

Julian Parkhill

List of Publications by Year in descending order

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678
papers

122,834
citations

186

151
h-index

162

323
g-index

754
all docs

754
docs citations

754
times ranked

84308
citing authors

#	ARTICLE	IF	CITATIONS
1	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010, 464, 59-65.	27.8	9,342
2	Deciphering the biology of <i>Mycobacterium tuberculosis</i> from the complete genome sequence. <i>Nature</i> , 1998, 393, 537-544.	27.8	7,357
3	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011, 473, 174-180.	27.8	5,800
4	Roary: rapid large-scale prokaryote pan genome analysis. <i>Bioinformatics</i> , 2015, 31, 3691-3693.	4.1	4,099
5	Complete genome sequence of the model actinomycete <i>Streptomyces coelicolor</i> A3(2). <i>Nature</i> , 2002, 417, 141-147.	27.8	2,940
6	Artemis: sequence visualization and annotation. <i>Bioinformatics</i> , 2000, 16, 944-945.	4.1	2,912
7	Reagent and laboratory contamination can critically impact sequence-based microbiome analyses. <i>BMC Biology</i> , 2014, 12, 87.	3.8	2,677
8	The genome sequence of the food-borne pathogen <i>Campylobacter jejuni</i> reveals hypervariable sequences. <i>Nature</i> , 2000, 403, 665-668.	27.8	1,869
9	Rapid phylogenetic analysis of large samples of recombinant bacterial whole genome sequences using Gubbins. <i>Nucleic Acids Research</i> , 2015, 43, e15-e15.	14.5	1,834
10	Massive gene decay in the leprosy bacillus. <i>Nature</i> , 2001, 409, 1007-1011.	27.8	1,607
11	ACT: the Artemis comparison tool. <i>Bioinformatics</i> , 2005, 21, 3422-3423.	4.1	1,536
12	Dominant and diet-responsive groups of bacteria within the human colonic microbiota. <i>ISME Journal</i> , 2011, 5, 220-230.	9.8	1,352
13	Complete genome sequence of a multiple drug resistant <i>Salmonella enterica</i> serovar Typhi CT18. <i>Nature</i> , 2001, 413, 848-852.	27.8	1,192
14	Genome sequence of <i>Yersinia pestis</i> , the causative agent of plague. <i>Nature</i> , 2001, 413, 523-527.	27.8	1,144
15	The minimum information about a genome sequence (MIGS) specification. <i>Nature Biotechnology</i> , 2008, 26, 541-547.	17.5	1,069
16	Evolution of MRSA During Hospital Transmission and Intercontinental Spread. <i>Science</i> , 2010, 327, 469-474.	12.6	1,054
17	Artemis: an integrated platform for visualization and analysis of high-throughput sequence-based experimental data. <i>Bioinformatics</i> , 2012, 28, 464-469.	4.1	1,029
18	The genome of the blood fluke <i>Schistosoma mansoni</i> . <i>Nature</i> , 2009, 460, 352-358.	27.8	945

