

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	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
2	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
3	Horizontal gene transfer and adaptive evolution in bacteria. <i>Nature Reviews Microbiology</i> , 2022, 20, 206-218.	28.6	214
4	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
5	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
6	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
7	Metrics to relate COVID-19 wastewater data to clinical testing dynamics. <i>Water Research</i> , 2022, 212, 118070.	11.3	68
8	Transmission from vaccinated individuals in a large SARS-CoV-2 Delta variant outbreak. <i>Cell</i> , 2022, 185, 485-492.e10.	28.9	38
9	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
10	Where is the next SARS-CoV-2 variant of concern?. <i>Lancet</i> , The, 2022, 399, 1938-1939.	13.7	16
11	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
12	Phylogenetic analysis of SARS-CoV-2 in Boston highlights the impact of superspreading events. <i>Science</i> , 2021, 371, .	12.6	226
13	Negative frequency-dependent selection and asymmetrical transformation stabilise multi-strain bacterial population structures. <i>ISME Journal</i> , 2021, 15, 1523-1538.	9.8	17
14	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
15	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
16	An early warning approach to monitor COVID-19 activity with multiple digital traces in near real time. <i>Science Advances</i> , 2021, 7, .	10.3	114
17	Snowball Sampling Study Design for Serosurveys Early in Disease Outbreaks. <i>American Journal of Epidemiology</i> , 2021, 190, 1918-1927.	3.4	21
18	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

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19	Partial immunity and SARS-CoV-2 mutations. <i>Science</i> , 2021, 372, 354-354.	12.6	9
20	Missing again: US racial and ethnic data for COVID-19 vaccination. <i>Lancet, The</i> , 2021, 397, 1259-1260.	13.7	17
21	Leveraging Pathogen Sequence and Contact Tracing Data to Enhance Vaccine Trials in Emerging Epidemics. <i>Epidemiology</i> , 2021, 32, 698-704.	2.7	3
22	Perfect as the enemy of good: tracing transmissions with low-sensitivity tests to mitigate SARS-CoV-2 outbreaks. <i>Lancet Microbe, The</i> , 2021, 2, e219-e224.	7.3	12
23	Reply to Shaw: Challenges for enrichment analysis of AMR gene-bearing plasmids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, e2104557118.	7.1	0
24	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
25	The devil in the details: Herd immunity and pandemic response. <i>Cell Host and Microbe</i> , 2021, 29, 1048-1051.	11.0	4
26	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
27	The role of interspecies recombination in the evolution of antibiotic-resistant pneumococci. <i>ELife</i> , 2021, 10, .	6.0	21
28	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
29	An omics-based framework for assessing the health risk of antimicrobial resistance genes. <i>Nature Communications</i> , 2021, 12, 4765.	12.8	248
30	Wastewater surveillance of SARS-CoV-2 across 40 U.S. states from February to June 2020. <i>Water Research</i> , 2021, 202, 117400.	11.3	119
31	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
32	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
33	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
34	376. Sensitivity and Specificity of the WHO Probable SARS-CoV-2 Case Definition Among Symptomatic Healthcare Personnel. <i>Open Forum Infectious Diseases</i> , 2021, 8, S290-S290.	0.9	0
35	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
36	<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

