

Keith A Jolley

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146
papers

10,486
citations

51
h-index

101
g-index

171
ext. papers

13,291
ext. citations

7.3
avg, IF

6.41
L-index

#	Paper	IF	Citations
146	BIGSdb: Scalable analysis of bacterial genome variation at the population level. <i>BMC Bioinformatics</i> , 2010 , 11, 595	3.6	1462
145	Open-access bacterial population genomics: BIGSdb software, the PubMLST.org website and their applications. <i>Wellcome Open Research</i> , 2018 , 3, 124	4.8	677
144	Multilocus sequence typing system for the endosymbiont <i>Wolbachia pipientis</i> . <i>Applied and Environmental Microbiology</i> , 2006 , 72, 7098-110	4.8	583
143	mlstdbNet - distributed multi-locus sequence typing (MLST) databases. <i>BMC Bioinformatics</i> , 2004 , 5, 86	3.6	416
142	MLST revisited: the gene-by-gene approach to bacterial genomics. <i>Nature Reviews Microbiology</i> , 2013 , 11, 728-36	22.2	410
141	Ribosomal multilocus sequence typing: universal characterization of bacteria from domain to strain. <i>Microbiology (United Kingdom)</i> , 2012 , 158, 1005-1015	2.9	325
140	Multilocus sequence typing of <i>Clostridium difficile</i> . <i>Journal of Clinical Microbiology</i> , 2010 , 48, 770-8	9.7	310
139	Description and nomenclature of <i>Neisseria meningitidis</i> capsule locus. <i>Emerging Infectious Diseases</i> , 2013 , 19, 566-73	10.2	214
138	Distribution of serogroups and genotypes among disease-associated and carried isolates of <i>Neisseria meningitidis</i> from the Czech Republic, Greece, and Norway. <i>Journal of Clinical Microbiology</i> , 2004 , 42, 5146-53	9.7	203
137	Genome-wide association study identifies vitamin B5 biosynthesis as a host specificity factor in <i>Campylobacter</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 11923-7	11.5	178
136	Genetic analysis of meningococci carried by children and young adults. <i>Journal of Infectious Diseases</i> , 2005 , 191, 1263-71	7	164
135	Genomic evidence for the evolution of <i>Streptococcus equi</i> : host restriction, increased virulence, and genetic exchange with human pathogens. <i>PLoS Pathogens</i> , 2009 , 5, e1000346	7.6	160
134	Genomic resolution of an aggressive, widespread, diverse and expanding meningococcal serogroup B, C and W lineage. <i>Journal of Infection</i> , 2015 , 71, 544-52	18.9	151
133	A chromosomally integrated bacteriophage in invasive meningococci. <i>Journal of Experimental Medicine</i> , 2005 , 201, 1905-13	16.6	148
132	Carried meningococci in the Czech Republic: a diverse recombining population. <i>Journal of Clinical Microbiology</i> , 2000 , 38, 4492-8	9.7	135
131	Molecular typing of meningococci: recommendations for target choice and nomenclature. <i>FEMS Microbiology Reviews</i> , 2007 , 31, 89-96	15.1	132
130	Clinical <i>Clostridium difficile</i> : clonality and pathogenicity locus diversity. <i>PLoS ONE</i> , 2011 , 6, e19993	3.7	131

