

Nicholas R Thomson

List of Publications by Year in descending order

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Version: 2024-02-01

214
papers

19,134
citations

18482

62
h-index

14759

127
g-index

245
all docs

245
docs citations

245
times ranked

17738
citing authors

#	ARTICLE	IF	CITATIONS
1	Population structure analysis and laboratory monitoring of <i>Shigella</i> by core-genome multilocus sequence typing. <i>Nature Communications</i> , 2022, 13, 551.	12.8	17
2	Reciprocally rewiring and repositioning the Integration Host Factor (IHF) subunit genes in <i>Salmonella enterica</i> serovar Typhimurium: impacts on physiology and virulence. <i>Microbial Genomics</i> , 2022, 8, .	2.0	3
3	Genomic and antigenic diversity of colonizing <i>Klebsiella pneumoniae</i> isolates mirrors that of invasive isolates in Blantyre, Malawi. <i>Microbial Genomics</i> , 2022, 8, .	2.0	5
4	Genomic Characteristics of Recently Recognized <i>Vibrio cholerae</i> El Tor Lineages Associated with Cholera in Bangladesh, 1991 to 2017. <i>Microbiology Spectrum</i> , 2022, 10, e0039122.	3.0	3
5	Characterisation of <i>Treponema pallidum</i> lineages within the contemporary syphilis outbreak in Australia: a genomic epidemiological analysis. <i>Lancet Microbe</i> , The, 2022, 3, e417-e426.	7.3	19
6	Mobility of antimicrobial resistance across serovars and disease presentations in non-typhoidal <i>Salmonella</i> from animals and humans in Vietnam. <i>Microbial Genomics</i> , 2022, 8, .	2.0	2
7	Exploring bacterial diversity via a curated and searchable snapshot of archived DNA. <i>Access Microbiology</i> , 2022, 4, .	0.5	1
8	Evolutionary histories and antimicrobial resistance in <i>Shigella flexneri</i> and <i>Shigella sonnei</i> in Southeast Asia. <i>Access Microbiology</i> , 2022, 4, .	0.5	0
9	Genomic dissection of <i>Klebsiella pneumoniae</i> infections in hospital patients reveals insights into an opportunistic pathogen. <i>Nature Communications</i> , 2022, 13, .	12.8	51
10	<i>Vibrio cholerae</i> O139 genomes provide a clue to why it may have failed to usher in the eighth cholera pandemic. <i>Nature Communications</i> , 2022, 13, .	12.8	8
11	“We realised we needed a new approach”: Government and law enforcement perspectives on the implementation and future of the drug decriminalisation policy in Vietnam. <i>International Journal of Drug Policy</i> , 2021, 87, 102990.	3.3	4
12	A comprehensive and high-quality collection of <i>Escherichia coli</i> genomes and their genes. <i>Microbial Genomics</i> , 2021, 7, .	2.0	38
13	Evolutionary histories and antimicrobial resistance in <i>Shigella flexneri</i> and <i>Shigella sonnei</i> in Southeast Asia. <i>Communications Biology</i> , 2021, 4, 353.	4.4	17
14	Epidemiologic and Genomic Reidentification of Yaws, Liberia. <i>Emerging Infectious Diseases</i> , 2021, 27, 1123-1132.	4.3	6
15	Progress towards an inducible, replication-proficient transposon delivery vector for <i>Chlamydia trachomatis</i> . <i>Wellcome Open Research</i> , 2021, 6, 82.	1.8	5
16	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.	12.8	65
17	<i>gbpA</i> and <i>chiA</i> genes are not uniformly distributed amongst diverse <i>Vibrio cholerae</i> . <i>Microbial Genomics</i> , 2021, 7, .	2.0	2
18	Ongoing evolution of <i>Chlamydia trachomatis</i> lymphogranuloma venereum: exploring the genomic diversity of circulating strains. <i>Microbial Genomics</i> , 2021, 7, .	2.0	11

