

# Keith A Jolley

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2754393/publications.pdf>

Version: 2024-02-01

149  
papers

15,097  
citations

25014

57  
h-index

20343

116  
g-index

172  
all docs

172  
docs citations

172  
times ranked

12294  
citing authors

#	ARTICLE	IF	CITATIONS
1	BIGSdb: Scalable analysis of bacterial genome variation at the population level. BMC Bioinformatics, 2010, 11, 595.	1.2	2,074
2	Open-access bacterial population genomics: BIGSdb software, the PubMLST.org website and their applications. Wellcome Open Research, 2018, 3, 124.	0.9	1,710
3	Multilocus Sequence Typing System for the Endosymbiont <i>Wolbachia pipientis</i> . Applied and Environmental Microbiology, 2006, 72, 7098-7110.	1.4	730
4	MLST revisited: the gene-by-gene approach to bacterial genomics. Nature Reviews Microbiology, 2013, 11, 728-736.	13.6	590
5	Ribosomal multilocus sequence typing: universal characterization of bacteria from domain to strain. Microbiology (United Kingdom), 2012, 158, 1005-1015.	0.7	497
6	mlstdbNet - distributed multi-locus sequence typing (MLST) databases. BMC Bioinformatics, 2004, 5, 86.	1.2	459
7	Multilocus Sequence Typing of <i>Clostridium difficile</i> . Journal of Clinical Microbiology, 2010, 48, 770-778.	1.8	399
8	Genome-wide association study identifies vitamin B <sub>5</sub> biosynthesis as a host specificity factor in <i>Campylobacter</i> . Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11923-11927.	3.3	267
9	Changes in the incidence of invasive disease due to <i>Streptococcus pneumoniae</i> , <i>Haemophilus influenzae</i> , and <i>Neisseria meningitidis</i> during the COVID-19 pandemic in 26 countries and territories in the Invasive Respiratory Infection Surveillance Initiative: a prospective analysis of surveillance data. The Lancet Digital Health, 2021, 3, e360-e370.	5.9	260
10	Description and Nomenclature of <i>Neisseria meningitidis</i> Capsule Locus. Emerging Infectious Diseases, 2013, 19, 566-573.	2.0	259
11	Distribution of Serogroups and Genotypes among Disease-Associated and Carried Isolates of <i>Neisseria meningitidis</i> from the Czech Republic, Greece, and Norway. Journal of Clinical Microbiology, 2004, 42, 5146-5153.	1.8	222
12	Genomic Evidence for the Evolution of <i>Streptococcus equi</i> : Host Restriction, Increased Virulence, and Genetic Exchange with Human Pathogens. PLoS Pathogens, 2009, 5, e1000346.	2.1	197
13	Genomic resolution of an aggressive, widespread, diverse and expanding meningococcal serogroup B, C and W lineage. Journal of Infection, 2015, 71, 544-552.	1.7	185
14	Genetic Analysis of Meningococci Carried by Children and Young Adults. Journal of Infectious Diseases, 2005, 191, 1263-1271.	1.9	178
15	A chromosomally integrated bacteriophage in invasive meningococci. Journal of Experimental Medicine, 2005, 201, 1905-1913.	4.2	166
16	A gene-by-gene population genomics platform: de novo assembly, annotation and genealogical analysis of 108 representative <i>Neisseria meningitidis</i> genomes. BMC Genomics, 2014, 15, 1138.	1.2	164
17	A genomic approach to bacterial taxonomy: an examination and proposed reclassification of species within the genus <i>Neisseria</i> . Microbiology (United Kingdom), 2012, 158, 1570-1580.	0.7	153
18	Molecular typing of meningococci: recommendations for target choice and nomenclature. FEMS Microbiology Reviews, 2007, 31, 89-96.	3.9	150