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37	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
38	Seroprevalence of SARS-CoV-2 in Hong Kong returnees. <i>Lancet Microbe</i> , The, 2020, 1, e147.	7.3	0
39	Scientific consensus on the COVID-19 pandemic: we need to act now. <i>Lancet</i> , The, 2020, 396, e71-e72.	13.7	189
40	Reproducibility in science: important or incremental?. <i>Lancet Microbe</i> , The, 2020, 1, e59-60.	7.3	5
41	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
42	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
43	SARS-CoV-2 Titers in Wastewater Are Higher than Expected from Clinically Confirmed Cases. <i>MSystems</i> , 2020, 5, .	3.8	649
44	US racial and ethnic data for COVID-19 cases: still missing in action. <i>Lancet</i> , The, 2020, 396, e81.	13.7	44
45	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
46	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
47	Making Sense of Mutation: What D614G Means for the COVID-19 Pandemic Remains Unclear. <i>Cell</i> , 2020, 182, 794-795.	28.9	353
48	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
49	Rapid inference of antibiotic resistance and susceptibility by genomic neighbour typing. <i>Nature Microbiology</i> , 2020, 5, 455-464.	13.3	74
50	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
51	Structure and Dynamics of Bacterial Populations: Pangenome Ecology. , 2020, , 115-128.		15
52	Phylogenetic interpretation during outbreaks requires caution. <i>Nature Microbiology</i> , 2020, 5, 876-877.	13.3	64
53	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
54	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . <i>PLoS Biology</i> , 2020, 18, e3000878.	5.6	24

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55	Previously undetected super-spreading of Mycobacterium tuberculosis revealed by deep sequencing. <i>ELife</i> , 2020, 9, .	6.0	38
56	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
57	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
58	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
59	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
60	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
61	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
62	Making sense of differences in pneumococcal serotype replacement. <i>Lancet Infectious Diseases</i> , The, 2019, 19, e213-e220.	9.1	100
63	Two Health or Not Two Health? That Is the Question. <i>MBio</i> , 2019, 10, .	4.1	9
64	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
65	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
66	561. Genomic Epidemiology of Methicillin-Resistant <i>Staphylococcus aureus</i> in Two Cohorts of High-Risk Military Trainees. <i>Open Forum Infectious Diseases</i> , 2019, 6, S266-S266.	0.9	0
67	Pneumococcal conjugate vaccines in different settings â€“ Authors' reply. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 1284.	9.1	0
68	The Relative Impact of Community and Hospital Antibiotic Use on the Selection of Extended-spectrum Beta-lactamaseâ€“producing <i>Escherichia coli</i> . <i>Clinical Infectious Diseases</i> , 2019, 69, 182-188.	5.8	23
69	Population genomics of pneumococcal carriage in Massachusetts children following introduction of PCV-13. <i>Microbial Genomics</i> , 2019, 5, .	2.0	12
70	Weak Epistasis May Drive Adaptation in Recombining Bacteria. <i>Genetics</i> , 2018, 208, 1247-1260.	2.9	51
71	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
72	Global emergence and population dynamics of divergent serotype 3 CC180 pneumococci. <i>PLoS Pathogens</i> , 2018, 14, e1007438.	4.7	74

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73	From bacterial genomics to clinical epidemiology: an interview with Bill Hanage. <i>BMC Biology</i> , 2018, 16, 122.	3.8	0
74	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
75	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
76	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
77	Panproteome-wide analysis of antibody responses to whole cell pneumococcal vaccination. <i>ELife</i> , 2018, 7, .	6.0	26
78	Genomic epidemiology of methicillin-resistant <i>Staphylococcus aureus</i> ST22 widespread in communities of the Gaza Strip, 2009. <i>Eurosurveillance</i> , 2018, 23, .	7.0	0
79	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
80	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.	7.1	158
81	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
82	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
83	Immunization, Antibiotic Use, and Pneumococcal Colonization Over a 15-Year Period. <i>Pediatrics</i> , 2017, 140, .	2.1	33
84	Frequency-dependent selection in vaccine-associated pneumococcal population dynamics. <i>Nature Ecology and Evolution</i> , 2017, 1, 1950-1960.	7.8	121
85	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
86	Efficient Inference of Recent and Ancestral Recombination within Bacterial Populations. <i>Molecular Biology and Evolution</i> , 2017, 34, 1167-1182.	8.9	168
87	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
88	Penicillin Resistance of Nonvaccine Type <i>Pneumococcus</i> before and after PCV13 Introduction, United States. <i>Emerging Infectious Diseases</i> , 2017, 23, 1012-1015.	4.3	13
89	Speciation trajectories in recombining bacterial species. <i>PLoS Computational Biology</i> , 2017, 13, e1005640.	3.2	24
90	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

