

Nicholas R Thomson

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211
papers

13,705
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58
h-index

114
g-index

245
ext. papers

17,153
ext. citations

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avg, IF

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L-index

#	Paper	IF	Citations
211	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	36.3	787
210	The pangenome structure of <i>Escherichia coli</i> : comparative genomic analysis of <i>E. coli</i> commensal and pathogenic isolates. <i>Journal of Bacteriology</i> , 2008 , 190, 6881-93	3.5	607
209	Genomic analysis of diversity, population structure, virulence, and antimicrobial resistance in <i>Klebsiella pneumoniae</i> , an urgent threat to public health. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E3574-81	11.5	588
208	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, 14240-5	11.5	569
207	<i>Escherichia coli</i> K-12: a cooperatively developed annotation snapshot--2005. <i>Nucleic Acids Research</i> , 2006 , 34, 1-9	20.1	525
206	Evidence for several waves of global transmission in the seventh cholera pandemic. <i>Nature</i> , 2011 , 477, 462-5	50.4	492
205	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, 17837-42	11.5	404
204	<i>Yersinia pestis</i> genome sequencing identifies patterns of global phylogenetic diversity. <i>Nature Genetics</i> , 2010 , 42, 1140-3	36.3	393
203	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, 2279-87	9.7	374
202	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, 1624-37	9.7	320
201	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, 632-9	36.3	305
200	The transcriptional landscape and small RNAs of <i>Salmonella enterica</i> serovar Typhimurium. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, E1277-86	11.5	294
199	Gut inflammation can boost horizontal gene transfer between pathogenic and commensal Enterobacteriaceae. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 1269-74	11.5	277
198	The genome of <i>Burkholderia cenocepacia</i> J2315, an epidemic pathogen of cystic fibrosis patients. <i>Journal of Bacteriology</i> , 2009 , 191, 261-77	3.5	270
197	Whole-genome analysis of diverse <i>Chlamydia trachomatis</i> strains identifies phylogenetic relationships masked by current clinical typing. <i>Nature Genetics</i> , 2012 , 44, 413-9, S1	36.3	222
196	Identification of capsule synthesis loci from whole genome data. <i>Microbial Genomics</i> , 2016 , 2, e000102	4.4	216
195	<i>Shigella sonnei</i> genome sequencing and phylogenetic analysis indicate recent global dissemination from Europe. <i>Nature Genetics</i> , 2012 , 44, 1056-9	36.3	203

194	Gastrointestinal Carriage Is a Major Reservoir of <i>Klebsiella pneumoniae</i> Infection in Intensive Care Patients. <i>Clinical Infectious Diseases</i> , 2017 , 65, 208-215	11.6	193
193	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	6	192
192	A strand-specific RNA-Seq analysis of the transcriptome of the typhoid bacillus <i>Salmonella typhi</i> . <i>PLoS Genetics</i> , 2009 , 5, e1000569	6	188
191	Proteomic and microarray characterization of the AggR regulon identifies a pheU pathogenicity island in enteroaggregative <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2006 , 61, 1267-82	4.1	185
190	Genomic history of the seventh pandemic of cholera in Africa. <i>Science</i> , 2017 , 358, 785-789	33.3	157
189	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, 863-8	11.5	154
188	<i>Chlamydia trachomatis</i> : genome sequence analysis of lymphogranuloma venereum isolates. <i>Genome Research</i> , 2008 , 18, 161-71	9.7	154
187	Genomic insights into the emergence and spread of antimicrobial-resistant bacterial pathogens. <i>Science</i> , 2018 , 360, 733-738	33.3	146
186	The <i>Chlamydomonas reinhardtii</i> genome sequence reveals an array of variable proteins that contribute to interspecies variation. <i>Genome Research</i> , 2005 , 15, 629-40	9.7	144
185	A commensal gone bad: complete genome sequence of the prototypical enterotoxigenic <i>Escherichia coli</i> strain H10407. <i>Journal of Bacteriology</i> , 2010 , 192, 5822-31	3.5	141
184	Intercontinental dissemination of azithromycin-resistant shigellosis through sexual transmission: a cross-sectional study. <i>Lancet Infectious Diseases</i> , 2015 , 15, 913-21	25.5	139
183	The genome of the heartwater agent <i>Ehrlichia ruminantium</i> contains multiple tandem repeats of actively variable copy number. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 838-43	11.5	139
182	Identification of enterotoxigenic <i>Escherichia coli</i> (ETEC) clades with long-term global distribution. <i>Nature Genetics</i> , 2014 , 46, 1321-6	36.3	134
181	<i>Salmonella bongori</i> provides insights into the evolution of the Salmonellae. <i>PLoS Pathogens</i> , 2011 , 7, e1002191	7.6	123
180	Pseudogene accumulation in the evolutionary histories of <i>Salmonella enterica</i> serovars Paratyphi A and Typhi. <i>BMC Genomics</i> , 2009 , 10, 36	4.5	120
179	Distinct <i>Salmonella enteritidis</i> lineages associated with enterocolitis in high-income settings and invasive disease in low-income settings. <i>Nature Genetics</i> , 2016 , 48, 1211-1217	36.3	116
178	Parallel independent evolution of pathogenicity within the genus <i>Yersinia</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 6768-73	11.5	114
177	Genome evolution and plasticity of <i>Serratia marcescens</i> , an important multidrug-resistant nosocomial pathogen. <i>Genome Biology and Evolution</i> , 2014 , 6, 2096-110	3.9	114

