

# Nicholas R Thomson

## List of Publications by Year in descending order

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214  
papers

19,134  
citations

18465

62  
h-index

14736

127  
g-index

245  
all docs

245  
docs citations

245  
times ranked

17738  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic analysis of diversity, population structure, virulence, and antimicrobial resistance in <i>Klebsiella pneumoniae</i> , an urgent threat to public health. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E3574-81.	3.3	942
2	Comparative analysis of the genome sequences of <i>Bordetella pertussis</i> , <i>Bordetella parapertussis</i> and <i>Bordetella bronchiseptica</i> . Nature Genetics, 2003, 35, 32-40.	9.4	898
3	The Pangenome Structure of <i>Escherichia coli</i> : Comparative Genomic Analysis of <i>E. coli</i> Commensal and Pathogenic Isolates. Journal of Bacteriology, 2008, 190, 6881-6893.	1.0	763
4	Genomic plasticity of the causative agent of melioidosis, <i>Burkholderia pseudomallei</i> . Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 14240-14245.	3.3	675
5	Evidence for several waves of global transmission in the seventh cholera pandemic. Nature, 2011, 477, 462-465.	13.7	649
6	<i>Escherichia coli</i> K-12: a cooperatively developed annotation snapshot--2005. Nucleic Acids Research, 2006, 34, 1-9.	6.5	606
7	Epidemic multiple drug resistant <i>Salmonella</i> Typhimurium causing invasive disease in sub-Saharan Africa have a distinct genotype. Genome Research, 2009, 19, 2279-2287.	2.4	504
8	<i>Yersinia pestis</i> genome sequencing identifies patterns of global phylogenetic diversity. Nature Genetics, 2010, 42, 1140-1143.	9.4	504
9	Microevolution and history of the plague bacillus, <i>Yersinia pestis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 17837-17842.	3.3	463
10	Phylogeographical analysis of the dominant multidrug-resistant H58 clade of <i>Salmonella</i> Typhi identifies inter- and intracontinental transmission events. Nature Genetics, 2015, 47, 632-639.	9.4	403
11	Gut inflammation can boost horizontal gene transfer between pathogenic and commensal <i>Enterobacteriaceae</i> . Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 1269-1274.	3.3	398
12	Comparative genome analysis of <i>Salmonella</i> Enteritidis PT4 and <i>Salmonella</i> Gallinarum 287/91 provides insights into evolutionary and host adaptation pathways. Genome Research, 2008, 18, 1624-1637.	2.4	394
13	Gastrointestinal Carriage Is a Major Reservoir of <i>Klebsiella pneumoniae</i> Infection in Intensive Care Patients. Clinical Infectious Diseases, 2017, 65, 208-215.	2.9	381
14	The transcriptional landscape and small RNAs of <i>Salmonella enterica</i> serovar Typhimurium. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1277-86.	3.3	373
15	Identification of <i>Klebsiella</i> capsule synthesis loci from whole genome data. Microbial Genomics, 2016, 2, e000102.	1.0	372
16	The Genome of <i>Burkholderia cenocepacia</i> J2315, an Epidemic Pathogen of Cystic Fibrosis Patients. Journal of Bacteriology, 2009, 191, 261-277.	1.0	329
17	Whole-genome analysis of diverse <i>Chlamydia trachomatis</i> strains identifies phylogenetic relationships masked by current clinical typing. Nature Genetics, 2012, 44, 413-419.	9.4	279
18	<i>Shigella sonnei</i> genome sequencing and phylogenetic analysis indicate recent global dissemination from Europe. Nature Genetics, 2012, 44, 1056-1059.	9.4	278

