Martin C J Maiden

List of Publications by Year
in descending order

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440 papers	39,650 citations	2669 95 h-index	3563 181 g-index
527 all docs	527 docs citations	527 times ranked	22663 citing authors

#	Article	IF	Citations
1	Multilocus sequence typing: A portable approach to the identification of clones within populations of pathogenic microorganisms. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 3140-3145.	3.3	3,333
2	BIGSdb: Scalable analysis of bacterial genome variation at the population level. BMC Bioinformatics, 2010, 11, 595.	1.2	2,074
3	Sex and virulence in Escherichia coli: an evolutionary perspective. Molecular Microbiology, 2006, 60, 1136-1151.	1.2	1,806
4	Open-access bacterial population genomics: BIGSdb software, the PubMLST.org website and their applications. Wellcome Open Research, 2018, 3, 124.	0.9	1,710
5	Report of the ad hoc committee for the re-evaluation of the species definition in bacteriology.. International Journal of Systematic and Evolutionary Microbiology, 2002, 52, 1043-1047.	0.8	971
6	Multilocus Sequence Typing of Bacteria. Annual Review of Microbiology, 2006, 60, 561-588.	2.9	798
7	Multilocus Sequence Typing System for Campylobacter jejuni. Journal of Clinical Microbiology, 2001, 39, 14-23.	1.8	771
8	Multilocus Sequence Typing System for the Endosymbiont Wolbachia pipientis. Applied and Environmental Microbiology, 2006, 72, 7098-7110.	1.4	730
9	MLST revisited: the gene-by-gene approach to bacterial genomics. Nature Reviews Microbiology, 2013, 11, 728-736.	13.6	590
10	Multi-locus sequence typing: a tool for global epidemiology. Trends in Microbiology, 2003, 11, 479-487.	3.5	574
11	Candida orthopsilosis and Candida metapsilosis spp. nov. To Replace Candida parapsilosis Groups II and III. Journal of Clinical Microbiology, 2005, 43, 284-292.	1.8	520
12	Ribosomal multilocus sequence typing: universal characterization of bacteria from domain to strain. Microbiology (United Kingdom), 2012, 158, 1005-1015.	0.7	497
13	mlstdbNet - distributed multi-locus sequence typing (MLST) databases. BMC Bioinformatics, 2004, 5, 86.	1.2	459
14	Identification of anthrax toxin genes in a Bacillus cereus associated with an illness resembling inhalation anthrax. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 8449-8454.	3.3	457
15	Mammalian and bacterial sugar transport proteins are homologous. Nature, 1987, 325, 641-643.	13.7	417
16	Impact of Meningococcal Serogroup C Conjugate Vaccines on Carriage and Herd Immunity. Journal of Infectious Diseases, 2008, 197, 737-743.	1.9	395
17	Carriage of serogroup C meningococci 1 year after meningococcal C conjugate polysaccharide vaccination. Lancet, The, 2002, 359, 1829-1830.	6.3	386
18	<i>Campylobacter</i>Genotyping to Determine the Source of Human Infection. Clinical Infectious Diseases, 2009, 48, 1072-1078.	2.9	358

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19	Population Structure and Evolution of the Bacillus cereus Group. Journal of Bacteriology, 2004, 186, 7959-7970.	1.0	337
20	Impact of recombination on bacterial evolution. Trends in Microbiology, 2010, 18, 315-322.	3.5	331
21	Meningococcal carriage and diseaseâ€"Population biology and evolution. Vaccine, 2009, 27, B64-B70.	1.7	302
22	The relative contributions of recombination and mutation to the divergence of clones of Neisseria meningitidis. Molecular Biology and Evolution, 1999, 16, 1496-1502.	3.5	290
23	Molecular Phylogenetics of Candida albicans. Eukaryotic Cell, 2007, 6, 1041-1052.	3.4	285
24	The maintenance of strain structure in populations of recombining infectious agents. Nature Medicine, 1996, 2, 437-442.	15.2	276
25	Genome-wide association study identifies vitamin B ₅ 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