176	A complete view of the genetic diversity of the Escherichia coli O-antigen biosynthesis gene cluster. <i>DNA Research</i> , 2015 , 22, 101-7	4.5	108
175	The role of prophage-like elements in the diversity of Salmonella enterica serovars. <i>Journal of Molecular Biology</i> , 2004 , 339, 279-300	6.5	102
174	The diversity of surface polysaccharides. <i>Microbial Genomics</i> , 2016 , 2, e000073	4.4	101
173	Co-evolution of genomes and plasmids within Chlamydia trachomatis and the emergence in Sweden of a new variant strain. <i>BMC Genomics</i> , 2009 , 10, 239	4.5	99
172	A bimodal pattern of relatedness between the Salmonella Paratyphi A and Typhi genomes: convergence or divergence by homologous recombination?. <i>Genome Research</i> , 2007 , 17, 61-8	9.7	98
171	Add, stir and reduce <i>Yersinia</i> spp. as model bacteria for pathogen evolution. <i>Nature Reviews Microbiology</i> , 2016 , 14, 177-90	22.2	95
170	Whole-genome sequences of Chlamydia trachomatis directly from clinical samples without culture. <i>Genome Research</i> , 2013 , 23, 855-66	9.7	95
169	Genomic insights into the 2016-2017 cholera epidemic in Yemen. <i>Nature</i> , 2019 , 565, 230-233	50.4	92
168	Tracking the establishment of local endemic populations of an emergent enteric pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 17522-7	11.5	89
167	The genomic signatures of Shigella evolution, adaptation and geographical spread. <i>Nature Reviews Microbiology</i> , 2016 , 14, 235-50	22.2	88
166	Integrated view of in the Americas. <i>Science</i> , 2017 , 358, 789-793	33.3	79
165	A simple method for directional transcriptome sequencing using Illumina technology. <i>Nucleic Acids Research</i> , 2009 , 37, e148	20.1	77
164	The genome sequence of the fish pathogen <i>Aeromonas salmonicida</i> strain LFI1238 shows extensive evidence of gene decay. <i>BMC Genomics</i> , 2008 , 9, 616	4.5	77
163	Genomic surveillance for hypervirulence and multi-drug resistance in invasive <i>Klebsiella pneumoniae</i> from South and Southeast Asia. <i>Genome Medicine</i> , 2020 , 12, 11	14.4	74
162	Variation in Salmonella enterica serovar typhi InChI1 plasmids during the global spread of resistant typhoid fever. <i>Antimicrobial Agents and Chemotherapy</i> , 2009 , 53, 716-27	5.9	73
161	Public health value of next-generation DNA sequencing of enterohemorrhagic Escherichia coli isolates from an outbreak. <i>Journal of Clinical Microbiology</i> , 2013 , 51, 232-7	9.7	67
160	A high-resolution genomic analysis of multidrug-resistant hospital outbreaks of <i>Klebsiella pneumoniae</i> . <i>EMBO Molecular Medicine</i> , 2015 , 7, 227-39	12	67
159	The Swedish new variant of Chlamydia trachomatis: genome sequence, morphology, cell tropism and phenotypic characterization. <i>Microbiology (United Kingdom)</i> , 2010 , 156, 1394-1404	2.9	67

