

William P Hanage

List of Publications by Year in descending order

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Version: 2024-02-01

171
papers

21,688
citations

17440

63
h-index

11308

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.	12.6	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.	2.2	1,697
3	Pandemic Potential of a Strain of Influenza A (H1N1): Early Findings. <i>Science</i> , 2009, 324, 1557-1561.	12.6	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.	27.0	1,069
5	Rapid Pneumococcal Evolution in Response to Clinical Interventions. <i>Science</i> , 2011, 331, 430-434.	12.6	828
6	SARS-CoV-2 Titers in Wastewater Are Higher than Expected from Clinically Confirmed Cases. <i>MSystems</i> , 2020, 5, .	3.8	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.	5.7	603
8	Recombination and the Nature of Bacterial Speciation. <i>Science</i> , 2007, 315, 476-480.	12.6	512
9	The Bacterial Species Challenge: Making Sense of Genetic and Ecological Diversity. <i>Science</i> , 2009, 323, 741-746.	12.6	381
10	Horizontal gene transfer and the evolution of bacterial and archaeal population structure. <i>Trends in Genetics</i> , 2013, 29, 170-175.	6.7	364
11	Population genomics of post-vaccine changes in pneumococcal epidemiology. <i>Nature Genetics</i> , 2013, 45, 656-663.	21.4	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.	7.1	363
13	Making Sense of Mutation: What D614G Means for the COVID-19 Pandemic Remains Unclear. <i>Cell</i> , 2020, 182, 794-795.	28.9	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.	2.0	320
15	Fuzzy species among recombinogenic bacteria. <i>BMC Biology</i> , 2005, 3, 6.	3.8	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.	7.1	262
17	Continued Impact of Pneumococcal Conjugate Vaccine on Carriage in Young Children. <i>Pediatrics</i> , 2009, 124, e1-e11.	2.1	258
18	An omics-based framework for assessing the health risk of antimicrobial resistance genes. <i>Nature Communications</i> , 2021, 12, 4765.	12.8	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, .	12.6	226
20	Horizontal gene transfer and adaptive evolution in bacteria. <i>Nature Reviews Microbiology</i> , 2022, 20, 206-218.	28.6	214
21	Comprehensive Identification of Single Nucleotide Polymorphisms Associated with Beta-lactam Resistance within Pneumococcal Mosaic Genes. <i>PLoS Genetics</i> , 2014, 10, e1004547.	3.5	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.	2.5	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.	9.1	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.	8.0	192
25	Scientific consensus on the COVID-19 pandemic: we need to act now. <i>Lancet</i> , The, 2020, 396, e71-e72.	13.7	189
26	Origin and Proliferation of Multiple-Drug Resistance in Bacterial Pathogens. <i>Microbiology and Molecular Biology Reviews</i> , 2015, 79, 101-116.	6.6	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.	5.8	181
28	Displaying the relatedness among isolates of bacterial species " the eBURST approach. <i>FEMS Microbiology Letters</i> , 2004, 241, 129-134.	1.8	179
29	Detection of recombination events in bacterial genomes from large population samples. <i>Nucleic Acids Research</i> , 2012, 40, e6-e6.	14.5	179
30	Restricted Gene Flow among Hospital Subpopulations of <i>Enterococcus faecium</i> . <i>MBio</i> , 2012, 3, e00151-12.	4.1	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.	8.6	173
32	Diversification of bacterial genome content through distinct mechanisms over different timescales. <i>Nature Communications</i> , 2014, 5, 5471.	12.8	173
33	Microbiology: Microbiome science needs a healthy dose of scepticism. <i>Nature</i> , 2014, 512, 247-248.	27.8	172
34	Efficient Inference of Recent and Ancestral Recombination within Bacterial Populations. <i>Molecular Biology and Evolution</i> , 2017, 34, 1167-1182.	8.9	168
35	Sequences, sequence clusters and bacterial species. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 1917-1927.	4.0	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, .	7.1	161