129	PorA variable regions of <i>Neisseria meningitidis</i> . <i>Emerging Infectious Diseases</i> , 2004 , 10, 674-8	10.2	131
128	A gene-by-gene population genomics platform: de novo assembly, annotation and genealogical analysis of 108 representative <i>Neisseria meningitidis</i> genomes. <i>BMC Genomics</i> , 2014 , 15, 1138	4.5	130
127	The influence of mutation, recombination, population history, and selection on patterns of genetic diversity in <i>Neisseria meningitidis</i> . <i>Molecular Biology and Evolution</i> , 2005 , 22, 562-9	8.3	128
126	A genomic approach to bacterial taxonomy: an examination and proposed reclassification of species within the genus <i>Neisseria</i> . <i>Microbiology (United Kingdom)</i> , 2012 , 158, 1570-1580	2.9	121
125	A surveillance network for meningococcal disease in Europe. <i>FEMS Microbiology Reviews</i> , 2007 , 31, 27-36	15.1	118
124	Role of selection in the emergence of lineages and the evolution of virulence in <i>Neisseria meningitidis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 15082-7	11.5	105
123	Real-time genomic epidemiological evaluation of human <i>Campylobacter</i> isolates by use of whole-genome multilocus sequence typing. <i>Journal of Clinical Microbiology</i> , 2013 , 51, 2526-34	9.7	104
122	A Gene-By-Gene Approach to Bacterial Population Genomics: Whole Genome MLST of <i>Campylobacter</i> . <i>Genes</i> , 2012 , 3, 261-77	4.2	102
121	<i>Cronobacter</i> , the emergent bacterial pathogen <i>Enterobacter sakazakii</i> comes of age; MLST and whole genome sequence analysis. <i>BMC Genomics</i> , 2014 , 15, 1121	4.5	100
120	Multilocus sequence typing for global surveillance of meningococcal disease. <i>FEMS Microbiology Reviews</i> , 2007 , 31, 15-26	15.1	100
119	Progressive genome-wide introgression in agricultural <i>Campylobacter coli</i> . <i>Molecular Ecology</i> , 2013 , 22, 1051-64	5.7	98
118	A reference pan-genome approach to comparative bacterial genomics: identification of novel epidemiological markers in pathogenic <i>Campylobacter</i> . <i>PLoS ONE</i> , 2014 , 9, e92798	3.7	89
117	Ecological Overlap and Horizontal Gene Transfer in <i>Staphylococcus aureus</i> and <i>Staphylococcus epidermidis</i> . <i>Genome Biology and Evolution</i> , 2015 , 7, 1313-28	3.9	86
116	Target gene sequencing to characterize the penicillin G susceptibility of <i>Neisseria meningitidis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2007 , 51, 2784-92	5.9	86
115	Antigenic shift and increased incidence of meningococcal disease. <i>Journal of Infectious Diseases</i> , 2006 , 193, 1266-74	7	82
114	Ribosomal proteins as biomarkers for bacterial identification by mass spectrometry in the clinical microbiology laboratory. <i>Journal of Microbiological Methods</i> , 2013 , 94, 390-6	2.8	81
113	Cryptic ecology among host generalist <i>Campylobacter jejuni</i> in domestic animals. <i>Molecular Ecology</i> , 2014 , 23, 2442-51	5.7	80
112	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	2.9	80

111	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, 480-6	9.7	79
110	Species status of <i>Neisseria gonorrhoeae</i> : evolutionary and epidemiological inferences from multilocus sequence typing. <i>BMC Biology</i> , 2007 , 5, 35	7.3	76
109	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, 675-86	7.86	72
108	Disease-associated genotypes of the commensal skin bacterium <i>Staphylococcus epidermidis</i> . <i>Nature Communications</i> , 2018 , 9, 5034	17.4	71
107	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	3.7	70
106	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, 3046-53	9.7	65
105	Population structure of the <i>Yersinia pseudotuberculosis</i> complex according to multilocus sequence typing. <i>Environmental Microbiology</i> , 2011 , 13, 3114-27	5.2	63
104	Genetic diversity and carriage dynamics of <i>Neisseria lactamica</i> in infants. <i>Infection and Immunity</i> , 2005 , 73, 2424-32	3.7	63
103	Core Genome Multilocus Sequence Typing Scheme for Stable, Comparative Analyses of <i>Campylobacter jejuni</i> and <i>C. coli</i> Human Disease Isolates. <i>Journal of Clinical Microbiology</i> , 2017 , 55, 2086-2097	9.7	61
102	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	5.2	61
101	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. <i>The Lancet Digital Health</i> , 2021 , 3, e360-e370	14.4	58
100	Getting a grip on strangles: recent progress towards improved diagnostics and vaccines. <i>Veterinary Journal</i> , 2007 , 173, 492-501	2.5	57
99	Using multilocus sequence typing to study bacterial variation: prospects in the genomic era. <i>Future Microbiology</i> , 2014 , 9, 623-30	2.9	56
98	Genomic epidemiology of age-associated meningococcal lineages in national surveillance: an observational cohort study. <i>Lancet Infectious Diseases</i> , 2015 , 15, 1420-8	25.5	56
97	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	3.7	56
96	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, 1420-8	4.8	54
95	Population structure of <i>Streptococcus oralis</i> . <i>Microbiology (United Kingdom)</i> , 2009 , 155, 2593-2602	2.9	50
94	Comparative Analysis of the Two Multilocus Sequence Typing (MLST) Schemes. <i>Frontiers in Microbiology</i> , 2019 , 10, 930	5.7	47