158	Comprehensive global genome dynamics of show ancient diversification followed by contemporary mixing and recent lineage expansion. <i>Genome Research</i> , 2017 , 27, 1220-1229	9.7	65
157	Species-wide whole genome sequencing reveals historical global spread and recent local persistence in <i>Shigella flexneri</i> . <i>ELife</i> , 2015 , 4, e07335	8.9	65
156	An O antigen capsule modulates bacterial pathogenesis in <i>Shigella sonnei</i> . <i>PLoS Pathogens</i> , 2015 , 11, e1004749	7.6	64
155	Sequencing and functional annotation of avian pathogenic <i>Escherichia coli</i> serogroup O78 strains reveal the evolution of <i>E. coli</i> lineages pathogenic for poultry via distinct mechanisms. <i>Infection and Immunity</i> , 2013 , 81, 838-49	3.7	64
154	Multidrug-resistant <i>Salmonella enterica</i> serovar paratyphi A harbors IncHI1 plasmids similar to those found in serovar typhi. <i>Journal of Bacteriology</i> , 2007 , 189, 4257-64	3.5	64
153	Horizontal antimicrobial resistance transfer drives epidemics of multiple <i>Shigella</i> species. <i>Nature Communications</i> , 2018 , 9, 1462	17.4	57
152	Antimicrobial-Resistant <i>Klebsiella pneumoniae</i> Carriage and Infection in Specialized Geriatric Care Wards Linked to Acquisition in the Referring Hospital. <i>Clinical Infectious Diseases</i> , 2018 , 67, 161-170	11.6	57
151	South Asia as a Reservoir for the Global Spread of Ciprofloxacin-Resistant <i>Shigella sonnei</i> : A Cross-Sectional Study. <i>PLoS Medicine</i> , 2016 , 13, e1002055	11.6	56
150	Novel Subclone of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Sequence Type 11 with Enhanced Virulence and Transmissibility, China. <i>Emerging Infectious Diseases</i> , 2020 , 26, 289-297	10.2	52
149	Global phylogeography and evolutionary history of <i>Shigella dysenteriae</i> type 1. <i>Nature Microbiology</i> , 2016 , 1, 16027	26.6	47
148	Genome and transcriptome adaptation accompanying emergence of the definitive type 2 host-restricted <i>Salmonella enterica</i> serovar Typhimurium pathovar. <i>MBio</i> , 2013 , 4, e00565-13	7.8	47
147	The sudden dominance of blaCTX-M harbouring plasmids in <i>Shigella</i> spp. Circulating in Southern Vietnam. <i>PLoS Neglected Tropical Diseases</i> , 2010 , 4, e702	4.8	45
146	Pan-genome Analysis of Ancient and Modern <i>Salmonella enterica</i> Demonstrates Genomic Stability of the Invasive Para C Lineage for Millennia. <i>Current Biology</i> , 2018 , 28, 2420-2428.e10	6.3	44
145	Genome-wide transposon mutagenesis indicates that <i>Mycobacterium marinum</i> customizes its virulence mechanisms for survival and replication in different hosts. <i>Infection and Immunity</i> , 2015 , 83, 1778-88	3.7	44
144	Prophage sequences defining hot spots of genome variation in <i>Salmonella enterica</i> serovar Typhimurium can be used to discriminate between field isolates. <i>Journal of Clinical Microbiology</i> , 2007 , 45, 2590-8	9.7	44
143	Plasmid deficiency in urogenital isolates of <i>Chlamydia trachomatis</i> reduces infectivity and virulence in a mouse model. <i>Pathogens and Disease</i> , 2014 , 70, 61-9	4.2	43
142	Gene array analysis of <i>Yersinia enterocolitica</i> FlhD and FlhC: regulation of enzymes affecting synthesis and degradation of carbamoylphosphate. <i>Microbiology (United Kingdom)</i> , 2004 , 150, 2289-2300	2.9	42
141	Assessing gut microbiota perturbations during the early phase of infectious diarrhea in Vietnamese children. <i>Gut Microbes</i> , 2018 , 9, 38-54	8.8	41