#	ARTICLE	IF	CITATIONS
19	Clinical <i>Clostridium difficile</i> : Clonality and Pathogenicity Locus Diversity. PLoS ONE, 2011, 6, e19993.	1.1	150
20	PorA Variable Regions of <i>Neisseria meningitidis</i> . Emerging Infectious Diseases, 2004, 10, 674-678.	2.0	142
21	Carried Meningococci in the Czech Republic: a Diverse Recombining Population. Journal of Clinical Microbiology, 2000, 38, 4492-4498.	1.8	142
22	The Influence of Mutation, Recombination, Population History, and Selection on Patterns of Genetic Diversity in <i>Neisseria meningitidis</i> . Molecular Biology and Evolution, 2005, 22, 562-569.	3.5	138
23	A Gene-By-Gene Approach to Bacterial Population Genomics: Whole Genome MLST of <i>Campylobacter</i> . Genes, 2012, 3, 261-277.	1.0	135
24	A surveillance network for meningococcal disease in Europe. FEMS Microbiology Reviews, 2007, 31, 27-36.	3.9	134
25	Comparative Analysis of the Two <i>Acinetobacter baumannii</i> Multilocus Sequence Typing (MLST) Schemes. Frontiers in Microbiology, 2019, 10, 930.	1.5	133
26	Cryptic ecology among host generalist <i>Campylobacter jejuni</i> in domestic animals. Molecular Ecology, 2014, 23, 2442-2451.	2.0	131
27	<i>Cronobacter</i> , the emergent bacterial pathogen <i>Enterobacter sakazakii</i> comes of age; MLST and whole genome sequence analysis. BMC Genomics, 2014, 15, 1121.	1.2	131
28	Ecological Overlap and Horizontal Gene Transfer in <i>Staphylococcus aureus</i> and <i>Staphylococcus epidermidis</i> . Genome Biology and Evolution, 2015, 7, 1313-1328.	1.1	130
29	Progressive genome-wide introgression in agricultural <i>Campylobacter coli</i> . Molecular Ecology, 2013, 22, 1051-1064.	2.0	128
30	Real-Time Genomic Epidemiological Evaluation of Human <i>Campylobacter</i> Isolates by Use of Whole-Genome Multilocus Sequence Typing. Journal of Clinical Microbiology, 2013, 51, 2526-2534.	1.8	124
31	A Reference Pan-Genome Approach to Comparative Bacterial Genomics: Identification of Novel Epidemiological Markers in Pathogenic <i>Campylobacter</i> . PLoS ONE, 2014, 9, e92798.	1.1	122
32	Role of selection in the emergence of lineages and the evolution of virulence in <i>Neisseria meningitidis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 15082-15087.	3.3	121
33	Ribosomal proteins as biomarkers for bacterial identification by mass spectrometry in the clinical microbiology laboratory. Journal of Microbiological Methods, 2013, 94, 390-396.	0.7	115
34	Disease-associated genotypes of the commensal skin bacterium <i>Staphylococcus epidermidis</i> . Nature Communications, 2018, 9, 5034.	5.8	115
35	Multilocus sequence typing for global surveillance of meningococcal disease. FEMS Microbiology Reviews, 2007, 31, 15-26.	3.9	105
36	Core Genome Multilocus Sequence Typing Scheme for Stable, Comparative Analyses of <i>Campylobacter jejuni</i> and <i>C. coli</i> Human Disease Isolates. Journal of Clinical Microbiology, 2017, 55, 2086-2097.	1.8	105