26	Changes in the incidence of invasive disease due to Streptococcus pneumoniae, Haemophilus influenzae, and Neisseria meningitidis 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
27	Description and Nomenclature of<i>Neisseria meningitidis</i>Capsule Locus. Emerging Infectious Diseases, 2013, 19, 566-573.	2.0	259
28	Horizontally Transmitted Symbionts and Host Colonization of Ecological Niches. Current Biology, 2013, 23, 1713-1717.	1.8	248
29	Capsular Serotypeâ€"Specific Attack Rates and Duration of Carriage ofStreptococcuspneumoniaein a Population of Children. Journal of Infectious Diseases, 2006, 194, 682-688.	1.9	247
30	Effect of a quadrivalent meningococcal ACWY glycoconjugate or a serogroup B meningococcal vaccine on meningococcal carriage: an observer-blind, phase 3 randomised clinical trial. Lancet, The, 2014, 384, 2123-2131.	6.3	247
31	Convergence of <i>Campylobacter</i> Species: Implications for Bacterial Evolution. Science, 2008, 320, 237-239.	6.0	231
32	Effect of a serogroup A meningococcal conjugate vaccine (PsAâ€"TT) on serogroup A meningococcal meningitis and carriage in Chad: a community study. Lancet, The, 2014, 383, 40-47.	6.3	230
33	Distribution of Serogroups and Genotypes among Disease-Associated and Carried Isolates of Neisseria meningitidis from the Czech Republic, Greece, and Norway. Journal of Clinical Microbiology, 2004, 42, 5146-5153.	1.8	222
34	Collaborative Consensus for Optimized Multilocus Sequence Typing of Candida albicans. Journal of Clinical Microbiology, 2003, 41, 5265-5266.	1.8	216
35	Molecular Characterization of<i>Campylobacter jejuni</i>Clones: A Basis for Epidemiologic Investigation. Emerging Infectious Diseases, 2002, 8, 949-955.	2.0	211
36	The influence of recombination on the population structure and evolution of the human pathogen Neisseria meningitidis. Molecular Biology and Evolution, 1999, 16, 741-749.	3.5	210

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37	Social Behavior and Meningococcal Carriage in British Teenagers. Emerging Infectious Diseases, 2006, 12, 950-957.	2.0	209
38	Genomic Evidence for the Evolution of Streptococcus equi: Host Restriction, Increased Virulence, and Genetic Exchange with Human Pathogens. PLoS Pathogens, 2009, 5, e1000346.	2.1	197
39	Population Structure and Properties of Candida albicans , as Determined by Multilocus Sequence Typing. Journal of Clinical Microbiology, 2005, 43, 5601-5613.	1.8	194
40	Multilocus Sequence Typing Scheme That Provides Both Species and Strain Differentiation for the Burkholderia cepacia Complex. Journal of Clinical Microbiology, 2005, 43, 4665-4673.	1.8	193
41	Molecular Characterization of<i>Campylobacter jejuni</i>Clones: A Basis for Epidemiologic Investigation. Emerging Infectious Diseases, 2002, 8, 949-955.	2.0	192
42	Silent Nucleotide Polymorphisms and a Phylogeny for<i>Mycobacterium tuberculosis</i>. Emerging Infectious Diseases, 2004, 10, 1568-1577.	2.0	189
43	Meningococcal vaccines and herd immunity: lessons learned from serogroup C conjugate vaccination programs. Expert Review of Vaccines, 2009, 8, 851-861.	2.0	185
44	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
45	Sequence Typing and Comparison of Population Biology of Campylobacter coli and Campylobacter jejuni. Journal of Clinical Microbiology, 2005, 43, 340-347.	1.8	183
46	Bacterial population genetics, evolution and epidemiology. Philosophical Transactions of the Royal Society B: Biological Sciences, 1999, 354, 701-710.	1.8	182
47	Distribution of Surface Protein Variants among Hyperinvasive Meningococci: Implications for Vaccine Design. Infection and Immunity, 2004, 72, 5955-5962.	1.0	180
48	Genetic Analysis of Meningococci Carried by Children and Young Adults. Journal of Infectious Diseases, 2005, 191, 1263-1271.	1.9	178