140	The <i>Yersinia pseudotuberculosis</i> complex: characterization and delineation of a new species, <i>Yersinia wautersii</i> . <i>International Journal of Medical Microbiology</i> , 2014 , 304, 452-63	3.7	38
139	Environmental marine pathogen isolation using mesocosm culture of sharpsnout seabream: striking genomic and morphological features of novel <i>Endozoicomonas</i> sp. <i>Scientific Reports</i> , 2015 , 5, 17609	4.9	38
138	Genomic epidemiology of <i>Shigella</i> in the United Kingdom shows transmission of pathogen sublineages and determinants of antimicrobial resistance. <i>Scientific Reports</i> , 2018 , 8, 7389	4.9	35
137	Genomic and phenotypic variation in epidemic-spanning <i>Salmonella enterica</i> serovar Enteritidis isolates. <i>BMC Microbiology</i> , 2009 , 9, 237	4.5	34
136	Molecular epidemiology of <i>Klebsiella pneumoniae</i> invasive infections over a decade at Kilifi County Hospital in Kenya. <i>International Journal of Medical Microbiology</i> , 2017 , 307, 422-429	3.7	33
135	Use of whole-genus genome sequence data to develop a multilocus sequence typing tool that accurately identifies <i>Yersinia</i> isolates to the species and subspecies levels. <i>Journal of Clinical Microbiology</i> , 2015 , 53, 35-42	9.7	32
134	Generating whole bacterial genome sequences of low-abundance species from complex samples with IMS-MDA. <i>Nature Protocols</i> , 2013 , 8, 2404-12	18.8	32
133	Genomic Analysis of <i>Salmonella enterica</i> Serovar Typhimurium from Wild Passerines in England and Wales. <i>Applied and Environmental Microbiology</i> , 2016 , 82, 6728-6735	4.8	32
132	Genomic epidemiology of syphilis reveals independent emergence of macrolide resistance across multiple circulating lineages. <i>Nature Communications</i> , 2019 , 10, 3255	17.4	31
131	Genomic epidemiology of <i>Vibrio cholerae</i> O1 associated with floods, Pakistan, 2010. <i>Emerging Infectious Diseases</i> , 2014 , 20, 13-20	10.2	30
130	<i>Chlamydia trachomatis</i> from Australian Aboriginal people with trachoma are polyphyletic composed of multiple distinctive lineages. <i>Nature Communications</i> , 2016 , 7, 10688	17.4	30
129	Genomic Epidemiology of <i>Vibrio cholerae</i> O1 Associated with Floods, Pakistan, 2010. <i>Emerging Infectious Diseases</i> , 2014 , 20, 13-20	10.2	29
128	<i>Vibrio cholerae</i> Serogroup O139: Isolation from Cholera Patients and Asymptomatic Household Family Members in Bangladesh between 2013 and 2014. <i>PLoS Neglected Tropical Diseases</i> , 2015 , 9, e00041183	4.8	29
127	Annotation of plasmid genes. <i>Plasmid</i> , 2017 , 91, 61-67	3.3	28
126	<i>Brucella neotomae</i> Infection in Humans, Costa Rica. <i>Emerging Infectious Diseases</i> , 2017 , 23, 997-1000	10.2	28
125	A genomic island in <i>Vibrio cholerae</i> with VPI-1 site-specific recombination characteristics contains CRISPR-Cas and type VI secretion modules. <i>Scientific Reports</i> , 2016 , 6, 36891	4.9	28
124	Long-Lasting Geomagnetically Induced Currents and Harmonic Distortion Observed in New Zealand During the 7-8 September 2017 Disturbed Period. <i>Space Weather</i> , 2018 , 16, 704-717	3.7	28
123	Genomic landscape of extended-spectrum β -lactamase resistance in <i>Escherichia coli</i> from an urban African setting. <i>Journal of Antimicrobial Chemotherapy</i> , 2017 , 72, 1602-1609	5.1	27