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19	Genomic history of the seventh pandemic of cholera in Africa. <i>Science</i> , 2017, 358, 785-789.	6.0	255
20	Genomic insights into the emergence and spread of antimicrobial-resistant bacterial pathogens. <i>Science</i> , 2018, 360, 733-738.	6.0	254
21	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.	1.5	227
22	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, 1267-1282.	1.2	216
23	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.	3.3	213
24	<i>Chlamydia trachomatis</i> : Genome sequence analysis of lymphogranuloma venereum isolates. <i>Genome Research</i> , 2008, 18, 161-171.	2.4	207
25	Intercontinental dissemination of azithromycin-resistant shigellosis through sexual transmission: a cross-sectional study. <i>Lancet Infectious Diseases</i> , 2015, 15, 913-921.	4.6	204
26	A Strand-Specific RNA-Seq Analysis of the Transcriptome of the Typhoid Bacillus <i>Salmonella Typhi</i> . <i>PLoS Genetics</i> , 2009, 5, e1000569.	1.5	202
27	Identification of enterotoxigenic <i>Escherichia coli</i> (ETEC) clades with long-term global distribution. <i>Nature Genetics</i> , 2014, 46, 1321-1326.	9.4	192
28	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.	9.4	191
29	The diversity of <i>Klebsiella pneumoniae</i> surface polysaccharides. <i>Microbial Genomics</i> , 2016, 2, e000073.	1.0	185
30	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.	3.6	178
31	<i>Salmonella bongori</i> Provides Insights into the Evolution of the Salmonellae. <i>PLoS Pathogens</i> , 2011, 7, e1002191.	2.1	171
32	A Commensal Gone Bad: Complete Genome Sequence of the Prototypical Enterotoxigenic <i>Escherichia coli</i> Strain H10407. <i>Journal of Bacteriology</i> , 2010, 192, 5822-5831.	1.0	168
33	Pseudogene accumulation in the evolutionary histories of <i>Salmonella enterica</i> serovars Paratyphi A and Typhi. <i>BMC Genomics</i> , 2009, 10, 36.	1.2	161
34	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, 838-843.	3.3	158
35	The <i>Chlamydomonas reinhardtii</i> genome sequence reveals an array of variable proteins that contribute to interspecies variation. <i>Genome Research</i> , 2005, 15, 629-640.	2.4	158
36	Genome Evolution and Plasticity of <i>Serratia marcescens</i> , an Important Multidrug-Resistant Nosocomial Pathogen. <i>Genome Biology and Evolution</i> , 2014, 6, 2096-2110.	1.1	155

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37	A complete view of the genetic diversity of the Escherichia coli O-antigen biosynthesis gene cluster. DNA Research, 2015, 22, 101-107.	1.5	155
38	Parallel independent evolution of pathogenicity within the genus <i>Yersinia</i> . Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6768-6773.	3.3	154
39	The genomic signatures of Shigella evolution, adaptation and geographical spread. Nature Reviews Microbiology, 2016, 14, 235-250.	13.6	142
40	'Add, stir and reduce': Yersinia spp. as model bacteria for pathogen evolution. Nature Reviews Microbiology, 2016, 14, 177-190.	13.6	130
41	Genomic insights into the 2016-2017 cholera epidemic in Yemen. Nature, 2019, 565, 230-233.	13.7	129
42	Integrated view of <i>Vibrio cholerae</i> in the Americas. Science, 2017, 358, 789-793.	6.0	128
43	Novel Subclone of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Sequence Type 11 with Enhanced Virulence and Transmissibility, China. Emerging Infectious Diseases, 2020, 26, 289-297.	2.0	126
44	Tracking the establishment of local endemic populations of an emergent enteric pathogen. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 17522-17527.	3.3	124
45	Horizontal antimicrobial resistance transfer drives epidemics of multiple Shigella species. Nature Communications, 2018, 9, 1462.	5.8	121
46	Co-evolution of genomes and plasmids within Chlamydia trachomatis and the emergence in Sweden of a new variant strain. BMC Genomics, 2009, 10, 239.	1.2	119
47	Whole-genome sequences of <i>Chlamydia trachomatis</i> directly from clinical samples without culture. Genome Research, 2013, 23, 855-866.	2.4	115
48	A bimodal pattern of relatedness between the Salmonella Paratyphi A and Typhi genomes: Convergence or divergence by homologous recombination?. Genome Research, 2006, 17, 61-68.	2.4	112
49	The Role of Prophage-like Elements in the Diversity of Salmonella enterica Serovars. Journal of Molecular Biology, 2004, 339, 279-300.	2.0	111
50	Antimicrobial-Resistant Klebsiella pneumoniae Carriage and Infection in Specialized Geriatric Care Wards Linked to Acquisition in the Referring Hospital. Clinical Infectious Diseases, 2018, 67, 161-170.	2.9	108
51	Comprehensive global genome dynamics of <i>Chlamydia trachomatis</i> show ancient diversification followed by contemporary mixing and recent lineage expansion. Genome Research, 2017, 27, 1220-1229.	2.4	106
52	A high-resolution genomic analysis of multidrug-resistant hospital outbreaks of <i>Klebsiella pneumoniae</i> . EMBO Molecular Medicine, 2015, 7, 227-239.	3.3	104
53	Species-wide whole genome sequencing reveals historical global spread and recent local persistence in Shigella flexneri. ELife, 2015, 4, e07335.	2.8	94
54	An O Antigen Capsule Modulates Bacterial Pathogenesis in Shigella sonnei. PLoS Pathogens, 2015, 11, e1004749.	2.1	92