49	Phasevarions Mediate Random Switching of Gene Expression in Pathogenic Neisseria. PLoS Pathogens, 2009, 5, e1000400.	2.1	170
50	Morphological autonomy and diachrony. Morphology, 2005, , 137-175.	0.3	168
51	A chromosomally integrated bacteriophage in invasive meningococci. Journal of Experimental Medicine, 2005, 201, 1905-1913.	4.2	166
52	A gene-by-gene population genomics platform: de novo assembly, annotation and genealogical analysis of 108 representative Neisseria meningitidis genomes. BMC Genomics, 2014, 15, 1138.	1.2	164
53	Campylobacter genotypes from food animals, environmental sources and clinical disease in Scotland 2005/6. International Journal of Food Microbiology, 2009, 134, 96-103.	2.1	158
54	Antigenic diversity of meningococcal enterobactin receptor FetA, a vaccine component. Microbiology (United Kingdom), 2003, 149, 1849-1858.	0.7	156

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55	Many carried meningococci lack the genes required for capsule synthesis and transport The GenBank accession number for the sequence of the cnl-1 allele is AJ308327.. Microbiology (United Kingdom), 2002, 148, 1813-1819.	0.7	154
56	A genomic approach to bacterial taxonomy: an examination and proposed reclassification of species within the genus Neisseria. Microbiology (United Kingdom), 2012, 158, 1570-1580.	0.7	153
57	Irregularity as a determinant of morphological change. Journal of Linguistics, 1992, 28, 285-312.	0.5	152
58	Molecular typing of meningococci: recommendations for target choice and nomenclature. FEMS Microbiology Reviews, 2007, 31, 89-96.	3.9	150
59	Comparative analysis of core genome MLST and SNP typing within a European Salmonella serovar Enteritidis outbreak. International Journal of Food Microbiology, 2018, 274, 1-11.	2.1	150
60	Genetic Diversity of Campylobacter jejuni Isolates from Farm Animals and the FarmEnvironment. Applied and Environmental Microbiology, 2003, 69, 7409-7413.	1.4	149
61	PorA Variable Regions of<i>Neisseria meningitidis</i>. Emerging Infectious Diseases, 2004, 10, 674-678.	2.0	142
62	Carried Meningococci in the Czech Republic: a Diverse Recombining Population. Journal of Clinical Microbiology, 2000, 38, 4492-4498.	1.8	142
63	Meningococcal conjugate vaccines: new opportunities and new challenges. Lancet, The, 1999, 354, 615-616.	6.3	141
64	The Influence of Mutation, Recombination, Population History, and Selection on Patterns of Genetic Diversity in Neisseria meningitidis. Molecular Biology and Evolution, 2005, 22, 562-569.	3.5	138
65	Candida albicans Strain Maintenance, Replacement, and Microvariation Demonstrated by Multilocus Sequence Typing. Journal of Clinical Microbiology, 2006, 44, 3647-3658.	1.8	138
66	Insect life history and the evolution of bacterial mutualism. Ecology Letters, 2015, 18, 516-525.	3.0	138
67	Role of horizontal genetic exchange in the antigenic variation of the class 1 outer membrane protein of Neisseria meningitidis. Molecular Microbiology, 1992, 6, 489-495.	1.2	137
68	Comparison of the class 1 outer membrane proteins of eight serological reference strains of Neisseria meningitidis. Molecular Microbiology, 1991, 5, 727-736.	1.2	136
69	A Gene-By-Gene Approach to Bacterial Population Genomics: Whole Genome MLST of Campylobacter. Genes, 2012, 3, 261-277.	1.0	135
70	Multilocus Sequence Typing for Differentiation of Strains of Candida tropicalis. Journal of Clinical Microbiology, 2005, 43, 5593-5600.	1.8	134
71	Host-associated Genetic Import in<i>Campylobacter jejuni</i>. Emerging Infectious Diseases, 2007, 13, 267-272.	2.0	134
72	A surveillance network for meningococcal disease in Europe. FEMS Microbiology Reviews, 2007, 31, 27-36.	3.9	134

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73	Meningococcal B Vaccine and Meningococcal Carriage in Adolescents in Australia. New England Journal of Medicine, 2020, 382, 318-327.	13.9	133