#	ARTICLE	IF	CITATIONS
37	Target Gene Sequencing To Characterize the Penicillin G Susceptibility of <i>Neisseria meningitidis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2007, 51, 2784-2792.	1.4	103
38	Development of an unambiguous and discriminatory multilocus sequence typing scheme for the <i>Streptococcus zooepidemicus</i> group. <i>Microbiology (United Kingdom)</i> , 2008, 154, 3016-3024.	0.7	102
39	Antigenic Shift and Increased Incidence of Meningococcal Disease. <i>Journal of Infectious Diseases</i> , 2006, 193, 1266-1274.	1.9	95
40	Sequence Variation of the SeM Gene of <i>Streptococcus equi</i> Allows Discrimination of the Source of Strangles Outbreaks. <i>Journal of Clinical Microbiology</i> , 2006, 44, 480-486.	1.8	95
41	Species status of <i>Neisseria gonorrhoeae</i> : evolutionary and epidemiological inferences from multilocus sequence typing. <i>BMC Biology</i> , 2007, 5, 35.	1.7	95
42	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
43	Multi Locus Sequence Typing of <i>Chlamydia</i> Reveals an Association between <i>Chlamydia psittaci</i> Genotypes and Host Species. <i>PLoS ONE</i> , 2010, 5, e14179.	1.1	90
44	Genome-wide association of functional traits linked with <i>Campylobacter jejuni</i> survival from farm to fork. <i>Environmental Microbiology</i> , 2017, 19, 361-380.	1.8	88
45	Population structure of the <i>Yersinia pseudotuberculosis</i> complex according to multilocus sequence typing. <i>Environmental Microbiology</i> , 2011, 13, 3114-3127.	1.8	84
46	Hospital effluent: A reservoir for carbapenemase-producing Enterobacterales?. <i>Science of the Total Environment</i> , 2019, 672, 618-624.	3.9	83
47	Using MLST to study bacterial variation: prospects in the genomic era. <i>Future Microbiology</i> , 2014, 9, 623-630.	1.0	80
48	Evolution of an Agriculture-Associated Disease Causing <i>Campylobacter coli</i> Clade: Evidence from National Surveillance Data in Scotland. <i>PLoS ONE</i> , 2010, 5, e15708.	1.1	75
49	Resolution of a Meningococcal Disease Outbreak from Whole-Genome Sequence Data with Rapid Web-Based Analysis Methods. <i>Journal of Clinical Microbiology</i> , 2012, 50, 3046-3053.	1.8	72
50	Defining the Estimated Core Genome of Bacterial Populations Using a Bayesian Decision Model. <i>PLoS Computational Biology</i> , 2014, 10, e1003788.	1.5	72
51	The Landscape of Realized Homologous Recombination in Pathogenic Bacteria. <i>Molecular Biology and Evolution</i> , 2016, 33, 456-471.	3.5	72
52	Genetic Diversity and Carriage Dynamics of <i>Neisseria lactamica</i> in Infants. <i>Infection and Immunity</i> , 2005, 73, 2424-2432.	1.0	70
53	Getting a grip on strangles: Recent progress towards improved diagnostics and vaccines. <i>Veterinary Journal</i> , 2007, 173, 492-501.	0.6	69
54	Genome evolution and the emergence of pathogenicity in avian <i>Escherichia coli</i> . <i>Nature Communications</i> , 2021, 12, 765.	5.8	69

#	ARTICLE	IF	CITATIONS
55	First Insights into the Evolution of <i>Streptococcus uberis</i> : a Multilocus Sequence Typing Scheme That Enables Investigation of Its Population Biology. <i>Applied and Environmental Microbiology</i> , 2006, 72, 1420-1428.	1.4	66
56	Genomic epidemiology of age-associated meningococcal lineages in national surveillance: an observational cohort study. <i>Lancet Infectious Diseases</i> , The, 2015, 15, 1420-1428.	4.6	63
57	Database for the ampC alleles in <i>Acinetobacter baumannii</i> . <i>PLoS ONE</i> , 2017, 12, e0176695.	1.1	63
58	Automated extraction of typing information for bacterial pathogens from whole genome sequence data: <i>Neisseria meningitidis</i> as an exemplar. <i>Eurosurveillance</i> , 2013, 18, 20379.	3.9	57
59	Identification of Three Novel Superantigen-Encoding Genes in <i>Streptococcus equi</i> subsp. <i>zooepidemicus</i> , <i>szf</i> , <i>szn</i> , and <i>szp</i> . <i>Infection and Immunity</i> , 2010, 78, 4817-4827.	1.0	56
60	Population structure of <i>Streptococcus oralis</i> . <i>Microbiology (United Kingdom)</i> , 2009, 155, 2593-2602.	0.7	55
61	Identifying <i>Neisseria</i> Species by Use of the 50S Ribosomal Protein L6 ( <i>rplF</i> ) Gene. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1375-1381.	1.8	55
62	<i>Neisseria</i> Adhesin A Variation and Revised Nomenclature Scheme. <i>Vaccine Journal</i> , 2014, 21, 966-971.	3.2	54
63	Agricultural intensification and the evolution of host specialism in the enteric pathogen <i>Campylobacter jejuni</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 11018-11028.	3.3	50
64	Defining a Core Genome Multilocus Sequence Typing Scheme for the Global Epidemiology of <i>Vibrio parahaemolyticus</i> . <i>Journal of Clinical Microbiology</i> , 2017, 55, 1682-1697.	1.8	49
65	Genotypic and Phenotypic Modifications of <i>Neisseria meningitidis</i> after an Accidental Human Passage. <i>PLoS ONE</i> , 2011, 6, e17145.	1.1	49
66	Biofilm Morphotypes and Population Structure among <i>Staphylococcus epidermidis</i> from Commensal and Clinical Samples. <i>PLoS ONE</i> , 2016, 11, e0151240.	1.1	49
67	Introgression in the genus <i>Campylobacter</i> : generation and spread of mosaic alleles. <i>Microbiology (United Kingdom)</i> , 2011, 157, 1066-1074.	0.7	47
68	Dihydrolipoamide dehydrogenase from the halophilic archaeon <i>Haloferax volcanii</i> : homologous overexpression of the cloned gene. <i>Journal of Bacteriology</i> , 1996, 178, 3044-3048.	1.0	46
69	Recombination-Mediated Host Adaptation by Avian <i>Staphylococcus aureus</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 830-842.	1.1	46
70	Changes in Serogroup and Genotype Prevalence Among Carried Meningococci in the United Kingdom During Vaccine Implementation. <i>Journal of Infectious Diseases</i> , 2011, 204, 1046-1053.	1.9	44
71	Genomics Reveals the Worldwide Distribution of Multidrug-Resistant Serotype 6E Pneumococci. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2271-2285.	1.8	44
72	Immunization with Recombinant Opc Outer Membrane Protein from <i>Neisseria meningitidis</i> : Influence of Sequence Variation and Levels of Expression on the Bactericidal Immune Response against Meningococci. <i>Infection and Immunity</i> , 2001, 69, 3809-3816.	1.0	43