122	A study on the geophylogeny of clinical and environmental <i>Vibrio cholerae</i> in Kenya. <i>PLoS ONE</i> , 2013 , 8, e74829	3.7	27
121	New Variant of Multidrug-Resistant Serovar Typhimurium Associated with Invasive Disease in Immunocompromised Patients in Vietnam. <i>MBio</i> , 2018 , 9,	7.8	26
120	The Murray collection of pre-antibiotic era Enterobacteriaceae: a unique research resource. <i>Genome Medicine</i> , 2015 , 7, 97	14.4	23
119	Quantitative Proteomics of the Infectious and Replicative Forms of <i>Chlamydia trachomatis</i> . <i>PLoS ONE</i> , 2016 , 11, e0149011	3.7	23
118	Whole genome sequencing of <i>Shigella sonnei</i> through PulseNet Latin America and Caribbean: advancing global surveillance of foodborne illnesses. <i>Clinical Microbiology and Infection</i> , 2017 , 23, 845-853	9.5	22
117	Minimal genetic change in <i>Vibrio cholerae</i> in Mozambique over time: Multilocus variable number tandem repeat analysis and whole genome sequencing. <i>PLoS Neglected Tropical Diseases</i> , 2017 , 11, e0003671	4.8	22
116	<i>Mycoplasma genitalium</i> : whole genome sequence analysis, recombination and population structure. <i>BMC Genomics</i> , 2017 , 18, 993	4.5	22
115	Defining endemic cholera at three levels of spatiotemporal resolution within Bangladesh. <i>Nature Genetics</i> , 2018 , 50, 951-955	36.3	22
114	Co-cultivation and transcriptome sequencing of two co-existing fish pathogens <i>Moritella viscosa</i> and <i>Aliivibrio wodanis</i> . <i>BMC Genomics</i> , 2015 , 16, 447	4.5	21
113	Emerging pathogens of gilthead seabream: characterisation and genomic analysis of novel intracellular ϵ proteobacteria. <i>ISME Journal</i> , 2016 , 10, 1791-803	11.9	21
112	Antimicrobial Drug Resistance of <i>Vibrio cholerae</i> , Democratic Republic of the Congo. <i>Emerging Infectious Diseases</i> , 2015 , 21, 847-51	10.2	21
111	The extant World War 1 dysentery bacillus NCTC1: a genomic analysis. <i>Lancet, The</i> , 2014 , 384, 1691-7	40	21
110	Diagnostics for Yaws Eradication: Insights From Direct Next-Generation Sequencing of Cutaneous Strains of <i>Treponema pallidum</i> . <i>Clinical Infectious Diseases</i> , 2018 , 66, 818-824	11.6	20
109	Relationship between Distinct African Cholera Epidemics Revealed via MLVA Haplotyping of 337 <i>Vibrio cholerae</i> Isolates. <i>PLoS Neglected Tropical Diseases</i> , 2015 , 9, e0003817	4.8	20
108	The population structure of <i>Vibrio cholerae</i> from the Chandigarh Region of Northern India. <i>PLoS Neglected Tropical Diseases</i> , 2014 , 8, e2981	4.8	20
107	RNA-seq analysis of the influence of anaerobiosis and FNR on <i>Shigella flexneri</i> . <i>BMC Genomics</i> , 2014 , 15, 438	4.5	20
106	European <i>Chlamydia abortus</i> livestock isolate genomes reveal unusual stability and limited diversity, reflected in geographical signatures. <i>BMC Genomics</i> , 2017 , 18, 344	4.5	19
105	<i>Brucella</i> Genetic Variability in Wildlife Marine Mammals Populations Relates to Host Preference and Ocean Distribution. <i>Genome Biology and Evolution</i> , 2017 , 9, 1901-1912	3.9	19