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55	The genome sequence of the fish pathogen <i>Aliivibrio salmonicida</i> strain LFI1238 shows extensive evidence of gene decay. <i>BMC Genomics</i> , 2008, 9, 616.	1.2	90
56	A simple method for directional transcriptome sequencing using Illumina technology. <i>Nucleic Acids Research</i> , 2009, 37, e148-e148.	6.5	88
57	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.	3.9	84
58	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, 838-849.	1.0	82
59	Variation in <i>Salmonella enterica</i> Serovar Typhi IncHI1 Plasmids during the Global Spread of Resistant Typhoid Fever. <i>Antimicrobial Agents and Chemotherapy</i> , 2009, 53, 716-727.	1.4	81
60	The Swedish new variant of <i>Chlamydia trachomatis</i> : genome sequence, morphology, cell tropism and phenotypic characterization. <i>Microbiology (United Kingdom)</i> , 2010, 156, 1394-1404.	0.7	81
61	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, 4257-4264.	1.0	80
62	Public Health Value of Next-Generation DNA Sequencing of Enterohemorrhagic <i>Escherichia coli</i> Isolates from an Outbreak. <i>Journal of Clinical Microbiology</i> , 2013, 51, 232-237.	1.8	79
63	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, 1778-1788.	1.0	72
64	Genomic epidemiology of syphilis reveals independent emergence of macrolide resistance across multiple circulating lineages. <i>Nature Communications</i> , 2019, 10, 3255.	5.8	72
65	Assessing gut microbiota perturbations during the early phase of infectious diarrhea in Vietnamese children. <i>Gut Microbes</i> , 2018, 9, 38-54.	4.3	66
66	Global phylogeography and evolutionary history of <i>Shigella dysenteriae</i> type 1. <i>Nature Microbiology</i> , 2016, 1, 16027.	5.9	65
67	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.	1.8	65
68	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.	1.6	65
69	Global population structure and genotyping framework for genomic surveillance of the major dysentery pathogen, <i>Shigella sonnei</i> . <i>Nature Communications</i> , 2021, 12, 2684.	5.8	65
70	Annotation of plasmid genes. <i>Plasmid</i> , 2017, 91, 61-67.	0.4	63
71	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.	1.5	61
72	Environmental marine pathogen isolation using mesocosm culture of sharpnose seabream: striking genomic and morphological features of novel <i>Endozoicomonas</i> sp.. <i>Scientific Reports</i> , 2015, 5, 17609.	1.6	60

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73	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, 2590-2598.	1.8	59
74	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, 61-69.	0.8	58
75	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.	1.8	57
76	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, 452-463.	1.5	54
77	New Variant of Multidrug-Resistant <i>Salmonella enterica</i> Serovar Typhimurium Associated with Invasive Disease in Immunocompromised Patients in Vietnam. <i>MBio</i> , 2018, 9, .	1.8	53
78	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.	1.4	51
79	Global phylogeny of <i>Treponema pallidum</i> lineages reveals recent expansion and spread of contemporary syphilis. <i>Nature Microbiology</i> , 2021, 6, 1549-1560.	5.9	51
80	Genomic dissection of <i>Klebsiella pneumoniae</i> infections in hospital patients reveals insights into an opportunistic pathogen. <i>Nature Communications</i> , 2022, 13, .	5.8	51
81	The Sudden Dominance of bla <sub>CTX-M</sub> Harboring Plasmids in <i>Shigella</i> spp. Circulating in Southern Vietnam. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e702.	1.3	48
82	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.	1.3	48
83	Quantitative Proteomics of the Infectious and Replicative Forms of <i>Chlamydia trachomatis</i> . <i>PLoS ONE</i> , 2016, 11, e0149011.	1.1	48
84	Genomic landscape of extended-spectrum $\beta$ -lactamase resistance in <i>Escherichia coli</i> from an urban African setting. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 1602-1609.	1.3	46
85	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.	0.7	45
86	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.	1.8	45
87	Genomic and phenotypic variation in epidemic-spanning <i>Salmonella enterica</i> serovar Enteritidis isolates. <i>BMC Microbiology</i> , 2009, 9, 237.	1.3	42
88	<i>Chlamydia trachomatis</i> from Australian Aboriginal people with trachoma are polyphyletic composed of multiple distinctive lineages. <i>Nature Communications</i> , 2016, 7, 10688.	5.8	42
89	Dissecting the molecular evolution of fluoroquinolone-resistant <i>Shigella sonnei</i> . <i>Nature Communications</i> , 2019, 10, 4828.	5.8	41
90	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.	1.6	40