74	The porA gene in serogroup A meningococci: evolutionary stability and mechanism of genetic variation. Molecular Microbiology, 1994, 12, 253-265.	1.2	132
75	Hyperinvasive Neonatal Group B Streptococcus Has Arisen from a Bovine Ancestor. Journal of Clinical Microbiology, 2004, 42, 2161-2167.	1.8	132
76	Cryptic ecology among host generalist <i>Campylobacter jejuni</i> in domestic animals. Molecular Ecology, 2014, 23, 2442-2451.	2.0	131
77	Structural and Evolutionary Inference from Molecular Variation in <i>Neisseria</i> Porins. Infection and Immunity, 1999, 67, 2406-2413.	1.0	131
78	Ecological Overlap and Horizontal Gene Transfer in Staphylococcus aureus and Staphylococcus epidermidis. Genome Biology and Evolution, 2015, 7, 1313-1328.	1.1	130
79	Progressive genomeâ€wide introgression in agricultural <i>Campylobacter coli</i>. Molecular Ecology, 2013, 22, 1051-1064.	2.0	128
80	Optimization and Validation of Multilocus Sequence Typing for Candida albicans. Journal of Clinical Microbiology, 2003, 41, 3765-3776.	1.8	125
81	Real-Time Genomic Epidemiological Evaluation of Human Campylobacter Isolates by Use of Whole-Genome Multilocus Sequence Typing. Journal of Clinical Microbiology, 2013, 51, 2526-2534.	1.8	124
82	A Reference Pan-Genome Approach to Comparative Bacterial Genomics: Identification of Novel Epidemiological Markers in Pathogenic Campylobacter. PLoS ONE, 2014, 9, e92798.	1.1	122
83	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
84	The Evolution of<i>Campylobacter jejuni</i>and<i>Campylobacter coli</i>. Cold Spring Harbor Perspectives in Biology, 2015, 7, a018119.	2.3	119
85	Attribution of<i>Campylobacter</i>Infections in Northeast Scotland to Specific Sources by Use of Multilocus Sequence Typing. Journal of Infectious Diseases, 2009, 199, 1205-1208.	1.9	117
86	When lexemes become allomorphs - On the genesis of suppletion. Folia Linguistica, 2004, 38, .	0.1	116
87	Host Association of <i>Campylobacter</i> Genotypes Transcends Geographic Variation. Applied and Environmental Microbiology, 2010, 76, 5269-5277.	1.4	116
88	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
89	Disease-associated genotypes of the commensal skin bacterium Staphylococcus epidermidis. Nature Communications, 2018, 9, 5034.	5.8	115
90	Environmental<i>Burkholderia cepacia</i>Complex Isolates from Human Infections. Emerging Infectious Diseases, 2007, 13, 458-461.	2.0	112

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91	Hybrid<i>Vibrio vulnificus</i>. Emerging Infectious Diseases, 2005, 11, 30-35.	2.0	109
92	Horizontal Genetic Exchange, Evolution, and Spread of Antibiotic Resistance in Bacteria. Clinical Infectious Diseases, 1998, 27, S12-S20.	2.9	108
93	Exploring the evolution of diversity in pathogen populations. Trends in Microbiology, 2001, 9, 181-185.	3.5	106
94	Multilocus sequence typing for global surveillance of meningococcal disease. FEMS Microbiology Reviews, 2007, 31, 15-26.	3.9	105
95	Niche segregation and genetic structure of <i>Campylobacter jejuni</i> populations from wild and agricultural host species. Molecular Ecology, 2011, 20, 3484-3490.	2.0	105
96	Core Genome Multilocus Sequence Typing Scheme for Stable, Comparative Analyses of Campylobacter jejuni and C. coli Human Disease Isolates. Journal of Clinical Microbiology, 2017, 55, 2086-2097.	1.8	105
97	Development of an unambiguous and discriminatory multilocus sequence typing scheme for the Streptococcus zooepidemicus group. Microbiology (United Kingdom), 2008, 154, 3016-3024.	0.7	102
98	Multilocus Sequence Typing and Antigen Gene Sequencing in the Investigation of a Meningococcal Disease Outbreak. Journal of Clinical Microbiology, 1999, 37, 3883-3887.	1.8	100