104	New insights into the bacterial fitness-associated mechanisms revealed by the characterization of large plasmids of an avian pathogenic <i>E. coli</i> . <i>PLoS ONE</i> , 2012 , 7, e29481	3.7	19
103	Genomic analysis of <i>Klebsiella pneumoniae</i> isolates from Malawi reveals acquisition of multiple ESBL determinants across diverse lineages. <i>Journal of Antimicrobial Chemotherapy</i> , 2019 , 74, 1223-1232	5.1	19
102	Detecting extra-ocular <i>Chlamydia trachomatis</i> in a trachoma-endemic community in Ethiopia: Identifying potential routes of transmission. <i>PLoS Neglected Tropical Diseases</i> , 2020 , 14, e0008120	4.8	18
101	Novel R pipeline for analyzing Biolog Phenotypic MicroArray data. <i>PLoS ONE</i> , 2015 , 10, e0118392	3.7	18
100	The genetic basis of plasmid tropism between <i>Chlamydia trachomatis</i> and <i>Chlamydia muridarum</i> . <i>Pathogens and Disease</i> , 2014 , 72, 19-23	4.2	18
99	Genomic characterisation of invasive non-typhoidal <i>Salmonella enterica</i> Subspecies <i>enterica</i> Serovar <i>Bovismorbificans</i> isolates from Malawi. <i>PLoS Neglected Tropical Diseases</i> , 2013 , 7, e2557	4.8	18
98	Dissecting the molecular evolution of fluoroquinolone-resistant <i>Shigella sonnei</i> . <i>Nature Communications</i> , 2019 , 10, 4828	17.4	17
97	Genomic variations leading to alterations in cell morphology of <i>Campylobacter</i> spp. <i>Scientific Reports</i> , 2016 , 6, 38303	4.9	17
96	Global phylogeny of <i>Shigella sonnei</i> strains from limited single nucleotide polymorphisms (SNPs) and development of a rapid and cost-effective SNP-typing scheme for strain identification by high-resolution melting analysis. <i>Journal of Clinical Microbiology</i> , 2013 , 51, 303-5	9.7	16
95	<i>Chlamydia trachomatis</i> : small genome, big challenges. <i>Future Microbiology</i> , 2010 , 5, 555-61	2.9	16
94	Strain 2308 Wisconsin Genome: Importance of the Definition of Reference Strains. <i>Frontiers in Microbiology</i> , 2016 , 7, 1557	5.7	16
93	Antimicrobial Resistance Diversity Suggestive of Distinct Typhimurium Sources or Selective Pressures in Food-Production Animals. <i>Frontiers in Microbiology</i> , 2019 , 10, 708	5.7	15
92	Directional gene flow and ecological separation in. <i>Microbial Genomics</i> , 2015 , 1, e000030	4.4	15
91	Dynamics of cholera epidemics from Benin to Mauritania. <i>PLoS Neglected Tropical Diseases</i> , 2018 , 12, e0006379	4.8	14
90	Travel- and Community-Based Transmission of Multidrug-Resistant <i>Shigella sonnei</i> Lineage among International Orthodox Jewish Communities. <i>Emerging Infectious Diseases</i> , 2016 , 22, 1545-53	10.2	14
89	Quantitative proteomic analysis of <i>Shigella flexneri</i> and <i>Shigella sonnei</i> Generalized Modules for Membrane Antigens (GMMA) reveals highly pure preparations. <i>International Journal of Medical Microbiology</i> , 2016 , 306, 99-108	3.7	13
88	Draft genome sequences of the type strains of <i>Shigella flexneri</i> held at Public Health England: comparison of classical phenotypic and novel molecular assays with whole genome sequence. <i>Gut Pathogens</i> , 2014 , 6, 7	5.4	13
87	Genomic evidence that the live <i>Chlamydia abortus</i> vaccine strain 1B is not attenuated and has the potential to cause disease. <i>Vaccine</i> , 2018 , 36, 3593-3598	4.1	13