#	ARTICLE	IF	CITATIONS
73	Lineage-specific plasmid acquisition and the evolution of specialized pathogens in <i>Bacillus thuringiensis</i> and the <i>Bacillus cereus</i> group. <i>Molecular Ecology</i> , 2018, 27, 1524-1540.	2.0	43
74	Opacity-Associated Adhesin Repertoire in Hyperinvasive <i>Neisseria meningitidis</i> . <i>Infection and Immunity</i> , 2006, 74, 5085-5094.	1.0	42
75	Genome sequence analyses show that <i>Neisseria oralis</i> is the same species as <i>Neisseria mucosa</i> var. <i>heidelbergensis</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 3920-3926.	0.8	42
76	Putatively novel serotypes and the potential for reduced vaccine effectiveness: capsular locus diversity revealed among 5405 pneumococcal genomes. <i>Microbial Genomics</i> , 2016, 2, 000090.	1.0	41
77	Sequence, distribution and chromosomal context of class I and class II pilin genes of <i>Neisseria meningitidis</i> identified in whole genome sequences. <i>BMC Genomics</i> , 2014, 15, 253.	1.2	40
78	Site-Directed Metagenesis and Halophilicity of Dihydrolipoamide Dehydrogenase from the Halophilic Archaeon, <i>Haloferax Volcanii</i> . <i>FEBS Journal</i> , 1997, 248, 362-368.	0.2	39
79	High diversity of invasive <i>Haemophilus influenzae</i> isolates in France and the emergence of resistance to third generation cephalosporins by alteration of <i>ftsI</i> gene. <i>Journal of Infection</i> , 2019, 79, 7-14.	1.7	39
80	Multicenter Study for Defining the Breakpoint for Rifampin Resistance in <i>Neisseria meningitidis</i> by <i>rpoB</i> Sequencing. <i>Antimicrobial Agents and Chemotherapy</i> , 2010, 54, 3651-3658.	1.4	37
81	Target Gene Sequencing To Define the Susceptibility of <i>Neisseria meningitidis</i> to Ciprofloxacin. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 1961-1964.	1.4	37
82	Local genes for local bacteria: Evidence of allopatry in the genomes of transatlantic <i>Campylobacter</i> populations. <i>Molecular Ecology</i> , 2017, 26, 4497-4508.	2.0	36
83	<i>Neisseria gonorrhoeae</i> Population Genomics: Use of the Gonococcal Core Genome to Improve Surveillance of Antimicrobial Resistance. <i>Journal of Infectious Diseases</i> , 2020, 222, 1816-1825.	1.9	36
84	Lack of Immunity in University Students before an Outbreak of Serogroup C Meningococcal Infection. <i>Journal of Infectious Diseases</i> , 2000, 181, 1172-1175.	1.9	34
85	Use of an improved <i>atpA</i> amplification and sequencing method to identify members of the <i>Campylobacteraceae</i> and <i>Helicobacteraceae</i> . <i>Letters in Applied Microbiology</i> , 2014, 58, 582-590.	1.0	34
86	Activation of human dendritic cells by the PorA protein of <i>Neisseria meningitidis</i> . <i>Cellular Microbiology</i> , 2004, 6, 651-662.	1.1	33
87	A RESTful application programming interface for the PubMLST molecular typing and genome databases. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	33
88	Multivalent liposome-based vaccines containing different serosubtypes of PorA protein induce cross-protective bactericidal immune responses against <i>Neisseria meningitidis</i> . <i>Vaccine</i> , 2006, 24, 36-44.	1.7	31
89	The Effect of Immune Selection on the Structure of the Meningococcal Opa Protein Repertoire. <i>PLoS Pathogens</i> , 2008, 4, e1000020.	2.1	31
90	A Dual Barcoding Approach to Bacterial Strain Nomenclature: Genomic Taxonomy of <i>Klebsiella pneumoniae</i> Strains. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	31