99	Marked host specificity and lack of phylogeographic population structure of <i>Campylobacter jejuni</i> in wild birds. Molecular Ecology, 2013, 22, 1463-1472.	2.0	96
100	Antigenic Shift and Increased Incidence of Meningococcal Disease. Journal of Infectious Diseases, 2006, 193, 1266-1274.	1.9	95
101	Sequence Variation of the SeM Gene of Streptococcus equi Allows Discrimination of the Source of Strangles Outbreaks. Journal of Clinical Microbiology, 2006, 44, 480-486.	1.8	95
102	Species status of Neisseria gonorrhoeae: evolutionary and epidemiological inferences from multilocus sequence typing. BMC Biology, 2007, 5, 35.	1.7	95
103	Nasal Inoculation of the Commensal Neisseria lactamica Inhibits Carriage of Neisseria meningitidis by Young Adults: A Controlled Human Infection Study. Clinical Infectious Diseases, 2015, 60, 1512-1520.	2.9	95
104	Population genetics of a transformable bacterium: The influence of horizontal genetic exchange on the biology ofNeisseria meningitidis. FEMS Microbiology Letters, 1993, 112, 243-250.	0.7	90
105	Comparison of <i>Campylobacter</i> Populations in Wild Geese with Those in Starlings and Free-Range Poultry on the Same Farm. Applied and Environmental Microbiology, 2008, 74, 3583-3590.	1.4	90
106	Multi Locus Sequence Typing of Chlamydia Reveals an Association between Chlamydia psittaci Genotypes and Host Species. PLoS ONE, 2010, 5, e14179.	1.1	90
107	<i>Campylobacter</i> infection of broiler chickens in a freeâ€range environment. Environmental Microbiology, 2008, 10, 2042-2050.	1.8	89
108	Genomeâ€wide association of functional traits linked with <scp><i>C</i></scp><i>ampylobacter jejuni</i> survival from farm to fork. Environmental Microbiology, 2017, 19, 361-380.	1.8	88

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109	Population genomics: diversity and virulence in the Neisseria. Current Opinion in Microbiology, 2008, 11, 467-471.	2.3	84
110	Population structure of the <i>Yersinia pseudotuberculosis</i> complex according to multilocus sequence typing. Environmental Microbiology, 2011, 13, 3114-3127.	1.8	84
111	Phylogenetic Evidence for Frequent Positive Selection and Recombination in the Meningococcal Surface Antigen PorB. Molecular Biology and Evolution, 2002, 19, 1686-1694.	3.5	83
112	Hospital effluent: A reservoir for carbapenemase-producing Enterobacterales?. Science of the Total Environment, 2019, 672, 618-624.	3.9	83
113	A global gene pool in the neisseriae. Molecular Microbiology, 1996, 21, 1297-1298.	1.2	82
114	<i>Campylobacter</i>Excreted into the Environment by Animal Sources: Prevalence, Concentration Shed, and Host Association. Foodborne Pathogens and Disease, 2009, 6, 1161-1170.	0.8	81
115	Sequence Typing Confirms that Campylobacter jejuni Strains Associated with Guillain-Barrel̀•and Miller-Fisher Syndromes Are of Diverse Genetic Lineage, Serotype, and Flagella Type. Journal of Clinical Microbiology, 2001, 39, 3346-3349.	1.8	80
116	Using MLST to study bacterial variation: prospects in the genomic era. Future Microbiology, 2014, 9, 623-630.	1.0	80
117	Clonal Nature of Campylobacter fetus as Defined by Multilocus Sequence Typing. Journal of Clinical Microbiology, 2005, 43, 5888-5898.	1.8	79
118	A Longitudinal 6-Year Study of the Molecular Epidemiology of Clinical Campylobacter Isolates in Oxfordshire, United Kingdom. Journal of Clinical Microbiology, 2012, 50, 3193-3201.	1.8	79
119	Variation of the factor H-binding protein of Neisseria meningitidis. Microbiology (United Kingdom), 2009, 155, 4155-4169.	0.7	79
120	A gonococcal porA pseudogene: implications for understanding the evolution and pathogenicity of Neisseria gonorrhoeae. Molecular Microbiology, 1998, 30, 647-656.	1.2	78
121	Evolution of an Agriculture-Associated Disease Causing Campylobacter coli Clade: Evidence from National Surveillance Data in Scotland. PLoS ONE, 2010, 5, e15708.	1.1	75