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37	Multi-institute analysis of carbapenem resistance reveals remarkable diversity, unexplained mechanisms, and limited clonal outbreaks. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 1135-1140.	7.1	158
38	Within-Host Bacterial Diversity Hinders Accurate Reconstruction of Transmission Networks from Genomic Distance Data. PLoS Computational Biology, 2014, 10, e1003549.	3.2	148
39	Neutral microepidemic evolution of bacterial pathogens. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1968-1973.	7.1	141
40	Invasiveness of Serotypes and Clones of Streptococcus pneumoniae among Children in Finland. Infection and Immunity, 2005, 73, 431-435.	2.2	137
41	Cryptic ecology among host generalist <i>Campylobacter jejuni</i> in domestic animals. Molecular Ecology, 2014, 23, 2442-2451.	3.9	131
42	No coexistence for free: Neutral null models for multistrain pathogens. Epidemics, 2009, 1, 2-13.	3.0	130
43	Ecological Overlap and Horizontal Gene Transfer in Staphylococcus aureus and Staphylococcus epidermidis. Genome Biology and Evolution, 2015, 7, 1313-1328.	2.5	130
44	Evidence that pneumococcal serotype replacement in Massachusetts following conjugate vaccination is now complete. Epidemics, 2010, 2, 80-84.	3.0	128
45	Diversity and Antibiotic Resistance among Nonvaccine Serotypes of Streptococcus pneumoniae Carriage Isolates in the Post-Heptavalent Conjugate Vaccine Era. Journal of Infectious Diseases, 2007, 195, 347-352.	4.0	127
46	Frequency-dependent selection in vaccine-associated pneumococcal population dynamics. Nature Ecology and Evolution, 2017, 1, 1950-1960.	7.8	121
47	Wastewater surveillance of SARS-CoV-2 across 40 U.S. states from February to June 2020. Water Research, 2021, 202, 117400.	11.3	119
48	An early warning approach to monitor COVID-19 activity with multiple digital traces in near real time. Science Advances, 2021, 7, .	10.3	114
49	Identifying Currents in the Gene Pool for Bacterial Populations Using an Integrative Approach. PLoS Computational Biology, 2009, 5, e1000455.	3.2	112
50	Serotype specific invasive capacity and persistent reduction in invasive pneumococcal disease. Vaccine, 2010, 29, 283-288.	3.8	112
51	Evidence for Soft Selective Sweeps in the Evolution of Pneumococcal Multidrug Resistance and Vaccine Escape. Genome Biology and Evolution, 2014, 6, 1589-1602.	2.5	112
52	The impact of homologous recombination on the generation of diversity in bacteria. Journal of Theoretical Biology, 2006, 239, 210-219.	1.7	106
53	Using Multilocus Sequence Data To Define the Pneumococcus. Journal of Bacteriology, 2005, 187, 6223-6230.	2.2	104
54	Making sense of differences in pneumococcal serotype replacement. Lancet Infectious Diseases, The, 2019, 19, e213-e220.	9.1	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.	3.3	93
56	Modelling bacterial speciation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 2039-2044.	4.0	88
57	HIV-1 Transmitting Couples Have Similar Viral Load Set-Points in Rakai, Uganda. <i>PLoS Pathogens</i> , 2010, 6, e1000876.	4.7	88
58	Heterogeneity in the Frequency and Characteristics of Homologous Recombination in Pneumococcal Evolution. <i>PLoS Genetics</i> , 2014, 10, e1004300.	3.5	84
59	Shared Genomic Variants: Identification of Transmission Routes Using Pathogen Deep-Sequence Data. <i>American Journal of Epidemiology</i> , 2017, 186, 1209-1216.	3.4	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.	2.2	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.	3.4	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.	1.3	78
63	Selective and Genetic Constraints on Pneumococcal Serotype Switching. <i>PLoS Genetics</i> , 2015, 11, e1005095.	3.5	78
64	Variable recombination dynamics during the emergence, transmission and –disarming– of a multidrug-resistant pneumococcal clone. <i>BMC Biology</i> , 2014, 12, 49.	3.8	75
65	Global emergence and population dynamics of divergent serotype 3 CC180 pneumococci. <i>PLoS Pathogens</i> , 2018, 14, e1007438.	4.7	74
66	Rapid inference of antibiotic resistance and susceptibility by genomic neighbour typing. <i>Nature Microbiology</i> , 2020, 5, 455-464.	13.3	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.	28.9	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.	2.0	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.	4.1	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.	7.1	68
71	Metrics to relate COVID-19 wastewater data to clinical testing dynamics. <i>Water Research</i> , 2022, 212, 118070.	11.3	68
72	Population genomic datasets describing the post-vaccine evolutionary epidemiology of <i>Streptococcus pneumoniae</i> . <i>Scientific Data</i> , 2015, 2, 150058.	5.3	67