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91	<i>Brucella neotomae</i> Infection in Humans, Costa Rica. Emerging Infectious Diseases, 2017, 23, 997-1000.	2.0	40
92	The Murray collection of pre-antibiotic era Enterobacteriaceae: a unique research resource. Genome Medicine, 2015, 7, 97.	3.6	39
93	A comprehensive and high-quality collection of Escherichia coli genomes and their genes. Microbial Genomics, 2021, 7, .	1.0	38
94	Vibrio cholerae Serogroup O139: Isolation from Cholera Patients and Asymptomatic Household Family Members in Bangladesh between 2013 and 2014. PLoS Neglected Tropical Diseases, 2015, 9, e0004183.	1.3	38
95	Genomic Epidemiology of <i>Vibrio cholerae</i> O1 Associated with Floods, Pakistan, 2010. Emerging Infectious Diseases, 2014, 20, 13-20.	2.0	37
96	Brucella abortus Strain 2308 Wisconsin Genome: Importance of the Definition of Reference Strains. Frontiers in Microbiology, 2016, 7, 1557.	1.5	37
97	Whole genome sequencing of Shigella sonnei through PulseNet Latin America and Caribbean: advancing global surveillance of foodborne illnesses. Clinical Microbiology and Infection, 2017, 23, 845-853.	2.8	37
98	Defining endemic cholera at three levels of spatiotemporal resolution within Bangladesh. Nature Genetics, 2018, 50, 951-955.	9.4	37
99	Generating whole bacterial genome sequences of low-abundance species from complex samples with IMS-MDA. Nature Protocols, 2013, 8, 2404-2412.	5.5	36
100	Genomic analysis of Klebsiella pneumoniae isolates from Malawi reveals acquisition of multiple ESBL determinants across diverse lineages. Journal of Antimicrobial Chemotherapy, 2019, 74, 1223-1232.	1.3	36
101	Mycoplasma genitalium: whole genome sequence analysis, recombination and population structure. BMC Genomics, 2017, 18, 993.	1.2	35
102	Emerging pathogens of gilthead seabream: characterisation and genomic analysis of novel intracellular $\beta$ -proteobacteria. ISME Journal, 2016, 10, 1791-1803.	4.4	34
103	A Study on the Geophylogeny of Clinical and Environmental Vibrio cholerae in Kenya. PLoS ONE, 2013, 8, e74829.	1.1	33
104	Co-cultivation and transcriptome sequencing of two co-existing fish pathogens Moritella viscosa and Aliivibrio wodanis. BMC Genomics, 2015, 16, 447.	1.2	32
105	Detecting extra-ocular Chlamydia trachomatis in a trachoma-endemic community in Ethiopia: Identifying potential routes of transmission. PLoS Neglected Tropical Diseases, 2020, 14, e0008120.	1.3	32
106	Genomic Epidemiology of <i>Vibrio cholerae</i> O1 Associated with Floods, Pakistan, 2010. Emerging Infectious Diseases, 2014, 20, 13-20.	2.0	31
107	European Chlamydia abortus livestock isolate genomes reveal unusual stability and limited diversity, reflected in geographical signatures. BMC Genomics, 2017, 18, 344.	1.2	31
108	Minimal genetic change in Vibrio cholerae in Mozambique over time: Multilocus variable number tandem repeat analysis and whole genome sequencing. PLoS Neglected Tropical Diseases, 2017, 11, e0005671.	1.3	31