122	Extended Sequence Typing of<i>Campylobacter</i>spp., United Kingdom. Emerging Infectious Diseases, 2008, 14, 1620-1622.	2.0	73
123	Resolution of a Meningococcal Disease Outbreak from Whole-Genome Sequence Data with Rapid Web-Based Analysis Methods. Journal of Clinical Microbiology, 2012, 50, 3046-3053.	1.8	72
124	Defining the Estimated Core Genome of Bacterial Populations Using a Bayesian Decision Model. PLoS Computational Biology, 2014, 10, e1003788.	1.5	72
125	The Landscape of Realized Homologous Recombination in Pathogenic Bacteria. Molecular Biology and Evolution, 2016, 33, 456-471.	3.5	72
126	Genetic evidence for recombination in Candida albicans based on haplotype analysis. Fungal Genetics and Biology, 2004, 41, 553-562.	0.9	71

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127	Genetic Diversity and Carriage Dynamics of Neisseria lactamica in Infants. Infection and Immunity, 2005, 73, 2424-2432.	1.0	70
128	Strain Typing and Determination of Population Structure of Candida krusei by Multilocus Sequence Typing. Journal of Clinical Microbiology, 2007, 45, 317-323.	1.8	70
129	Molecular analysis of the serotyping antigens of Neisseria meningitidis. Infection and Immunity, 1992, 60, 3620-3629.	1.0	69
130	<i>Campylobacter</i> populations in wild and domesticated Mallard ducks (<i>Anas) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 622 Td (plat	1.0	68
131	The Diversity of Meningococcal Carriage Across the African Meningitis Belt and the Impact of Vaccination With a Group A Meningococcal Conjugate Vaccine. Journal of Infectious Diseases, 2015, 212, 1298-1307.	1.9	68
132	First Insights into the Evolution of Streptococcus uberis : a Multilocus Sequence Typing Scheme That Enables Investigation of Its Population Biology. Applied and Environmental Microbiology, 2006, 72, 1420-1428.	1.4	66
133	Campylobacter sequence typing databases: applications and future prospects. Microbiology (United) Tj ETQq1 1 0.784314 rgBT /Overlo	0.7	64
134	Dynamics of <i>Campylobacter</i> colonization of a natural host, <i>Sturnus vulgaris</i> (European) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.8	63
135	Genomic epidemiology of age-associated meningococcal lineages in national surveillance: an observational cohort study. Lancet Infectious Diseases, The, 2015, 15, 1420-1428.	4.6	63
136	Distribution of BexseroÂ® Antigen Sequence Types (BASTs) in invasive meningococcal disease isolates: Implications for immunisation. Vaccine, 2016, 34, 4690-4697.	1.7	63
137	Association of a Bacteriophage with Meningococcal Disease in Young Adults. PLoS ONE, 2008, 3, e3885.	1.1	62
138	Molecular Evidence for Dissemination of Unique Campylobacter jejuni Clones in CuracÌ§ao, Netherlands Antilles. Journal of Clinical Microbiology, 2003, 41, 5593-5597.	1.8	61
139	Independent evolution of the core and accessory gene sets in the genus Neisseria: insights gained from the genome of Neisseria lactamica isolate 020-06. BMC Genomics, 2010, 11, 652.	1.2	61
140	Wild birdâ€associated <scp><i>C</i></scp><i>ampylobacter jejuni</i> isolates are a consistent source of human disease, in <scp>O</scp>xfordshire, <scp>U</scp>nited <scp>K</scp>ingdom. Environmental Microbiology Reports, 2015, 7, 782-788.	1.0	61
141	Specificity of the ModA11, ModA12 and ModD1 epigenetic regulator N6-adenine DNA methyltransferases of Neisseria meningitidis. Nucleic Acids Research, 2015, 43, 4150-4162.	6.5	58
142	Influence of the combination and phase variation status of the haemoglobin receptors HmbR and HpuAB on meningococcal virulence. Microbiology (United Kingdom), 2011, 157, 1446-1456.	0.7	58
143	Widespread acquisition of antimicrobial resistance among Campylobacter isolates from UK retail poultry and evidence for clonal expansion of resistant lineages. BMC Microbiology, 2013, 13, 160.	1.3	57