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91	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
92	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
93	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
94	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
95	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
96	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
97	Population genomic datasets describing the post-vaccine evolutionary epidemiology of <i>Streptococcus pneumoniae</i> . <i>Scientific Data</i> , 2015, 2, 150058.	5.3	67
98	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
99	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
100	Identification of pneumococcal colonization determinants in the stringent response pathway facilitated by genomic diversity. <i>BMC Genomics</i> , 2015, 16, 369.	2.8	13
101	Origin and Proliferation of Multiple-Drug Resistance in Bacterial Pathogens. <i>Microbiology and Molecular Biology Reviews</i> , 2015, 79, 101-116.	6.6	183
102	Stability of the pneumococcal population structure in Massachusetts as PCV13 was introduced. <i>BMC Infectious Diseases</i> , 2015, 15, 68.	2.9	26
103	Selective and Genetic Constraints on Pneumococcal Serotype Switching. <i>PLoS Genetics</i> , 2015, 11, e1005095.	3.5	78
104	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
105	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
106	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.	2.5	130
107	Mechanisms of genome evolution of <i>Streptococcus</i> . <i>Infection, Genetics and Evolution</i> , 2015, 33, 334-342.	2.3	63
108	Recombination produces coherent bacterial species clusters in both core and accessory genomes. <i>Microbial Genomics</i> , 2015, 1, e000038.	2.0	37

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109	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
110	Evolutionary and Population Biology of <i>Streptococcus Pneumoniae</i> . , 2014, , 117-135.		6
111	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
112	Within-Host Bacterial Diversity Hinders Accurate Reconstruction of Transmission Networks from Genomic Distance Data. <i>PLoS Computational Biology</i> , 2014, 10, e1003549.	3.2	148
113	Heterogeneity in the Frequency and Characteristics of Homologous Recombination in Pneumococcal Evolution. <i>PLoS Genetics</i> , 2014, 10, e1004300.	3.5	84
114	Diversification of bacterial genome content through distinct mechanisms over different timescales. <i>Nature Communications</i> , 2014, 5, 5471.	12.8	173
115	The Distribution of Pairwise Genetic Distances: A Tool for Investigating Disease Transmission. <i>Genetics</i> , 2014, 198, 1395-1404.	2.9	43
116	Cryptic ecology among host generalist <i>Campylobacter jejuni</i> in domestic animals. <i>Molecular Ecology</i> , 2014, 23, 2442-2451.	3.9	131
117	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.	2.5	112
118	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
119	Random projection based clustering for population genomics. , 2014, , .		13
120	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
121	A Pluralistic Account of Homology: Adapting the Models to the Data. <i>Molecular Biology and Evolution</i> , 2014, 31, 501-516.	8.9	37
122	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
123	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
124	Microbiology: Microbiome science needs a healthy dose of scepticism. <i>Nature</i> , 2014, 512, 247-248.	27.8	172
125	Fuzzy species revisited. <i>BMC Biology</i> , 2013, 11, 41.	3.8	27
126	The haunting reality of meningococcal meningitis. <i>Lancet Infectious Diseases</i> , The, 2013, 13, 400.	9.1	0