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19	Circlator: automated circularization of genome assemblies using long sequencing reads. <i>Genome Biology</i> , 2015, 16, 294.	8.8	910
20	<i>Salmonella enterica</i> Serovar Typhimurium Exploits Inflammation to Compete with the Intestinal Microbiota. <i>PLoS Biology</i> , 2007, 5, e244.	5.6	905
21	Out-of-Africa migration and Neolithic coexpansion of <i>Mycobacterium tuberculosis</i> with modern humans. <i>Nature Genetics</i> , 2013, 45, 1176-1182.	21.4	900
22	Comparative analysis of the genome sequences of <i>Bordetella pertussis</i> , <i>Bordetella parapertussis</i> and <i>Bordetella bronchiseptica</i> . <i>Nature Genetics</i> , 2003, 35, 32-40.	21.4	898
23	The complete genome sequence of <i>Mycobacterium bovis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 7877-7882.	7.1	882
24	Complete genomes of two clinical <i>Staphylococcus aureus</i> strains: Evidence for the rapid evolution of virulence and drug resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 9786-9791.	7.1	830
25	Rapid Pneumococcal Evolution in Response to Clinical Interventions. <i>Science</i> , 2011, 331, 430-434.	12.6	828
26	The multidrug-resistant human pathogen <i>Clostridium difficile</i> has a highly mobile, mosaic genome. <i>Nature Genetics</i> , 2006, 38, 779-786.	21.4	821
27	DNAPlotter: circular and linear interactive genome visualization. <i>Bioinformatics</i> , 2009, 25, 119-120.	4.1	801
28	Whole-genome sequencing to delineate <i>Mycobacterium tuberculosis</i> outbreaks: a retrospective observational study. <i>Lancet Infectious Diseases</i> , The, 2013, 13, 137-146.	9.1	786
29	Meticillin-resistant <i>Staphylococcus aureus</i> with a novel <i>mecA</i> homologue in human and bovine populations in the UK and Denmark: a descriptive study. <i>Lancet Infectious Diseases</i> , The, 2011, 11, 595-603.	9.1	751
30	Complete DNA sequence of a serogroup A strain of <i>Neisseria meningitidis</i> Z2491. <i>Nature</i> , 2000, 404, 502-506.	27.8	687
31	Genomic plasticity of the causative agent of melioidosis, <i>Burkholderia pseudomallei</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 14240-14245.	7.1	675
32	Emergence and global spread of epidemic healthcare-associated <i>Clostridium difficile</i> . <i>Nature Genetics</i> , 2013, 45, 109-113.	21.4	669
33	Genetic Analysis of the Capsular Biosynthetic Locus from All 90 Pneumococcal Serotypes. <i>PLoS Genetics</i> , 2006, 2, e31.	3.5	661
34	Evidence for several waves of global transmission in the seventh cholera pandemic. <i>Nature</i> , 2011, 477, 462-465.	27.8	649
35	Rapid Whole-Genome Sequencing for Investigation of a Neonatal MRSA Outbreak. <i>New England Journal of Medicine</i> , 2012, 366, 2267-2275.	27.0	609
36	High-throughput clone library analysis of the mucosa-associated microbiota reveals dysbiosis and differences between inflamed and non-inflamed regions of the intestine in inflammatory bowel disease. <i>BMC Microbiology</i> , 2011, 11, 7.	3.3	596

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37	Whole-genome sequencing to identify transmission of <i>Mycobacterium abscessus</i> between patients with cystic fibrosis: a retrospective cohort study. <i>Lancet</i> , The, 2013, 381, 1551-1560.	13.7	596
38	Artemis and ACT: viewing, annotating and comparing sequences stored in a relational database. <i>Bioinformatics</i> , 2008, 24, 2672-2676.	4.1	578
39	Whole-genome sequencing for prediction of <i>Mycobacterium tuberculosis</i> drug susceptibility and resistance: a retrospective cohort study. <i>Lancet Infectious Diseases</i> , The, 2015, 15, 1193-1202.	9.1	553
40	Simultaneous assay of every <i>Salmonella</i> Typhi gene using one million transposon mutants. <i>Genome Research</i> , 2009, 19, 2308-2316.	5.5	544
41	Whole-genome sequencing for analysis of an outbreak of methicillin-resistant <i>Staphylococcus aureus</i> : a descriptive study. <i>Lancet Infectious Diseases</i> , The, 2013, 13, 130-136.	9.1	531
42	Human placenta has no microbiome but can contain potential pathogens. <i>Nature</i> , 2019, 572, 329-334.	27.8	513
43	Pre-Columbian mycobacterial genomes reveal seals as a source of New World human tuberculosis. <i>Nature</i> , 2014, 514, 494-497.	27.8	506
44	Epidemic multiple drug resistant <i>Salmonella</i> Typhimurium causing invasive disease in sub-Saharan Africa have a distinct genotype. <i>Genome Research</i> , 2009, 19, 2279-2287.	5.5	504
45	Targeted Restoration of the Intestinal Microbiota with a Simple, Defined Bacteriotherapy Resolves Relapsing <i>Clostridium difficile</i> Disease in Mice. <i>PLoS Pathogens</i> , 2012, 8, e1002995.	4.7	504
46	Sequencing ancient calcified dental plaque shows changes in oral microbiota with dietary shifts of the Neolithic and Industrial revolutions. <i>Nature Genetics</i> , 2013, 45, 450-455.	21.4	500
47	The genome of <i>Rhizobium leguminosarum</i> has recognizable core and accessory components. <i>Genome Biology</i> , 2006, 7, R34.	9.6	489
48	Expanding the biotechnology potential of lactobacilli through comparative genomics of 213 strains and associated genera. <i>Nature Communications</i> , 2015, 6, 8322.	12.8	488
49	Genome plasticity of BCG and impact on vaccine efficacy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 5596-5601.	7.1	486
50	ARIBA: rapid antimicrobial resistance genotyping directly from sequencing reads. <i>Microbial Genomics</i> , 2017, 3, e000131.	2.0	478
51	Insights from the complete genome sequence of <i>Mycobacterium marinum</i> on the evolution of <i>Mycobacterium tuberculosis</i> . <i>Genome Research</i> , 2008, 18, 729-741.	5.5	471
52	Microevolution and history of the plague bacillus, <i>Yersinia pestis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 17837-17842.	7.1	463
53	Emergence and spread of a human-transmissible multidrug-resistant nontuberculous mycobacterium. <i>Science</i> , 2016, 354, 751-757.	12.6	462
54	High-throughput sequencing provides insights into genome variation and evolution in <i>Salmonella</i> Typhi. <i>Nature Genetics</i> , 2008, 40, 987-993.	21.4	453