86	Contrasting patterns of longitudinal population dynamics and antimicrobial resistance mechanisms in two priority bacterial pathogens over 70 years in a single center. <i>Genome Biology</i> , 2019 , 20, 184	18.3	12
85	Determining antimicrobial susceptibility in <i>Salmonella enterica</i> serovar Typhimurium through whole genome sequencing: a comparison against multiple phenotypic susceptibility testing methods. <i>BMC Microbiology</i> , 2019 , 19, 148	4.5	12
84	Clinical and laboratory-induced colistin-resistance mechanisms in <i>Acinetobacter baumannii</i> . <i>Microbial Genomics</i> , 2019 , 5,	4.4	12
83	Retrospective Analysis of Serotype Switching of <i>Vibrio cholerae</i> O1 in a Cholera Endemic Region Shows It Is a Non-random Process. <i>PLoS Neglected Tropical Diseases</i> , 2016 , 10, e0005044	4.8	12
82	A comprehensive and high-quality collection of genomes and their genes. <i>Microbial Genomics</i> , 2021 , 7,	4.4	12
81	Morphological, genomic and transcriptomic responses of <i>Klebsiella pneumoniae</i> to the last-line antibiotic colistin. <i>Scientific Reports</i> , 2018 , 8, 9868	4.9	11
80	Genome Sequence of <i>Klebsiella pneumoniae</i> Ecl8, a Reference Strain for Targeted Genetic Manipulation. <i>Genome Announcements</i> , 2013 , 1,		11
79	Type II and type IV toxin-antitoxin systems show different evolutionary patterns in the global <i>Klebsiella pneumoniae</i> population. <i>Nucleic Acids Research</i> , 2020 , 48, 4357-4370	20.1	10
78	Bacillary dysentery from World War 1 and NCTC1, the first bacterial isolate in the National Collection. <i>Lancet, The</i> , 2014 , 384, 1720	40	10
77	Whole-genome sequencing of bacterial sexually transmitted infections: implications for clinicians. <i>Current Opinion in Infectious Diseases</i> , 2013 , 26, 90-8	5.4	10
76	Differential phenotypic and genotypic characteristics of qnrS1-harboring plasmids carried by hospital and community commensal enterobacteria. <i>Antimicrobial Agents and Chemotherapy</i> , 2011 , 55, 1798-802	5.9	10
75	An untypeable enterotoxigenic represents one of the dominant types causing human disease. <i>Microbial Genomics</i> , 2017 , 3, e000121	4.4	10
74	Genetic and Phenotypic Characterization of the Etiological Agent of Canine Orchiepididymitis Smooth sp. BCCN84.3. <i>Frontiers in Veterinary Science</i> , 2019 , 6, 175	3.1	9
73	<i>Galleria mellonella</i> is low cost and suitable surrogate host for studying virulence of human pathogenic <i>Vibrio cholerae</i> . <i>Gene</i> , 2017 , 628, 1-7	3.8	9
72	Caribbean multi-centre study of <i>Klebsiella pneumoniae</i> : whole-genome sequencing, antimicrobial resistance and virulence factors. <i>Microbial Genomics</i> , 2019 , 5,	4.4	9
71	The speciation and hybridization history of the genus. <i>Microbial Genomics</i> , 2019 , 5,	4.4	9
70	Millennia of genomic stability within the invasive Para C Lineage of <i>Salmonella enterica</i>		9
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29	Genomic surveillance for hypervirulence and multi-drug resistance in invasive <i>Klebsiella pneumoniae</i> from south and southeast Asia		3
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