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19	Canine brucellosis in Costa Rica reveals widespread <i>Brucella canis</i> infection and the recent introduction of foreign strains. <i>Veterinary Microbiology</i> , 2021, 257, 109072.	1.9	2
20	Genomic contextualisation of ancient DNA molecular data from an Argentinian fifth pandemic <i>Vibrio cholerae</i> infection. <i>Microbial Genomics</i> , 2021, 7, .	2.0	0
21	<i>Brucella</i> sp. sequence-type 27 associated with abortion in dwarf sperm whale <i>Kogia sima</i> . <i>European Journal of Wildlife Research</i> , 2021, 67, 1.	1.4	6
22	Different evolutionary trends form the twilight zone of the bacterial pan-genome. <i>Microbial Genomics</i> , 2021, 7, .	2.0	17
23	Genomics, social media and mobile phone data enable mapping of SARS-CoV-2 lineages to inform health policy in Bangladesh. <i>Nature Microbiology</i> , 2021, 6, 1271-1278.	13.3	13
24	Global phylogeny of <i>Treponema pallidum</i> lineages reveals recent expansion and spread of contemporary syphilis. <i>Nature Microbiology</i> , 2021, 6, 1549-1560.	13.3	51
25	The evolutionary history of <i>Shigella flexneri</i> serotype 6 in Asia. <i>Microbial Genomics</i> , 2021, 7, .	2.0	3
26	Linkage of Whole Genome Sequencing, Epidemiological, and Clinical Data to Understand the Genetic Diversity and Clinical Outcomes of <i>Shigella flexneri</i> among Men Who Have Sex with Men in England. <i>Microbiology Spectrum</i> , 2021, 9, e0121321.	3.0	3
27	Emergence of carbapenemase-producing Enterobacteriaceae in Malawi. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 20, 225-227.	2.2	9
28	Genomics of the Argentinian cholera epidemic elucidate the contrasting dynamics of epidemic and endemic <i>Vibrio cholerae</i> . <i>Nature Communications</i> , 2020, 11, 4918.	12.8	12
29	Viability PCR shows that non-ocular surfaces could contribute to transmission of <i>Chlamydia trachomatis</i> infection in trachoma. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008449.	3.0	18
30	Yaws re-emergence and bacterial drug resistance selection after mass administration of azithromycin: a genomic epidemiology investigation. <i>Lancet Microbe</i> , The, 2020, 1, e263-e271.	7.3	19
31	Network Rewiring: Physiological Consequences of Reciprocally Exchanging the Physical Locations and Growth-Phase-Dependent Expression Patterns of the <i>Salmonella flexneri</i> and <i>Salmonella dysenteriae</i> Genes. <i>MBio</i> , 2020, 11, .	4.1	11
32	Fine capsule variation affects bacteriophage susceptibility in <i>Klebsiella pneumoniae</i> ST258. <i>FASEB Journal</i> , 2020, 34, 10801-10817.	0.5	17
33	The Nature and Extent of Plasmid Variation in <i>Chlamydia trachomatis</i> . <i>Microorganisms</i> , 2020, 8, 373.	3.6	11
34	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.	3.0	32
35	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.	8.2	178
36	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.	4.3	126