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55	The complete genome, comparative and functional analysis of <i>Stenotrophomonas maltophilia</i> reveals an organism heavily shielded by drug resistance determinants. <i>Genome Biology</i> , 2008, 9, R74.	9.6	452
56	Evolution and transmission of drug-resistant tuberculosis in a Russian population. <i>Nature Genetics</i> , 2014, 46, 279-286.	21.4	451
57	Routine Use of Microbial Whole Genome Sequencing in Diagnostic and Public Health Microbiology. <i>PLoS Pathogens</i> , 2012, 8, e1002824.	4.7	450
58	Comparative genome and phenotypic analysis of <i>Clostridium difficile</i> O27 strains provides insight into the evolution of a hypervirulent bacterium. <i>Genome Biology</i> , 2009, 10, R102.	9.6	431
59	Producing polished prokaryotic pangenomes with the Panaroo pipeline. <i>Genome Biology</i> , 2020, 21, 180.	8.8	419
60	A genomic portrait of the emergence, evolution, and global spread of a methicillin-resistant <i>Staphylococcus aureus</i> pandemic. <i>Genome Research</i> , 2013, 23, 653-664.	5.5	412
61	Phylogeographical analysis of the dominant multidrug-resistant H58 clade of <i>Salmonella</i> Typhi identifies inter- and intracontinental transmission events. <i>Nature Genetics</i> , 2015, 47, 632-639.	21.4	403
62	Comparative genome analysis of <i>Salmonella</i> Enteritidis PT4 and <i>Salmonella</i> Gallinarum 287/91 provides insights into evolutionary and host adaptation pathways. <i>Genome Research</i> , 2008, 18, 1624-1637.	5.5	394
63	Genome Project Standards in a New Era of Sequencing. <i>Science</i> , 2009, 326, 236-237.	12.6	382
64	Interpolated variable order motifs for identification of horizontally acquired DNA: revisiting the <i>Salmonella</i> pathogenicity islands. <i>Bioinformatics</i> , 2006, 22, 2196-2203.	4.1	377
65	Dense genomic sampling identifies highways of pneumococcal recombination. <i>Nature Genetics</i> , 2014, 46, 305-309.	21.4	371
66	Genomic and genetic analyses of diversity and plant interactions of <i>Pseudomonas fluorescens</i> . <i>Genome Biology</i> , 2009, 10, R51.	9.6	370
67	Intracontinental spread of human invasive <i>Salmonella</i> Typhimurium pathovariants in sub-Saharan Africa. <i>Nature Genetics</i> , 2012, 44, 1215-1221.	21.4	370
68	Genome sequence of the enterobacterial phytopathogen <i>Erwinia carotovora</i> subsp. <i>atroseptica</i> and characterization of virulence factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 11105-11110.	7.1	366
69	Population genomics of post-vaccine changes in pneumococcal epidemiology. <i>Nature Genetics</i> , 2013, 45, 656-663.	21.4	364
70	Evolutionary dynamics of <i>Clostridium difficile</i> over short and long time scales. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 7527-7532.	7.1	346
71	Reductive evolution and niche adaptation inferred from the genome of <i>Mycobacterium ulcerans</i> , the causative agent of Buruli ulcer. <i>Genome Research</i> , 2007, 17, 192-200.	5.5	345
72	The Genome of <i>Burkholderia cenocepacia</i> J2315, an Epidemic Pathogen of Cystic Fibrosis Patients. <i>Journal of Bacteriology</i> , 2009, 191, 261-277.	2.2	329