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73	Serotype-specific problems associated with pneumococcal conjugate vaccination. <i>Future Microbiology</i> , 2008, 3, 23-30.	2.0	64
74	Phylogenetic interpretation during outbreaks requires caution. <i>Nature Microbiology</i> , 2020, 5, 876-877.	13.3	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.	2.5	63
76	Mechanisms of genome evolution of <i>Streptococcus</i> . <i>Infection, Genetics and Evolution</i> , 2015, 33, 334-342.	2.3	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.	3.8	60
78	Carried Pneumococci in Massachusetts Children. <i>Pediatric Infectious Disease Journal</i> , 2011, 30, 302-308.	2.0	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.	2.5	55
80	Modelling infectious disease – time to think outside the box?. <i>Nature Reviews Microbiology</i> , 2006, 4, 307-312.	28.6	54
81	Navigating the future of bacterial molecular epidemiology. <i>Current Opinion in Microbiology</i> , 2010, 13, 640-645.	5.1	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.	4.7	52
83	Weak Epistasis May Drive Adaptation in Recombining Bacteria. <i>Genetics</i> , 2018, 208, 1247-1260.	2.9	51
84	Not So Simple After All: Bacteria, Their Population Genetics, and Recombination. <i>Cold Spring Harbor Perspectives in Biology</i> , 2016, 8, a018069.	5.5	50
85	Recombination in <i>Streptococcus pneumoniae</i> Lineages Increase with Carriage Duration and Size of the Polysaccharide Capsule. <i>MBio</i> , 2016, 7, .	4.1	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.	3.4	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.	3.9	44
88	US racial and ethnic data for COVID-19 cases: still missing in action. <i>Lancet</i> , The, 2020, 396, e81.	13.7	44
89	The Distribution of Pairwise Genetic Distances: A Tool for Investigating Disease Transmission. <i>Genetics</i> , 2014, 198, 1395-1404.	2.9	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.	6.3	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.	5.7	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.	0.9	38
93	Previously undetected super-spreading of <i>Mycobacterium tuberculosis</i> revealed by deep sequencing. <i>ELife</i> , 2020, 9, .	6.0	38
94	Transmission from vaccinated individuals in a large SARS-CoV-2 Delta variant outbreak. <i>Cell</i> , 2022, 185, 485-492.e10.	28.9	38
95	A Pluralistic Account of Homology: Adapting the Models to the Data. <i>Molecular Biology and Evolution</i> , 2014, 31, 501-516.	8.9	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.	3.5	37
97	Recombination produces coherent bacterial species clusters in both core and accessory genomes. <i>Microbial Genomics</i> , 2015, 1, e000038.	2.0	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.	3.4	33
99	Immunization, Antibiotic Use, and Pneumococcal Colonization Over a 15-Year Period. <i>Pediatrics</i> , 2017, 140, .	2.1	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.	4.0	31
101	Effects of <i>Streptococcus pneumoniae</i> Strain Background on Complement Resistance. <i>PLoS ONE</i> , 2011, 6, e24581.	2.5	27
102	Fuzzy species revisited. <i>BMC Biology</i> , 2013, 11, 41.	3.8	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.	3.8	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.	8.9	27
105	Stability of the pneumococcal population structure in Massachusetts as PCV13 was introduced. <i>BMC Infectious Diseases</i> , 2015, 15, 68.	2.9	26
106	Panproteome-wide analysis of antibody responses to whole cell pneumococcal vaccination. <i>ELife</i> , 2018, 7, .	6.0	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.	4.7	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.	5.5	25