93	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	19.8	47
92	<i>Neisseria</i> adhesin A variation and revised nomenclature scheme. <i>Vaccine Journal</i> , 2014 , 21, 966-71		46
91	Identification of three novel superantigen-encoding genes in <i>Streptococcus equi</i> subsp. <i>zooepidemicus</i> , <i>szef</i> , <i>szen</i> , and <i>szep</i> . <i>Infection and Immunity</i> , 2010 , 78, 4817-27	3.7	46
90	Hospital effluent: A reservoir for carbapenemase-producing Enterobacterales?. <i>Science of the Total Environment</i> , 2019 , 672, 618-624	10.2	45
89	Identifying <i>Neisseria</i> species by use of the 50S ribosomal protein L6 (rplF) gene. <i>Journal of Clinical Microbiology</i> , 2014 , 52, 1375-81	9.7	44
88	Defining the estimated core genome of bacterial populations using a Bayesian decision model. <i>PLoS Computational Biology</i> , 2014 , 10, e1003788	5	42
87	Dihydrolipoamide dehydrogenase from the halophilic archaeon <i>Haloferax volcanii</i> : homologous overexpression of the cloned gene. <i>Journal of Bacteriology</i> , 1996 , 178, 3044-8	3.5	42
86	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, 3809-16	3.7	41
85	Genotypic and phenotypic modifications of <i>Neisseria meningitidis</i> after an accidental human passage. <i>PLoS ONE</i> , 2011 , 6, e17145	3.7	41
84	The Landscape of Realized Homologous Recombination in Pathogenic Bacteria. <i>Molecular Biology and Evolution</i> , 2016 , 33, 456-71	8.3	40
83	Changes in serogroup and genotype prevalence among carried meningococci in the United Kingdom during vaccine implementation. <i>Journal of Infectious Diseases</i> , 2011 , 204, 1046-53	7	40
82	Opacity-associated adhesin repertoire in hyperinvasive <i>Neisseria meningitidis</i> . <i>Infection and Immunity</i> , 2006 , 74, 5085-94	3.7	38
81	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	9.7	36
80	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	2.2	36
79	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	4.5	35
78	Biofilm Morphotypes and Population Structure among <i>Staphylococcus epidermidis</i> from Commensal and Clinical Samples. <i>PLoS ONE</i> , 2016 , 11, e0151240	3.7	34
77	Introgression in the genus <i>Campylobacter</i> : generation and spread of mosaic alleles. <i>Microbiology (United Kingdom)</i> , 2011 , 157, 1066-1074	2.9	33
76	Activation of human dendritic cells by the PorA protein of <i>Neisseria meningitidis</i> . <i>Cellular Microbiology</i> , 2004 , 6, 651-62	3.9	32

75	Multicenter study for defining the breakpoint for rifampin resistance in <i>Neisseria meningitidis</i> by rpoB sequencing. <i>Antimicrobial Agents and Chemotherapy</i> , 2010 , 54, 3651-8	5.9	31
74	Lack of immunity in university students before an outbreak of serogroup C meningococcal infection. <i>Journal of Infectious Diseases</i> , 2000 , 181, 1172-5	7	31
73	Use of an improved atpA amplification and sequencing method to identify members of the Campylobacteraceae and Helicobacteraceae. <i>Letters in Applied Microbiology</i> , 2014 , 58, 582-90	2.9	30
72	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	4.1	30
71	Recombination-Mediated Host Adaptation by Avian <i>Staphylococcus aureus</i> . <i>Genome Biology and Evolution</i> , 2017 , 9, 830-842	3.9	29
70	Long-term evolution of antigen repertoires among carried meningococci. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2010 , 277, 1635-41	4.4	29
69	Agricultural intensification and the evolution of host specialism in the enteric pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 11018-11028	11.5	27
68	Site-directed mutagenesis and halophilicity of dihydrolipoamide dehydrogenase from the halophilic archaeon, <i>Haloferax volcanii</i> . <i>FEBS Journal</i> , 1997 , 248, 362-8		27
67	The effect of immune selection on the structure of the meningococcal opa protein repertoire. <i>PLoS Pathogens</i> , 2008 , 4, e1000020	7.6	27
66	Target gene sequencing to define the susceptibility of <i>Neisseria meningitidis</i> to ciprofloxacin. <i>Antimicrobial Agents and Chemotherapy</i> , 2013 , 57, 1961-4	5.9	26
65	AgdbNet - antigen sequence database software for bacterial typing. <i>BMC Bioinformatics</i> , 2006 , 7, 314	3.6	26
64	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	5.7	25
63	Naturally occurring isolates of <i>Neisseria gonorrhoeae</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	2.9	25
62	Database for the ampC alleles in <i>Acinetobacter baumannii</i> . <i>PLoS ONE</i> , 2017 , 12, e0176695	3.7	24
61	2-Oxoacid dehydrogenase multienzyme complexes in the halophilic Archaea? Gene sequences and protein structural predictions. <i>Microbiology (United Kingdom)</i> , 2000 , 146 (Pt 5), 1061-1069	2.9	24
60	Clonal Expansion of New Penicillin-Resistant Clade of <i>Neisseria meningitidis</i> Serogroup W Clonal Complex 11, Australia. <i>Emerging Infectious Diseases</i> , 2017 , 23, 1364-1367	10.2	23
59	A common gene pool for the <i>Neisseria FetA</i> antigen. <i>International Journal of Medical Microbiology</i> , 2009 , 299, 133-9	3.7	23
58	Genome-Based Characterization of Emergent Invasive <i>Neisseria meningitidis</i> Serogroup Y Isolates in Sweden from 1995 to 2012. <i>Journal of Clinical Microbiology</i> , 2015 , 53, 2154-62	9.7	22