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73	Microbiology in the post-genomic era. <i>Nature Reviews Microbiology</i> , 2008, 6, 419-430.	28.6	324
74	Newly introduced genomic prophage islands are critical determinants of in vivo competitiveness in the Liverpool Epidemic Strain of <i>Pseudomonas aeruginosa</i> . <i>Genome Research</i> , 2009, 19, 12-23.	5.5	317
75	Antibiotic Treatment of <i>Clostridium difficile</i> Carrier Mice Triggers a Supershedder State, Spore-Mediated Transmission, and Severe Disease in Immunocompromised Hosts. <i>Infection and Immunity</i> , 2009, 77, 3661-3669.	2.2	315
76	Accelerated telomere shortening in ataxia telangiectasia. <i>Nature Genetics</i> , 1996, 13, 350-353.	21.4	314
77	Distinguishable Epidemics of Multidrug-Resistant <i>Salmonella</i> Typhimurium DT104 in Different Hosts. <i>Science</i> , 2013, 341, 1514-1517.	12.6	310
78	Modulation of the human gut microbiota by dietary fibres occurs at the species level. <i>BMC Biology</i> , 2016, 14, 3.	3.8	308
79	The Transcription Factor T-bet Regulates Intestinal Inflammation Mediated by Interleukin-7 Receptor+ Innate Lymphoid Cells. <i>Immunity</i> , 2012, 37, 674-684.	14.3	305
80	Complete Genome Sequence and Comparative Genome Analysis of Enteropathogenic <i>Escherichia coli</i> O127:H6 Strain E2348/69. <i>Journal of Bacteriology</i> , 2009, 191, 347-354.	2.2	299
81	Comparative Genomic Structure of Prokaryotes. <i>Annual Review of Genetics</i> , 2004, 38, 771-791.	7.6	293
82	The complete genome sequence and analysis of <i>Corynebacterium diphtheriae</i> NCTC13129. <i>Nucleic Acids Research</i> , 2003, 31, 6516-6523.	14.5	285
83	Whole-genome analysis of diverse <i>Chlamydia trachomatis</i> strains identifies phylogenetic relationships masked by current clinical typing. <i>Nature Genetics</i> , 2012, 44, 413-419.	21.4	279
84	Whole Genome Comparison of <i>Campylobacter jejuni</i> Human Isolates Using a Low-Cost Microarray Reveals Extensive Genetic Diversity. <i>Genome Research</i> , 2001, 11, 1706-1715.	5.5	278
85	<i>Shigella sonnei</i> genome sequencing and phylogenetic analysis indicate recent global dissemination from Europe. <i>Nature Genetics</i> , 2012, 44, 1056-1059.	21.4	278
86	Extensive DNA Inversions in the <i>B. fragilis</i> Genome Control Variable Gene Expression. <i>Science</i> , 2005, 307, 1463-1465.	12.6	275
87	Genome-wide analysis of multi- and extensively drug-resistant <i>Mycobacterium tuberculosis</i> . <i>Nature Genetics</i> , 2018, 50, 307-316.	21.4	271
88	Complete Sequence and Organization of pBtoxis, the Toxin-Coding Plasmid of <i>Bacillus thuringiensis</i> subsp. israelensis. <i>Applied and Environmental Microbiology</i> , 2002, 68, 5082-5095.	3.1	270
89	Complete Genome Sequence and Lytic Phase Transcription Profile of a <i>Coccolithovirus</i> . <i>Science</i> , 2005, 309, 1090-1092.	12.6	270
90	Genome-wide association study identifies vitamin B ₅ 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, 11923-11927.	7.1	267