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109	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . <i>PLoS Biology</i> , 2020, 18, e3000878.	5.6	24
110	Speciation trajectories in recombining bacterial species. <i>PLoS Computational Biology</i> , 2017, 13, e1005640.	3.2	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.	5.8	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.	4.3	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.	5.8	22
114	Snowball Sampling Study Design for Serosurveys Early in Disease Outbreaks. <i>American Journal of Epidemiology</i> , 2021, 190, 1918-1927.	3.4	21
115	The role of interspecies recombination in the evolution of antibiotic-resistant pneumococci. <i>ELife</i> , 2021, 10, .	6.0	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.	8.2	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.	10.3	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.	3.1	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.	4.0	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.	11.1	18
121	Negative frequency-dependent selection and asymmetrical transformation stabilise multi-strain bacterial population structures. <i>ISME Journal</i> , 2021, 15, 1523-1538.	9.8	17
122	Missing again: US racial and ethnic data for COVID-19 vaccination. <i>Lancet, The</i> , 2021, 397, 1259-1260.	13.7	17
123	Where is the next SARS-CoV-2 variant of concern?. <i>Lancet, The</i> , 2022, 399, 1938-1939.	13.7	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.	2.8	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.	1.7	13
128	Penicillin Resistance of Nonvaccine Type Pneumococcus before and after PCV13 Introduction, United States. <i>Emerging Infectious Diseases</i> , 2017, 23, 1012-1015.	4.3	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, .	3.9	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.	7.3	12
131	Population genomics of pneumococcal carriage in Massachusetts children following introduction of PCV-13. <i>Microbial Genomics</i> , 2019, 5, .	2.0	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.	3.2	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.	5.8	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.	1.9	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.	10.3	10
136	Two Health or Not Two Health? That Is the Question. <i>MBio</i> , 2019, 10, .	4.1	9
137	Early Signals of Vaccine-driven Perturbation Seen in Pneumococcal Carriage Population Genomic Data. <i>Clinical Infectious Diseases</i> , 2020, 70, 1294-1303.	5.8	9
138	Partial immunity and SARS-CoV-2 mutations. <i>Science</i> , 2021, 372, 354-354.	12.6	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.	4.4	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.	7.1	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.	5.7	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.	1.8	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.	2.5	5

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145	Reproducibility in science: important or incremental?. <i>Lancet Microbe</i> , The, 2020, 1, e59-60.	7.3	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, .	3.2	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.	5.9	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.	5.8	4
149	The devil in the details: Herd immunity and pandemic response. <i>Cell Host and Microbe</i> , 2021, 29, 1048-1051.	11.0	4
150	Leveraging Pathogen Sequence and Contact Tracing Data to Enhance Vaccine Trials in Emerging Epidemics. <i>Epidemiology</i> , 2021, 32, 698-704.	2.7	3
151	Responseâ€”Influenza. <i>Science</i> , 2009, 325, 1072-1073.	12.6	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.	7.1	2
153	Coming to America: Genomic surveillance and how B.1.1.7 arrived in the US. <i>Cell</i> , 2021, 184, 2532-2534.	28.9	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, .	7.1	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, .	2.0	1
156	The haunting reality of meningococcal meningitis. <i>Lancet Infectious Diseases</i> , The, 2013, 13, 400.	9.1	0
157	1165. Comparing Patient Risk Factors, Sequence Type, and Resistance Loci Identification Approaches for Predicting Antibiotic Resistance in <i>Escherichia coli</i> Bloodstream Infections. <i>Open Forum Infectious Diseases</i> , 2018, 5, S351-S351.	0.9	0
158	From bacterial genomics to clinical epidemiology: an interview with Bill Hanage. <i>BMC Biology</i> , 2018, 16, 122.	3.8	0
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