> , 2017, 140, .	1.0	33
100	Carriage burden, multiple colonization and antibiotic pressure promote emergence of resistant vaccine escape pneumococci. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140342.	1.8	31
101	Effects of <i>Streptococcus pneumoniae</i> Strain Background on Complement Resistance. <i>PLoS ONE</i> , 2011, 6, e24581.	1.1	27
102	Fuzzy species revisited. <i>BMC Biology</i> , 2013, 11, 41.	1.7	27
103	Population genetic structure, antibiotic resistance, capsule switching and evolution of invasive pneumococci before conjugate vaccination in Malawi. <i>Vaccine</i> , 2017, 35, 4594-4602.	1.7	27
104	Fine-Scale Haplotype Structure Reveals Strong Signatures of Positive Selection in a Recombining Bacterial Pathogen. <i>Molecular Biology and Evolution</i> , 2020, 37, 417-428.	3.5	27
105	Stability of the pneumococcal population structure in Massachusetts as PCV13 was introduced. <i>BMC Infectious Diseases</i> , 2015, 15, 68.	1.3	26
106	Panproteome-wide analysis of antibody responses to whole cell pneumococcal vaccination. <i>ELife</i> , 2018, 7, .	2.8	26
107	The impact of serotype-specific vaccination on phylodynamic parameters of <i>Streptococcus pneumoniae</i> and the pneumococcal pan-genome. <i>PLoS Pathogens</i> , 2018, 14, e1006966.	2.1	25
108	Optimal SARS-CoV-2 vaccine allocation using real-time attack-rate estimates in Rhode Island and Massachusetts. <i>BMC Medicine</i> , 2021, 19, 162.	2.3	25

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109	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . <i>PLoS Biology</i> , 2020, 18, e3000878.	2.6	24
110	Speciation trajectories in recombining bacterial species. <i>PLoS Computational Biology</i> , 2017, 13, e1005640.	1.5	24
111	The Relative Impact of Community and Hospital Antibiotic Use on the Selection of Extended-spectrum Beta-lactamase-producing <i>Escherichia coli</i> . <i>Clinical Infectious Diseases</i> , 2019, 69, 182-188.	2.9	23
112	Use of Genome Sequencing to Define Institutional Influenza Outbreaks, Toronto, Ontario, Canada, 2014-15. <i>Emerging Infectious Diseases</i> , 2018, 24, 492-497.	2.0	22
113	Early Introduction and Rise of the Omicron Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Variant in Highly Vaccinated University Populations. <i>Clinical Infectious Diseases</i> , 2023, 76, e400-e408.	2.9	22
114	Snowball Sampling Study Design for Serosurveys Early in Disease Outbreaks. <i>American Journal of Epidemiology</i> , 2021, 190, 1918-1927.	1.6	21
115	The role of interspecies recombination in the evolution of antibiotic-resistant pneumococci. <i>ELife</i> , 2021, 10, .	2.8	21
116	Identifying the effect of patient sharing on between-hospital genetic differentiation of methicillin-resistant <i>Staphylococcus aureus</i> . <i>Genome Medicine</i> , 2016, 8, 18.	3.6	20
117	Horizontal gene transfer rate is not the primary determinant of observed antibiotic resistance frequencies in <i>Streptococcus pneumoniae</i> . <i>Science Advances</i> , 2020, 6, eaaz6137.	4.7	19
118	Distribution of Pneumococcal Surface Protein A Families 1 and 2 among <i>Streptococcus pneumoniae</i> Isolates from Children in Finland Who Had Acute Otitis Media or Were Nasopharyngeal Carriers. <i>Vaccine Journal</i> , 2008, 15, 1555-1563.	3.2	18
119	Pneumococcal protein antigen serology varies with age and may predict antigenic profile of colonizing isolates. <i>Journal of Infectious Diseases</i> , 2017, 215, jiw628.	1.9	18
120	High-resolution genomic surveillance elucidates a multilayered hierarchical transfer of resistance between WWTP- and human/animal-associated bacteria. <i>Microbiome</i> , 2022, 10, 16.	4.9	18
121	Negative frequency-dependent selection and asymmetrical transformation stabilise multi-strain bacterial population structures. <i>ISME Journal</i> , 2021, 15, 1523-1538.	4.4	17
122	Missing again: US racial and ethnic data for COVID-19 vaccination. <i>Lancet, The</i> , 2021, 397, 1259-1260.	6.3	17
123	Where is the next SARS-CoV-2 variant of concern?. <i>Lancet, The</i> , 2022, 399, 1938-1939.	6.3	16
124	Structure and Dynamics of Bacterial Populations: Pangenome Ecology. , 2020, , 115-128.		15
125	Random projection based clustering for population genomics. , 2014, , .		13
126	Identification of pneumococcal colonization determinants in the stringent response pathway facilitated by genomic diversity. <i>BMC Genomics</i> , 2015, 16, 369.	1.2	13