#	ARTICLE	IF	CITATIONS
91	Long-term evolution of antigen repertoires among carried meningococci. Proceedings of the Royal Society B: Biological Sciences, 2010, 277, 1635-1641.	1.2	30
92	Frequent capsule switching in "ultra-virulent" meningococci " Are we ready for a serogroup B ST-11 complex outbreak?. Journal of Infection, 2017, 75, 95-103.	1.7	30
93	Clonal Expansion of New Penicillin-Resistant Clade of <i>Neisseria meningitidis</i> Serogroup W Clonal Complex 11, Australia. Emerging Infectious Diseases, 2017, 23, 1364-1367.	2.0	30
94	The domestication of the probiotic bacterium <i>Lactobacillus acidophilus</i> . Scientific Reports, 2014, 4, 7202.	1.6	29
95	Meningococcal Deduced Vaccine Antigen Reactivity (MenDeVAR) Index: a Rapid and Accessible Tool That Exploits Genomic Data in Public Health and Clinical Microbiology Applications. Journal of Clinical Microbiology, 2020, 59, .	1.8	29
96	AgdbNet " antigen sequence database software for bacterial typing. BMC Bioinformatics, 2006, 7, 314.	1.2	28
97	Naturally occurring isolates of <i>Neisseria gonorrhoea</i> , which display anomalous serovar properties, express PIA/PIB hybrid porins, deletions in PIB or novel PIA molecules. FEMS Microbiology Letters, 1998, 162, 75-82.	0.7	27
98	Genomic analyses of the <i>Chlamydia trachomatis</i> core genome show an association between chromosomal genome, plasmid type and disease. BMC Genomics, 2018, 19, 130.	1.2	27
99	A curated public database for multilocus sequence typing (MLST) and analysis of <i>Haemophilus parasuis</i> based on an optimized typing scheme. Veterinary Microbiology, 2013, 162, 899-906.	0.8	26
100	2-Oxoacid dehydrogenase multienzyme complexes in the halophilic Archaea? Gene sequences and protein structural predictions The GenBank accession number for the sequence reported in this paper is AF068743.. Microbiology (United Kingdom), 2000, 146, 1061-1069.	0.7	26
101	Not all <i>Pseudomonas aeruginosa</i> are equal: strains from industrial sources possess uniquely large multireplicon genomes. Microbial Genomics, 2019, 5, .	1.0	26
102	Domestication of <i>Campylobacter jejuni</i> NCTC 11168. Microbial Genomics, 2019, 5, .	1.0	26
103	Genome-Based Characterization of Emergent Invasive <i>Neisseria meningitidis</i> Serogroup Y Isolates in Sweden from 1995 to 2012. Journal of Clinical Microbiology, 2015, 53, 2154-2162.	1.8	25
104	Detection of OXA-48-like-producing Enterobacterales in Irish recreational water. Science of the Total Environment, 2019, 690, 1-6.	3.9	25
105	A common gene pool for the <i>Neisseria FetA</i> antigen. International Journal of Medical Microbiology, 2009, 299, 133-139.	1.5	24
106	Meningococcal carriage in periods of high and low invasive meningococcal disease incidence in the UK: comparison of UKMenCar1 "4 cross-sectional survey results. Lancet Infectious Diseases, The, 2021, 21, 677-687.	4.6	24
107	Multi-Locus Sequence Typing. , 2001, 67, 173-186.		23
108	<i>Neisseria</i> genomics: current status and future perspectives. Pathogens and Disease, 2017, 75, .	0.8	23