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37	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.	14.5	14
38	Persistence of <i>Brucella abortus</i> lineages revealed by genomic characterization and phylodynamic analysis. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008235.	3.0	13
39	Community evolution of laboratory strains and pedigrees in the age of genomics. <i>Microbiology (United Kingdom)</i> , 2020, 166, 233-238.	1.8	8
40	Genetic Markers in <i>S. Paratyphi C</i> Reveal Primary Adaptation to Pigs. <i>Microorganisms</i> , 2020, 8, 657.	3.6	5
41	Genetic and Phenotypic Characterization of the Etiological Agent of Canine Orchiepididymitis Smooth <i>Brucella</i> sp. BCCN84.3. <i>Frontiers in Veterinary Science</i> , 2019, 6, 175.	2.2	18
42	Genomic epidemiology of syphilis reveals independent emergence of macrolide resistance across multiple circulating lineages. <i>Nature Communications</i> , 2019, 10, 3255.	12.8	72
43	Type III secretion system confers enhanced virulence in clinical non-O1/non-O139 <i>Vibrio cholerae</i> . <i>Microbial Pathogenesis</i> , 2019, 135, 103645.	2.9	17
44	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.	3.3	20
45	Dissecting the molecular evolution of fluoroquinolone-resistant <i>Shigella sonnei</i> . <i>Nature Communications</i> , 2019, 10, 4828.	12.8	41
46	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.	8.8	22
47	Whole genome sequence of <i>Vibrio cholerae</i> directly from dried spotted filter paper. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007330.	3.0	7
48	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.	3.5	28
49	The history, genome and biology of NCTC 30: a non-pandemic <i>Vibrio cholerae</i> isolate from World War One. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20182025.	2.6	18
50	High quality reference genomes for toxigenic and non-toxigenic <i>Vibrio cholerae</i> serogroup O139. <i>Scientific Reports</i> , 2019, 9, 5865.	3.3	13
51	Collecting and exploiting data to understand a nation's sexual health needs: Implications for the British National Surveys of Sexual Attitudes and Lifestyles (Natsal). <i>Sexually Transmitted Infections</i> , 2019, 95, 159-161.	1.9	3
52	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.	3.0	36
53	Genomic insights into the 2016-2017 cholera epidemic in Yemen. <i>Nature</i> , 2019, 565, 230-233.	27.8	129
54	Using human iPSC derived small intestinal organoids as a model for enteric disease caused by Enterotoxigenic <i>E. coli</i> and <i>Vibrio cholerae</i> . <i>Access Microbiology</i> , 2019, 1, .	0.5	2

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55	Clinical and laboratory-induced colistin-resistance mechanisms in <i>Acinetobacter baumannii</i> . <i>Microbial Genomics</i> , 2019, 5, .	2.0	30
56	rPinecone: Define sub-lineages of a clonal expansion via a phylogenetic tree. <i>Microbial Genomics</i> , 2019, 5, .	2.0	10
57	Caribbean multi-centre study of <i>Klebsiella pneumoniae</i> : whole-genome sequencing, antimicrobial resistance and virulence factors. <i>Microbial Genomics</i> , 2019, 5, .	2.0	19
58	The speciation and hybridization history of the genus <i>Salmonella</i> . <i>Microbial Genomics</i> , 2019, 5, .	2.0	13
59	Use of whole-genome sequencing to identify clusters of <i>Shigella flexneri</i> associated with sexual transmission in men who have sex with men in England: a validation study using linked behavioural data. <i>Microbial Genomics</i> , 2019, 5, .	2.0	16
60	The genomic (re)definition of EPEC. <i>Access Microbiology</i> , 2019, 1, .	0.5	0
61	Horizontal antimicrobial resistance transfer drives epidemics of multiple <i>Shigella</i> species. <i>Nature Communications</i> , 2018, 9, 1462.	12.8	121
62	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.	5.8	108
63	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.	5.8	30
64	Assessing gut microbiota perturbations during the early phase of infectious diarrhea in Vietnamese children. <i>Gut Microbes</i> , 2018, 9, 38-54.	9.8	66
65	Complement Susceptibility in Relation to Genome Sequence of Recent <i>Klebsiella pneumoniae</i> Isolates from Thai Hospitals. <i>MSphere</i> , 2018, 3, .	2.9	25
66	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, .	4.1	53
67	Direct Whole-Genome Sequencing of Cutaneous Strains of <i>Haemophilus ducreyi</i> . <i>Emerging Infectious Diseases</i> , 2018, 24, 786-789.	4.3	7
68	Genomic insights into the emergence and spread of antimicrobial-resistant bacterial pathogens. <i>Science</i> , 2018, 360, 733-738.	12.6	254
69	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.	3.8	25
70	Defining endemic cholera at three levels of spatiotemporal resolution within Bangladesh. <i>Nature Genetics</i> , 2018, 50, 951-955.	21.4	37
71	Morphological, genomic and transcriptomic responses of <i>Klebsiella pneumoniae</i> to the last-line antibiotic colistin. <i>Scientific Reports</i> , 2018, 8, 9868.	3.3	20
72	Microevolution and Patterns of Transmission of <i>Shigella sonnei</i> within Cyclic Outbreaks Shigellosis, Israel. <i>Emerging Infectious Diseases</i> , 2018, 24, 1335-1339.	4.3	6