144	Multilocus Sequence Typing. Methods in Molecular Biology, 2009, 551, 129-140.	0.4	57

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145	Automated extraction of typing information for bacterial pathogens from whole genome sequence data: Neisseria meningitidis as an exemplar. Eurosurveillance, 2013, 18, 20379.	3.9	57
146	Diversity in pathogenicity can cause outbreaks of meningococcal disease. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 10229-10234.	3.3	55
147	Population structure of Streptococcus oralis. Microbiology (United Kingdom), 2009, 155, 2593-2602.	0.7	55
148	Identifying Neisseria Species by Use of the 50S Ribosomal Protein L6 (<i>rplF</i>) Gene. Journal of Clinical Microbiology, 2014, 52, 1375-1381.	1.8	55
149	Neisseria Adhesin A Variation and Revised Nomenclature Scheme. Vaccine Journal, 2014, 21, 966-971.	3.2	54
150	Genomic analyses of Neisseria gonorrhoeae reveal an association of the gonococcal genetic island with antimicrobial resistance. Journal of Infection, 2016, 73, 578-587.	1.7	54
151	The cloning, DNA sequence, and overexpression of the gene araE coding for arabinose-proton symport in Escherichia coli K12. Journal of Biological Chemistry, 1988, 263, 8003-10.	1.6	54
152	The evolution of genetic structure in the marine pathogen, Vibrio vulnificus. Infection, Genetics and Evolution, 2007, 7, 685-693.	1.0	52
153	Diversity and distribution of nuclease bacteriocins in bacterial genomes revealed using Hidden Markov Models. PLoS Computational Biology, 2017, 13, e1005652.	1.5	52
154	Agricultural intensification and the evolution of host specialism in the enteric pathogen <i>Campylobacter jejuni</i>. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 11018-11028.	3.3	50
155	A systematic review of source attribution of human campylobacteriosis using multilocus sequence typing. Eurosurveillance, 2019, 24, .	3.9	50
156	Genotypic and Phenotypic Modifications of Neisseria meningitidis after an Accidental Human Passage. PLoS ONE, 2011, 6, e17145.	1.1	49
157	Biofilm Morphotypes and Population Structure among Staphylococcus epidermidis from Commensal and Clinical Samples. PLoS ONE, 2016, 11, e0151240.	1.1	49
158	Vaccination Drives Changes in Metabolic and Virulence Profiles of Streptococcus pneumoniae. PLoS Pathogens, 2015, 11, e1005034.	2.1	49
159	Monoclonal antibody recognition of members of the meningococcal P1.10 variable region family: implications for serological typing and vaccine design. Microbiology (United Kingdom), 1996, 142, 63-69.	0.7	48
160	Monitoring chicken flock behaviour provides early warning of infection by human pathogen <i>Campylobacter</i>. Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20152323.	1.2	47
161	Pharyngeal carriage of Neisseria species inÂthe African meningitis belt. Journal of Infection, 2016, 72, 667-677.	1.7	47
162	Pan-GWAS of Streptococcus agalactiae Highlights Lineage-Specific Genes Associated with Virulence and Niche Adaptation. MBio, 2020, 11, .	1.8	47

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163	The Romance Verb. , 2018, , .		47
164	Introgression in the genus Campylobacter: generation and spread of mosaic alleles. Microbiology (United Kingdom), 2011, 157, 1066-1074.	0.7	47
165	Identification of meningococcal serosubtypes by polymerase chain reaction. Journal of Clinical Microbiology, 1992, 30, 2835-2841.	1.8	47
166	Campylobacter Infection in Children in Malawi Is Common and Is Frequently Associated with Enteric Virus Co-Infections. PLoS ONE, 2013, 8, e59663.	1.1	47
167	Recombination-Mediated Host Adaptation by Avian Staphylococcus aureus. Genome Biology and Evolution, 2017, 9, 830-842.	1.1	46
168	A Strange Affinity: â€˜Perfecto y tiempos afinesâ€™. Bulletin of Hispanic Studies, 2001, 78, 441-464.	0.0	45
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