#	ARTICLE	IF	CITATIONS
109	A public database for the new MLST scheme for <i>Treponema pallidum</i> subsp. <i>pallidum</i> : surveillance and epidemiology of the causative agent of syphilis. <i>PeerJ</i> , 2019, 6, e6182.	0.9	23
110	Association of <i>Neisseria gonorrhoeae</i> Plasmids With Distinct Lineages and The Economic Status of Their Country of Origin. <i>Journal of Infectious Diseases</i> , 2020, 222, 1826-1836.	1.9	22
111	Clonal Distribution of Disease-Associated and Healthy Carrier Isolates of <i>Neisseria meningitidis</i> between 1983 and 2005 in Cuba. <i>Journal of Clinical Microbiology</i> , 2010, 48, 802-810.	1.8	21
112	PubMLST.org – The new home for the <i>Borrelia</i> MLSA database. <i>Ticks and Tick-borne Diseases</i> , 2015, 6, 869-871.	1.1	20
113	Genomic epidemiology of <i>Campylobacter jejuni</i> associated with asymptomatic pediatric infection in the Peruvian Amazon. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008533.	1.3	20
114	Inferring <i>Mycobacterium bovis</i> transmission between cattle and badgers using isolates from the Randomised Badger Culling Trial. <i>PLoS Pathogens</i> , 2021, 17, e1010075.	2.1	20
115	Implications of Differential Age Distribution of Disease-Associated Meningococcal Lineages for Vaccine Development. <i>Vaccine Journal</i> , 2014, 21, 847-853.	3.2	19
116	Integration of Genomic and Other Epidemiologic Data to Investigate and Control a Cross-Institutional Outbreak of <i>Streptococcus pyogenes</i> . <i>Emerging Infectious Diseases</i> , 2016, 22, 973-980.	2.0	18
117	Potential Coverage of the 4CMenB Vaccine against Invasive Serogroup B <i>Neisseria meningitidis</i> Isolated from 2009 to 2013 in the Republic of Ireland. <i>MSphere</i> , 2018, 3, .	1.3	18
118	A Whole-Genome-Based Gene-by-Gene Typing System for Standardized High-Resolution Strain Typing of <i>Bacillus anthracis</i> . <i>Journal of Clinical Microbiology</i> , 2021, 59, e0288920.	1.8	17
119	Host ecology regulates interspecies recombination in bacteria of the genus <i>Campylobacter</i> . <i>ELife</i> , 2022, 11, .	2.8	17
120	Resolution of a Protracted Serogroup B Meningococcal Outbreak with Whole-Genome Sequencing Shows Interspecies Genetic Transfer. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2891-2899.	1.8	16
121	Phylogenetic Analysis of Invasive Serotype 1 <i>Pneumococcus</i> in South Africa, 1989 to 2013. <i>Journal of Clinical Microbiology</i> , 2016, 54, 1326-1334.	1.8	16
122	An MLST approach to support tracking of plasmids carrying OXA-48-like carbapenemase. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1856-1862.	1.3	16
123	Opa Protein Repertoires of Disease-Causing and Carried Meningococci. <i>Journal of Clinical Microbiology</i> , 2008, 46, 3033-3041.	1.8	15
124	The global meningitis genome partnership. <i>Journal of Infection</i> , 2020, 81, 510-520.	1.7	13
125	Dam inactivation in <i>Neisseria meningitidis</i> : prevalence among diverse hyperinvasive lineages. <i>BMC Microbiology</i> , 2004, 4, 34.	1.3	12
126	Comparison of three molecular typing methods to assess genetic diversity for <i>Mycobacterium tuberculosis</i> . <i>Journal of Microbiological Methods</i> , 2013, 93, 42-48.	0.7	12