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127	Horizontal gene transfer and the evolution of bacterial and archaeal population structure. Trends in Genetics, 2013, 29, 170-175.	6.7	364
128	Population genomics of post-vaccine changes in pneumococcal epidemiology. Nature Genetics, 2013, 45, 656-663.	21.4	364
129	Comparative Genomics of Recent Shiga Toxin-Producing Escherichia coli O104:H4: Short-Term Evolution of an Emerging Pathogen. MBio, 2013, 4, e00452-12.	4.1	68
130	Historical Zoonoses and Other Changes in Host Tropism of Staphylococcus aureus, Identified by Phylogenetic Analysis of a Population Dataset. PLoS ONE, 2013, 8, e62369.	2.5	55
131	Population structure in the <i>Neisseria</i> , and the biological significance of fuzzy species. Journal of the Royal Society Interface, 2012, 9, 1208-1215.	3.4	33
132	Detection of recombination events in bacterial genomes from large population samples. Nucleic Acids Research, 2012, 40, e6-e6.	14.5	179
133	Genomic epidemiology of the <i>Escherichia coli</i> O104:H4 outbreaks in Europe, 2011. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 3065-3070.	7.1	262
134	Reply to Guy et al.: Support for a bottleneck in the 2011 Escherichia coli O104:H4 outbreak in Germany. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E3629-E3630.	7.1	2
135	Pneumococcal Carriage and Antibiotic Resistance in Young Children Before 13-valent Conjugate Vaccine. Pediatric Infectious Disease Journal, 2012, 31, 249-254.	2.0	71
136	Restricted Gene Flow among Hospital Subpopulations of Enterococcus faecium. MBio, 2012, 3, e00151-12.	4.1	177
137	Rapid Pneumococcal Evolution in Response to Clinical Interventions. Science, 2011, 331, 430-434.	12.6	828
138	Effects of Streptococcus pneumoniae Strain Background on Complement Resistance. PLoS ONE, 2011, 6, e24581.	2.5	27
139	Carried Pneumococci in Massachusetts Children. Pediatric Infectious Disease Journal, 2011, 30, 302-308.	2.0	55
140	Population biology of Gram-positive pathogens: high-risk clones for dissemination of antibiotic resistance. FEMS Microbiology Reviews, 2011, 35, 872-900.	8.6	173
141	What is the mechanism for persistent coexistence of drug-susceptible and drug-resistant strains of <i>Streptococcus pneumoniae</i> ?. Journal of the Royal Society Interface, 2010, 7, 905-919.	3.4	83
142	HIV-1 Transmitting Couples Have Similar Viral Load Set-Points in Rakai, Uganda. PLoS Pathogens, 2010, 6, e1000876.	4.7	88
143	Evidence that pneumococcal serotype replacement in Massachusetts following conjugate vaccination is now complete. Epidemics, 2010, 2, 80-84.	3.0	128
144	Navigating the future of bacterial molecular epidemiology. Current Opinion in Microbiology, 2010, 13, 640-645.	5.1	54

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145	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
146	Serotype specific invasive capacity and persistent reduction in invasive pneumococcal disease. <i>Vaccine</i> , 2010, 29, 283-288.	3.8	112
147	Pandemic Potential of a Strain of Influenza A (H1N1): Early Findings. <i>Science</i> , 2009, 324, 1557-1561.	12.6	1,665
148	Response to Influenza. <i>Science</i> , 2009, 325, 1072-1073.	12.6	2
149	Identifying Currents in the Gene Pool for Bacterial Populations Using an Integrative Approach. <i>PLoS Computational Biology</i> , 2009, 5, e1000455.	3.2	112
150	Continued Impact of Pneumococcal Conjugate Vaccine on Carriage in Young Children. <i>Pediatrics</i> , 2009, 124, e1-e11.	2.1	258
151	No coexistence for free: Neutral null models for multistrain pathogens. <i>Epidemics</i> , 2009, 1, 2-13.	3.0	130
152	The Bacterial Species Challenge: Making Sense of Genetic and Ecological Diversity. <i>Science</i> , 2009, 323, 741-746.	12.6	381
153	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
154	Serotype-specific problems associated with pneumococcal conjugate vaccination. <i>Future Microbiology</i> , 2008, 3, 23-30.	2.0	64
155	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.	4.0	127
156	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
157	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
158	Recombination and the Nature of Bacterial Speciation. <i>Science</i> , 2007, 315, 476-480.	12.6	512
159	Modelling infectious disease – time to think outside the box?. <i>Nature Reviews Microbiology</i> , 2006, 4, 307-312.	28.6	54
160	The impact of homologous recombination on the generation of diversity in bacteria. <i>Journal of Theoretical Biology</i> , 2006, 239, 210-219.	1.7	106
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