57	The domestication of the probiotic bacterium <i>Lactobacillus acidophilus</i> . <i>Scientific Reports</i> , 2014 , 4, 7202	4.9	22
56	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	4.4	22
55	Frequent capsule switching in ultra-virulent meningococci - Are we ready for a serogroup B ST-11 complex outbreak?. <i>Journal of Infection</i> , 2017 , 75, 95-103	18.9	21
54	Genomics Reveals the Worldwide Distribution of Multidrug-Resistant Serotype 6E Pneumococci. <i>Journal of Clinical Microbiology</i> , 2015 , 53, 2271-85	9.7	21
53	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	5.7	20
52	Implications of differential age distribution of disease-associated meningococcal lineages for vaccine development. <i>Vaccine Journal</i> , 2014 , 21, 847-53		19
51	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	18.9	18
50	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,	5	18
49	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, 802-10	9.7	18
48	<i>Neisseria</i> genomics: current status and future perspectives. <i>Pathogens and Disease</i> , 2017 , 75,	4.2	16
47	Detection of OXA-48-like-producing Enterobacterales in Irish recreational water. <i>Science of the Total Environment</i> , 2019 , 690, 1-6	10.2	16
46	Genomic analyses of the <i>Chlamydia trachomatis</i> core genome show an association between chromosomal genome, plasmid type and disease. <i>BMC Genomics</i> , 2018 , 19, 130	4.5	15
45	A curated public database for multilocus sequence typing (MLST) and analysis of <i>Haemophilus parasuis</i> based on an optimized typing scheme. <i>Veterinary Microbiology</i> , 2013 , 162, 899-906	3.3	15
44	Opa protein repertoires of disease-causing and carried meningococci. <i>Journal of Clinical Microbiology</i> , 2008 , 46, 3033-41	9.7	15
43	Genome evolution and the emergence of pathogenicity in avian <i>Escherichia coli</i> . <i>Nature Communications</i> , 2021 , 12, 765	17.4	15
42	PubMLST.org--The new home for the <i>Borrelia</i> MLSA database. <i>Ticks and Tick-borne Diseases</i> , 2015 , 6, 869-71	3.6	14
41	A public database for the new MLST scheme for subsp. : surveillance and epidemiology of the causative agent of syphilis. <i>PeerJ</i> , 2019 , 6, e6182	3.1	14
40	Domestication of <i>Campylobacter jejuni</i> NCTC 11168. <i>Microbial Genomics</i> , 2019 , 5,	4.4	14