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109	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.	2.9	30
110	Clinical and laboratory-induced colistin-resistance mechanisms in <i>Acinetobacter baumannii</i> . <i>Microbial Genomics</i> , 2019, 5, .	1.0	30
111	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.	0.8	29
112	Antimicrobial Drug Resistance of <i>Vibrio cholerae</i> , Democratic Republic of the Congo. <i>Emerging Infectious Diseases</i> , 2015, 21, 847-851.	2.0	29
113	Novel R Pipeline for Analyzing Biolog Phenotypic Microarray Data. <i>PLoS ONE</i> , 2015, 10, e0118392.	1.1	29
114	Antimicrobial Resistance Diversity Suggestive of Distinct <i>Salmonella</i> Typhimurium Sources or Selective Pressures in Food-Production Animals. <i>Frontiers in Microbiology</i> , 2019, 10, 708.	1.5	28
115	RNA-seq analysis of the influence of anaerobiosis and FNR on <i>Shigella flexneri</i> . <i>BMC Genomics</i> , 2014, 15, 438.	1.2	27
116	The extant World War 1 dysentery bacillus NCTC1: a genomic analysis. <i>Lancet, The</i> , 2014, 384, 1691-1697.	6.3	27
117	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.	1.3	26
118	<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.	1.1	26
119	Genomic variations leading to alterations in cell morphology of <i>Campylobacter</i> spp. <i>Scientific Reports</i> , 2016, 6, 38303.	1.6	25
120	Complement Susceptibility in Relation to Genome Sequence of Recent <i>Klebsiella pneumoniae</i> Isolates from Thai Hospitals. <i>MSphere</i> , 2018, 3, .	1.3	25
121	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.	1.7	25
122	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.	1.1	24
123	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.	1.3	24
124	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, 1545-1553.	2.0	23
125	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.	1.3	23
126	Contrasting patterns of longitudinal population dynamics and antimicrobial resistance mechanisms in two priority bacterial pathogens over 7 years in a single center. <i>Genome Biology</i> , 2019, 20, 184.	3.8	22



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127	The Population Structure of <i>Vibrio cholerae</i> from the Chandigarh Region of Northern India. PLoS Neglected Tropical Diseases, 2014, 8, e2981.	1.3	21
128	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. Journal of Clinical Microbiology, 2013, 51, 303-305.	1.8	20
129	Morphological, genomic and transcriptomic responses of <i>Klebsiella pneumoniae</i> to the last-line antibiotic colistin. Scientific Reports, 2018, 8, 9868.	1.6	20
130	Determining antimicrobial susceptibility in <i>Salmonella enterica</i> serovar Typhimurium through whole genome sequencing: a comparison against multiple phenotypic susceptibility testing methods. BMC Microbiology, 2019, 19, 148.	1.3	20
131	The <i>Chlamydia muridarum</i> plasmid revisited : new insights into growth kinetics. Wellcome Open Research, 2018, 3, 25.	0.9	20
132	<i>Chlamydia trachomatis</i> : small genome, big challenges. Future Microbiology, 2010, 5, 555-561.	1.0	19
133	Quantitative proteomic analysis of <i>Shigella flexneri</i> and <i>Shigella sonnei</i> Generalized Modules for Membrane Antigens (GMMA) reveals highly pure preparations. International Journal of Medical Microbiology, 2016, 306, 99-108.	1.5	19
134	Yaws re-emergence and bacterial drug resistance selection after mass administration of azithromycin: a genomic epidemiology investigation. Lancet Microbe, The, 2020, 1, e263-e271.	3.4	19
135	Caribbean multi-centre study of <i>Klebsiella pneumoniae</i> : whole-genome sequencing, antimicrobial resistance and virulence factors. Microbial Genomics, 2019, 5, .	1.0	19
136	Characterisation of <i>Treponema pallidum</i> lineages within the contemporary syphilis outbreak in Australia: a genomic epidemiological analysis. Lancet Microbe, The, 2022, 3, e417-e426.	3.4	19
137	Dynamics of cholera epidemics from Benin to Mauritania. PLoS Neglected Tropical Diseases, 2018, 12, e0006379.	1.3	18
138	Population-based analysis of ocular <i>Chlamydia trachomatis</i> in trachoma-endemic West African communities identifies genomic markers of disease severity. Genome Medicine, 2018, 10, 15.	3.6	18
139	Genetic and Phenotypic Characterization of the Etiological Agent of Canine Orchiepididymitis Smooth <i>Brucella</i> sp. BCCN84.3. Frontiers in Veterinary Science, 2019, 6, 175.	0.9	18
140	The history, genome and biology of NCTC 30: a non-pandemic <i>Vibrio cholerae</i> isolate from World War One. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20182025.	1.2	18
141	Viability PCR shows that non-ocular surfaces could contribute to transmission of <i>Chlamydia trachomatis</i> infection in trachoma. PLoS Neglected Tropical Diseases, 2020, 14, e0008449.	1.3	18
142	Molecular characterisation of the <i>Chlamydia pecorum</i> plasmid from porcine, ovine, bovine, and koala strains indicates plasmid-strain co-evolution. PeerJ, 2016, 4, e1661.	0.9	18
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