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73	Dynamics of cholera epidemics from Benin to Mauritania. PLoS Neglected Tropical Diseases, 2018, 12, e0006379.	3.0	18
74	Pan-genome Analysis of Ancient and Modern Salmonella enterica Demonstrates Genomic Stability of the Invasive Para C Lineage for Millennia. Current Biology, 2018, 28, 2420-2428.e10.	3.9	65
75	Population-based analysis of ocular Chlamydia trachomatis in trachoma-endemic West African communities identifies genomic markers of disease severity. Genome Medicine, 2018, 10, 15.	8.2	18
76	Genomic epidemiology of Shigella in the United Kingdom shows transmission of pathogen sublineages and determinants of antimicrobial resistance. Scientific Reports, 2018, 8, 7389.	3.3	65
77	The role of intra-NAPL diffusion on mass transfer from MGP residuals. Journal of Contaminant Hydrology, 2018, 213, 49-61.	3.3	7
78	Long-lasting Geomagnetically Induced Currents and Harmonic Distortion Observed in New Zealand During the 7 th -8 September 2017 Disturbed Period. Space Weather, 2018, 16, 704-717.	3.7	48
79	PlasmidTron: assembling the cause of phenotypes and genotypes from NGS data. Microbial Genomics, 2018, 4, .	2.0	5
80	Whole-genome sequencing revealed concurrent outbreaks of shigellosis in the English Orthodox Jewish Community caused by multiple importations of Shigella sonnei from Israel. Microbial Genomics, 2018, 4, .	2.0	14
81	An outbreak of a rare Shiga-toxin-producing Escherichia coli serotype (O117:H7) among men who have sex with men. Microbial Genomics, 2018, 4, .	2.0	13
82	The Chlamydia muridarum plasmid revisited : new insights into growth kinetics. Wellcome Open Research, 2018, 3, 25.	1.8	20
83	Identification and initial characterisation of a protein involved in Campylobacter jejuni cell shape. Microbial Pathogenesis, 2017, 104, 202-211.	2.9	12
84	Genomic landscape of extended-spectrum β -lactamase resistance in Escherichia coli from an urban African setting. Journal of Antimicrobial Chemotherapy, 2017, 72, 1602-1609.	3.0	46
85	European Chlamydia abortus livestock isolate genomes reveal unusual stability and limited diversity, reflected in geographical signatures. BMC Genomics, 2017, 18, 344.	2.8	31
86	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.	5.5	106
87	Annotation of plasmid genes. Plasmid, 2017, 91, 61-67.	1.4	63
88	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.	6.0	37
89	Common determinants of antimicrobial resistance in sequential episodes of sexually transmitted shigellosis in men who have sex with men: a cross-sectional study. Lancet, The, 2017, 389, S24.	13.7	2
90	Gastrointestinal Carriage Is a Major Reservoir of Klebsiella pneumoniae Infection in Intensive Care Patients. Clinical Infectious Diseases, 2017, 65, 208-215.	5.8	381