#	ARTICLE	IF	CITATIONS
127	A comprehensive resource for <i>Bordetella</i> genomic epidemiology and biodiversity studies. <i>Nature Communications</i> , 2022, 13, .	5.8	11
128	The Applied Development of a Tiered Multilocus Sequence Typing (MLST) Scheme for <i>Dichelobacter nodosus</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 551.	1.5	10
129	Genomic Analyses of >3,100 Nasopharyngeal <i>Pneumococci</i> Revealed Significant Differences Between <i>Pneumococci</i> Recovered in Four Different Geographical Regions. <i>Frontiers in Microbiology</i> , 2019, 10, 317.	1.5	9
130	<i>Neisseria meningitidis</i> Serogroup X Sequence Type 767 in Turkey. <i>Journal of Clinical Microbiology</i> , 2010, 48, 4340-4341.	1.8	7
131	TypOn: the microbial typing ontology. <i>Journal of Biomedical Semantics</i> , 2014, 5, 43.	0.9	7
132	cgMLST characterisation of invasive <i>Neisseria meningitidis</i> serogroup C and W strains associated with increasing disease incidence in the Republic of Ireland. <i>PLoS ONE</i> , 2019, 14, e0216771.	1.1	7
133	Relationships among streptococci from the mitis group, misidentified as <i>Streptococcus pneumoniae</i> . <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2020, 39, 1865-1878.	1.3	7
134	Evolution of Sequence Type 4821 Clonal Complex Hyperinvasive and Quinolone-Resistant Meningococci. <i>Emerging Infectious Diseases</i> , 2021, 27, 1110-1122.	2.0	7
135	Internet-Based Sequence-Typing Databases for Bacterial Molecular Epidemiology. <i>Methods in Molecular Biology</i> , 2009, 551, 305-312.	0.4	7
136	Typing complex meningococcal vaccines to understand diversity and population structure of key vaccine antigens. <i>Wellcome Open Research</i> , 2018, 3, 151.	0.9	7
137	Recombinant Proteins in Vaccine Development. , 2001, 66, 167-180.		5
138	Typing complex meningococcal vaccines to understand diversity and population structure of key vaccine antigens. <i>Wellcome Open Research</i> , 2018, 3, 151.	0.9	5
139	Establishment of a Publicly Available Core Genome Multilocus Sequence Typing Scheme for <i>Clostridium perfringens</i> . <i>Microbiology Spectrum</i> , 2021, 9, e0053321.	1.2	5
140	Genomic epidemiology of group B streptococci spanning 10 years in an Irish maternity hospital, 2008â€“2017. <i>Journal of Infection</i> , 2021, 83, 37-45.	1.7	4
141	Methods for Typing of Meningococci. , 2006, , 37-52.		2
142	Genetic and Antigenic Characterization of <i>Neisseria meningitidis</i> Strains from Turkish Recruits in 2006. <i>Internal Medicine</i> , 2008, 47, 1949-1950.	0.3	2
143	Integration of Genomic and Other Epidemiologic Data to Investigate and Control a Cross-Institutional Outbreak of <i>Streptococcus pyogenes</i> . <i>Emerging Infectious Diseases</i> , 2016, 22, 973-980.	2.0	2
144	Computational Methods for Meningococcal Population Studies. , 2001, 67, 357-373.		1

#	ARTICLE	IF	CITATIONS
145	Naturally occurring isolates of <i>Neisseria gonorrhoea</i> , which display anomalous serovar properties, express PIA/PIB hybrid porins, deletions in PIB or novel PIA molecules. <i>FEMS Microbiology Letters</i> , 1998, 162, 75-82.	0.7	1
146	Worth its salt. <i>Trends in Biotechnology</i> , 1996, 14, 446.	4.9	0
147	Sequence data management for scientific purposes. <i>Infection, Genetics and Evolution</i> , 2017, 54, 508.	1.0	0
148	P1.06â€¦In silico multilocus sequence typing of <i>Chlamydia trachomatis</i> plasmids shows clustering of isolates according to the disease related biovars. , 2017, , .		0
149	Mobile antimicrobial resistance in <i>Neisseria gonorrhoeae</i> . <i>Access Microbiology</i> , 2022, 4, .	0.2	0