39	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, 973-80	10.2	13
38	<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	7	12
37	Potential Coverage of the 4CMenB Vaccine against Invasive Serogroup B Isolated from 2009 to 2013 in the Republic of Ireland. <i>MSphere</i> , 2018 , 3,	5	12
36	Dam inactivation in <i>Neisseria meningitidis</i> : prevalence among diverse hyperinvasive lineages. <i>BMC Microbiology</i> , 2004 , 4, 34	4.5	12
35	Multi-locus sequence typing. <i>Methods in Molecular Medicine</i> , 2001 , 67, 173-86		12
34	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	9.7	12
33	Phylogenetic Analysis of Invasive Serotype 1 Pneumococcus in South Africa, 1989 to 2013. <i>Journal of Clinical Microbiology</i> , 2016 , 54, 1326-34	9.7	11
32	Comparison of three molecular typing methods to assess genetic diversity for <i>Mycobacterium tuberculosis</i> . <i>Journal of Microbiological Methods</i> , 2013 , 93, 42-8	2.8	11
31	Carried Meningococci in the Czech Republic: a Diverse Recombining Population. <i>Journal of Clinical Microbiology</i> , 2002 , 40, 3549-3550	9.7	11
30	Not all <i>Pseudomonas aeruginosa</i> are equal: strains from industrial sources possess uniquely large multireplicon genomes. <i>Microbial Genomics</i> , 2019 , 5,	4.4	11
29	Meningococcal Deduced Vaccine Antigen Reactivity (MenDeVAR) Index: a Rapid and Accessible Tool That Exploits Genomic Data in Public Health and Clinical Microbiology Applications. <i>Journal of Clinical Microbiology</i> , 2020 , 59,	9.7	9
28	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	4.8	9
27	The Applied Development of a Tiered Multilocus Sequence Typing (MLST) Scheme for. <i>Frontiers in Microbiology</i> , 2018 , 9, 551	5.7	8
26	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	3.7	6
25	Internet-based sequence-typing databases for bacterial molecular epidemiology. <i>Methods in Molecular Biology</i> , 2009 , 551, 305-12	1.4	6
24	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	9.7	6
23	Genomic Analyses of >3,100 Nasopharyngeal Pneumococci Revealed Significant Differences Between Pneumococci Recovered in Four Different Geographical Regions. <i>Frontiers in Microbiology</i> , 2019 , 10, 317	5.7	5
22	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	7	5

21	TypOn: the microbial typing ontology. <i>Journal of Biomedical Semantics</i> , 2014 , 5, 43	2.2	5
20	<i>Neisseria meningitidis</i> serogroup X sequence type 767 in Turkey. <i>Journal of Clinical Microbiology</i> , 2010 , 48, 4340-1	9.7	5
19	Typing complex meningococcal vaccines to understand diversity and population structure of key vaccine antigens. <i>Wellcome Open Research</i> , 2018 , 3, 151	4.8	5
18	Heterogeneity among estimates of the core genome and pan-genome in different pneumococcal populations		5
17	An MLST approach to support tracking of plasmids carrying OXA-48-like carbapenemase. <i>Journal of Antimicrobial Chemotherapy</i> , 2019 , 74, 1856-1862	5.1	4
16	The global meningitis genome partnership. <i>Journal of Infection</i> , 2020 , 81, 510-520	18.9	4
15	Recombinant proteins in vaccine development. <i>Methods in Molecular Medicine</i> , 2001 , 66, 167-80		4
14	Typing complex meningococcal vaccines to understand diversity and population structure of key vaccine antigens. <i>Wellcome Open Research</i> , 2018 , 3, 151	4.8	4
13	Meningococcal carriage in periods of high and low invasive meningococcal disease incidence in the UK: comparison of UKMenCar1-4 cross-sectional survey results. <i>Lancet Infectious Diseases</i> , 2021 , 21, 677-687	25.5	4
12	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	7.6	3
11	The Invasive Respiratory Infection Surveillance (IRIS) Initiative reveals significant reductions in invasive bacterial infections during the COVID-19 pandemic		3
10	Genetic and antigenic characterization of <i>Neisseria meningitidis</i> strains from Turkish recruits in 2006. <i>Internal Medicine</i> , 2008 , 47, 1949-50	1.1	2
9	Methods for Typing of Meningococci 2006 , 37-52		2
8	A dual barcoding approach to bacterial strain nomenclature: Genomic taxonomy of <i>Klebsiella pneumoniae</i> strains		2
7	Computational methods for meningococcal population studies. <i>Methods in Molecular Medicine</i> , 2001 , 67, 357-73		1
6	Establishment of a Publicly Available Core Genome Multilocus Sequence Typing Scheme for <i>Clostridium perfringens</i> . <i>Microbiology Spectrum</i> , 2021 , 9, e0053321	8.9	1
5	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	5.3	1
4	Evolution of Sequence Type 4821 Clonal Complex Hyperinvasive and Quinolone-Resistant Meningococci. <i>Emerging Infectious Diseases</i> , 2021 , 27, 1110-1122	10.2	1

- 3 Genomic epidemiology of group B streptococci spanning 10 years in an Irish maternity hospital, 2008-2017. *Journal of Infection*, **2021**, 83, 37-45 18.9 ○
- 2 Sequence data management for scientific purposes. *Infection, Genetics and Evolution*, **2017**, 54, 508 4.5
- 1 Integration of Genomic and Other Epidemiologic Data to Investigate and Control a Cross-Institutional Outbreak of *Streptococcus pyogenes*. *Emerging Infectious Diseases*, **2016**, 22, 973-980^{10.2}