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91	Genomic analysis of smooth tubercle bacilli provides insights into ancestry and pathoadaptation of <i>Mycobacterium tuberculosis</i> . <i>Nature Genetics</i> , 2013, 45, 172-179.	21.4	264
92	Description and Nomenclature of <i>Neisseria meningitidis</i> Capsule Locus. <i>Emerging Infectious Diseases</i> , 2013, 19, 566-573.	4.3	259
93	Global Population Structure and Evolution of <i>Bordetella pertussis</i> and Their Relationship with Vaccination. <i>MBio</i> , 2014, 5, e01074.	4.1	257
94	Genomic history of the seventh pandemic of cholera in Africa. <i>Science</i> , 2017, 358, 785-789.	12.6	255
95	Recognizing the reagent microbiome. <i>Nature Microbiology</i> , 2018, 3, 851-853.	13.3	255
96	Comparative Genomic Analyses of Seventeen <i>Streptococcus pneumoniae</i> Strains: Insights into the Pneumococcal Supragenome. <i>Journal of Bacteriology</i> , 2007, 189, 8186-8195.	2.2	249
97	Reverse Transcriptase-Mediated Tropism Switching in <i>Bordetella</i> Bacteriophage. <i>Science</i> , 2002, 295, 2091-2094.	12.6	247
98	Microbial genome-wide association studies: lessons from human GWAS. <i>Nature Reviews Genetics</i> , 2017, 18, 41-50.	16.3	239
99	The Impact of Different DNA Extraction Kits and Laboratories upon the Assessment of Human Gut Microbiota Composition by 16S rRNA Gene Sequencing. <i>PLoS ONE</i> , 2014, 9, e88982.	2.5	236
100	Sequencing and analysis of the genome of the Whipple's disease bacterium <i>Tropheryma whippelii</i> . <i>Lancet</i> , The, 2003, 361, 637-644.	13.7	232
101	Systematic longitudinal survey of invasive <i>Escherichia coli</i> in England demonstrates a stable population structure only transiently disturbed by the emergence of ST131. <i>Genome Research</i> , 2017, 27, 1437-1449.	5.5	231
102	Complete Genome Sequence of Uropathogenic <i>Proteus mirabilis</i> , a Master of both Adherence and Motility. <i>Journal of Bacteriology</i> , 2008, 190, 4027-4037.	2.2	229
103	Genome sequence of a proteolytic (Group I) <i>Clostridium botulinum</i> strain Hall A and comparative analysis of the clostridial genomes. <i>Genome Research</i> , 2007, 17, 1082-1092.	5.5	228
104	A decade of advances in transposon-insertion sequencing. <i>Nature Reviews Genetics</i> , 2020, 21, 526-540.	16.3	228
105	The Complete Genome Sequence and Comparative Genome Analysis of the High Pathogenicity <i>Yersinia enterocolitica</i> Strain 8081. <i>PLoS Genetics</i> , 2006, 2, e206.	3.5	227
106	Partitioning core and satellite taxa from within cystic fibrosis lung bacterial communities. <i>ISME Journal</i> , 2011, 5, 780-791.	9.8	222
107	Diarrhea in young children from low-income countries leads to large-scale alterations in intestinal microbiota composition. <i>Genome Biology</i> , 2014, 15, R76.	9.6	219
108	GeneDB--an annotation database for pathogens. <i>Nucleic Acids Research</i> , 2012, 40, D98-D108.	14.5	217

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109	Proteomic and microarray characterization of the AggR regulon identifies a pheU pathogenicity island in enteroaggregative Escherichia coli. <i>Molecular Microbiology</i> , 2006, 61, 1267-1282.	2.5	216
110	Multireplicon genome architecture of <i>Lactobacillus salivarius</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 6718-6723.	7.1	216
111	Rapid Evolution of Virulence and Drug Resistance in the Emerging Zoonotic Pathogen <i>Streptococcus suis</i> . <i>PLoS ONE</i> , 2009, 4, e6072.	2.5	214
112	Patterns of genome evolution that have accompanied host adaptation in <i>Salmonella</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 863-868.	7.1	213
113	Genome Sequence of a Recently Emerged, Highly Transmissible, Multi-Antibiotic- and Antiseptic-Resistant Variant of Methicillin-Resistant <i>Staphylococcus aureus</i> , Sequence Type 239 (TW). <i>Journal of Bacteriology</i> , 2010, 192, 888-892.	2.2	211
114	Genome Evolution of <i>Wolbachia</i> Strain wPip from the <i>Culex pipiens</i> Group. <i>Molecular Biology and Evolution</i> , 2008, 25, 1877-1887.	8.9	210
115	Proteomic and Genomic Characterization of Highly Infectious <i>Clostridium difficile</i> 630 Spores. <i>Journal of Bacteriology</i> , 2009, 191, 5377-5386.	2.2	210
116	Sequence-Based Analysis Uncovers an Abundance of Non-Coding RNA in the Total Transcriptome of <i>Mycobacterium tuberculosis</i> . <i>PLoS Pathogens</i> , 2011, 7, e1002342.	4.7	210
117	<i>Streptococcus agalactiae</i> clones infecting humans were selected and fixed through the extensive use of tetracycline. <i>Nature Communications</i> , 2014, 5, 4544.	12.8	208
118	16S rRNA gene-based profiling of the human infant gut microbiota is strongly influenced by sample processing and PCR primer choice. <i>Microbiome</i> , 2015, 3, 26.	11.1	208
119	Robust high-throughput prokaryote de novo assembly and improvement pipeline for Illumina data. <i>Microbial Genomics</i> , 2016, 2, e000083.	2.0	208
120	<i>Chlamydia trachomatis</i> : Genome sequence analysis of lymphogranuloma venereum isolates. <i>Genome Research</i> , 2008, 18, 161-171.	5.5	207
121	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
122	Intercontinental dissemination of azithromycin-resistant shigellosis through sexual transmission: a cross-sectional study. <i>Lancet Infectious Diseases</i> , The, 2015, 15, 913-921.	9.1	204
123	A Strand-Specific RNA-Seq Analysis of the Transcriptome of the Typhoid Bacillus <i>Salmonella Typhi</i> . <i>PLoS Genetics</i> , 2009, 5, e1000569.	3.5	202
124	Novel staphylococcal species that form part of a <i>Staphylococcus aureus</i> -related complex: the non-pigmented <i>Staphylococcus argenteus</i> sp. nov. and the non-human primate-associated <i>Staphylococcus schweitzeri</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 15-22.	1.7	201
125	GeneDB: a resource for prokaryotic and eukaryotic organisms. <i>Nucleic Acids Research</i> , 2004, 32, 339D-343.	14.5	199
126	Large-scale whole genome sequencing of <i>M. tuberculosis</i> provides insights into transmission in a high prevalence area. <i>ELife</i> , 2015, 4, .	6.0	198