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127	The impact of host metapopulation structure on the population genetics of colonizing bacteria. <i>Journal of Theoretical Biology</i> , 2016, 396, 53-62.	0.8	13
128	Penicillin Resistance of Nonvaccine Type Pneumococcus before and after PCV13 Introduction, United States. <i>Emerging Infectious Diseases</i> , 2017, 23, 1012-1015.	2.0	13
129	Comparing Patient Risk Factor-, Sequence Type-, and Resistance Locus Identification-Based Approaches for Predicting Antibiotic Resistance in <i>Escherichia coli</i> Bloodstream Infections. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	12
130	Perfect as the enemy of good: tracing transmissions with low-sensitivity tests to mitigate SARS-CoV-2 outbreaks. <i>Lancet Microbe</i> , The, 2021, 2, e219-e224.	3.4	12
131	Population genomics of pneumococcal carriage in Massachusetts children following introduction of PCV-13. <i>Microbial Genomics</i> , 2019, 5, .	1.0	12
132	Towards global control of parasitic diseases in the Covid-19 era: One Health and the future of multisectoral global health governance. <i>Advances in Parasitology</i> , 2021, 114, 1-26.	1.4	12
133	<i>Streptococcus pyogenes</i> With Reduced Susceptibility to β -Lactams: How Big an Alarm Bell?. <i>Clinical Infectious Diseases</i> , 2020, 71, 205-206.	2.9	11
134	Evaluating the contributions of strategies to prevent SARS-CoV-2 transmission in the healthcare setting: a modelling study. <i>BMJ Open</i> , 2021, 11, e044644.	0.8	10
135	SARS-CoV-2 epidemic after social and economic reopening in three U.S. states reveals shifts in age structure and clinical characteristics. <i>Science Advances</i> , 2022, 8, eabf9868.	4.7	10
136	Two Health or Not Two Health? That Is the Question. <i>MBio</i> , 2019, 10, .	1.8	9
137	Early Signals of Vaccine-driven Perturbation Seen in Pneumococcal Carriage Population Genomic Data. <i>Clinical Infectious Diseases</i> , 2020, 70, 1294-1303.	2.9	9
138	Partial immunity and SARS-CoV-2 mutations. <i>Science</i> , 2021, 372, 354-354.	6.0	9
139	Combining genomic and epidemiological data to compare the transmissibility of SARS-CoV-2 variants Alpha and Iota. <i>Communications Biology</i> , 2022, 5, 439.	2.0	9
140	Substitutions of short heterologous DNA segments of intragenomic or extragenomic origins produce clustered genomic polymorphisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 15066-15071.	3.3	8
141	Transmission of SARS-CoV-2 before and after symptom onset: impact of nonpharmaceutical interventions in China. <i>European Journal of Epidemiology</i> , 2021, 36, 429-439.	2.5	8
142	Impact of Host Heterogeneity on the Efficacy of Interventions to Reduce <i>Staphylococcus aureus</i> Carriage. <i>Infection Control and Hospital Epidemiology</i> , 2016, 37, 197-204.	1.0	7
143	Evolutionary and Population Biology of <i>Streptococcus Pneumoniae</i> . , 2014, , 117-135.		6
144	Biomedical Ph.D. Students Enrolled in Two Elite Universities in the United Kingdom and the United States Report Adopting Multiple Learning Relationships. <i>PLoS ONE</i> , 2014, 9, e103075.	1.1	5

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145	Reproducibility in science: important or incremental?. <i>Lancet Microbe</i> , The, 2020, 1, e59-60.	3.4	5
146	Using Genetic Distance from Archived Samples for the Prediction of Antibiotic Resistance in <i>Escherichia coli</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	5
147	SARS-CoV-2 Attack Rate and Population Immunity in Southern New England, March 2020 to May 2021. <i>JAMA Network Open</i> , 2022, 5, e2214171.	2.8	5
148	Potential for Erosion of Efficacy in Noninferiority Trials of Decreasing Duration of Antibiotic Therapy. <i>Clinical Infectious Diseases</i> , 2019, 69, 1262-1262.	2.9	4
149	The devil in the details: Herd immunity and pandemic response. <i>Cell Host and Microbe</i> , 2021, 29, 1048-1051.	5.1	4
150	Leveraging Pathogen Sequence and Contact Tracing Data to Enhance Vaccine Trials in Emerging Epidemics. <i>Epidemiology</i> , 2021, 32, 698-704.	1.2	3
151	Responseâ€”Influenza. <i>Science</i> , 2009, 325, 1072-1073.	6.0	2
152	Reply to Guy et al.: Support for a bottleneck in the 2011 <i>Escherichia coli</i> O104:H4 outbreak in Germany. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E3629-E3630.	3.3	2
153	Coming to America: Genomic surveillance and how B.1.1.7 arrived in the US. <i>Cell</i> , 2021, 184, 2532-2534.	13.5	2
154	Reply to Partridge et al.: Complementary bioinformatics and experimental approaches to investigate the transfer of AMR genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	2
155	Widespread sharing of pneumococcal strains in a rural African setting: proximate villages are more likely to share similar strains that are carried at multiple timepoints. <i>Microbial Genomics</i> , 2022, 8, .	1.0	1
156	The haunting reality of meningococcal meningitis. <i>Lancet Infectious Diseases</i> , The, 2013, 13, 400.	4.6	0
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