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127	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.	4.7	197
128	Whole-Genome Sequencing for Rapid Susceptibility Testing of <i>M. tuberculosis</i> . <i>New England Journal of Medicine</i> , 2013, 369, 290-292.	27.0	195
129	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
130	Methicillin-resistant <i>Staphylococcus aureus</i> emerged long before the introduction of methicillin into clinical practice. <i>Genome Biology</i> , 2017, 18, 130.	8.8	193
131	Whole genome sequencing identifies zoonotic transmission of MRSA isolates with the novel <i>mecA</i> homologue <i>mecC</i> . <i>EMBO Molecular Medicine</i> , 2013, 5, 509-515.	6.9	192
132	Whole-Genome Sequencing for Routine Pathogen Surveillance in Public Health: a Population Snapshot of Invasive <i>Staphylococcus aureus</i> in Europe. <i>MBio</i> , 2016, 7, .	4.1	192
133	Distinct <i>Salmonella</i> Enteritidis lineages associated with enterocolitis in high-income settings and invasive disease in low-income settings. <i>Nature Genetics</i> , 2016, 48, 1211-1217.	21.4	191
134	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. <i>PLoS Biology</i> , 2014, 12, e1001920.	5.6	190
135	Sequence element enrichment analysis to determine the genetic basis of bacterial phenotypes. <i>Nature Communications</i> , 2016, 7, 12797.	12.8	190
136	Re-annotation and re-analysis of the <i>Campylobacter jejuni</i> NCTC11168 genome sequence. <i>BMC Genomics</i> , 2007, 8, 162.	2.8	189
137	Whole-genome sequencing to establish relapse or re-infection with <i>Mycobacterium tuberculosis</i> : a retrospective observational study. <i>Lancet Respiratory Medicine</i> , the, 2013, 1, 786-792.	10.7	184
138	Rapid Bacterial Whole-Genome Sequencing to Enhance Diagnostic and Public Health Microbiology. <i>JAMA Internal Medicine</i> , 2013, 173, 1397.	5.1	181
139	Inferring patient to patient transmission of <i>Mycobacterium tuberculosis</i> from whole genome sequencing data. <i>BMC Infectious Diseases</i> , 2013, 13, 110.	2.9	180
140	Comprehensive Assignment of Roles for <i>Salmonella</i> Typhimurium Genes in Intestinal Colonization of Food-Producing Animals. <i>PLoS Genetics</i> , 2013, 9, e1003456.	3.5	176
141	Molecular tracing of the emergence, diversification, and transmission of <i>S. aureus</i> sequence type 8 in a New York community. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6738-6743.	7.1	176
142	Molecular tracing of the emergence, adaptation, and transmission of hospital-associated methicillin-resistant <i>Staphylococcus aureus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 9107-9112.	7.1	174
143	Microevolution of extensively drug-resistant tuberculosis in Russia. <i>Genome Research</i> , 2012, 22, 735-745.	5.5	173
144	Pneumococcal Capsular Switching: A Historical Perspective. <i>Journal of Infectious Diseases</i> , 2013, 207, 439-449.	4.0	172

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145	Salmonella bongori Provides Insights into the Evolution of the Salmonellae. PLoS Pathogens, 2011, 7, e1002191.	4.7	171
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