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91	The Hidden Genomics of <i>Chlamydia trachomatis</i> . <i>Current Topics in Microbiology and Immunology</i> , 2017, 412, 107-131.	1.1	6
92	Genome-wide profiling of humoral immunity and pathogen genes under selection identifies immune evasion tactics of <i>Chlamydia trachomatis</i> during ocular infection. <i>Scientific Reports</i> , 2017, 7, 9634.	3.3	12
93	<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.	2.2	13
94	<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.	2.5	26
95	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.	3.6	61
96	Genomic history of the seventh pandemic of cholera in Africa. <i>Science</i> , 2017, 358, 785-789.	12.6	255
97	Integrated view of <i>Vibrio cholerae</i> in the Americas. <i>Science</i> , 2017, 358, 789-793.	12.6	128
98	<i>Brucella neotomae</i> Infection in Humans, Costa Rica. <i>Emerging Infectious Diseases</i> , 2017, 23, 997-1000.	4.3	40
99	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, e0005671.	3.0	31
100	<i>Mycoplasma genitalium</i> : whole genome sequence analysis, recombination and population structure. <i>BMC Genomics</i> , 2017, 18, 993.	2.8	35
101	Concern regarding the alleged spread of hypervirulent lymphogranuloma venereum <i>Chlamydia trachomatis</i> strain in Europe. <i>Eurosurveillance</i> , 2017, 22, .	7.0	7
102	An untypeable enterotoxigenic <i>Escherichia coli</i> represents one of the dominant types causing human disease. <i>Microbial Genomics</i> , 2017, 3, e000121.	2.0	13
103	Transcriptome and proteome analysis of <i>Salmonella enterica</i> serovar Typhimurium systemic infection of wild type and immune-deficient mice. <i>PLoS ONE</i> , 2017, 12, e0181365.	2.5	6
104	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.	4.3	23
105	The diversity of <i>Klebsiella pneumoniae</i> surface polysaccharides. <i>Microbial Genomics</i> , 2016, 2, e000073.	2.0	185
106	Identification of <i>Klebsiella</i> capsule synthesis loci from whole genome data. <i>Microbial Genomics</i> , 2016, 2, e000102.	2.0	372
107	<i>Salmonella</i> Enteritidis Isolate Harboring Multiple Efflux Pumps and Pathogenicity Factors, Shows Absence of O Antigen Polymerase Gene. <i>Frontiers in Microbiology</i> , 2016, 7, 1130.	3.5	1
108	<i>Brucella abortus</i> Strain 2308 Wisconsin Genome: Importance of the Definition of Reference Strains. <i>Frontiers in Microbiology</i> , 2016, 7, 1557.	3.5	37

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109	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.	3.0	23
110	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.	8.4	84
111	<i>Chlamydia trachomatis</i> from Australian Aboriginal people with trachoma are polyphyletic composed of multiple distinctive lineages. <i>Nature Communications</i> , 2016, 7, 10688.	12.8	42
112	Genomic variations leading to alterations in cell morphology of <i>Campylobacter</i> spp. <i>Scientific Reports</i> , 2016, 6, 38303.	3.3	25
113	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.	3.1	51
114	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
115	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.	3.3	40
116	Global phylogeography and evolutionary history of <i>Shigella dysenteriae</i> type 1. <i>Nature Microbiology</i> , 2016, 1, 16027.	13.3	65
117	The Type III Secretion System Effector SeoC of <i>Salmonella enterica</i> subsp. <i>salamae</i> and <i>S. enterica</i> subsp. <i>arizonae</i> ADP-Ribosylates Src and Inhibits Opsonophagocytosis. <i>Infection and Immunity</i> , 2016, 84, 3618-3628.	2.2	7
118	'Add, stir and reduce': <i>Yersinia</i> spp. as model bacteria for pathogen evolution. <i>Nature Reviews Microbiology</i> , 2016, 14, 177-190.	28.6	130
119	Emerging pathogens of gilthead seabream: characterisation and genomic analysis of novel intracellular β -proteobacteria. <i>ISME Journal</i> , 2016, 10, 1791-1803.	9.8	34
120	The genomic signatures of <i>Shigella</i> evolution, adaptation and geographical spread. <i>Nature Reviews Microbiology</i> , 2016, 14, 235-250.	28.6	142
121	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.	3.6	19
122	Quantitative Proteomics of the Infectious and Replicative Forms of <i>Chlamydia trachomatis</i> . <i>PLoS ONE</i> , 2016, 11, e0149011.	2.5	48
123	Molecular characterisation of the <i>Chlamydia pecorum</i> plasmid from porcine, ovine, bovine, and koala strains indicates plasmid-strain co-evolution. <i>PeerJ</i> , 2016, 4, e1661.	2.0	18
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.	4.3	5
125	A high-resolution genomic analysis of multidrug-resistant hospital outbreaks of <i>Klebsiella pneumoniae</i> . <i>EMBO Molecular Medicine</i> , 2015, 7, 227-239.	6.9	104
126	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.	3.3	60

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127	The Murray collection of pre-antibiotic era Enterobacteriaceae: a unique research resource. <i>Genome Medicine</i> , 2015, 7, 97.	8.2	39
128	Draft Genome Sequence of 24570, the Type Strain of <i>Shigella flexneri</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	7
129	Antimicrobial Drug Resistance of <i>Vibrio cholerae</i> , Democratic Republic of the Congo. <i>Emerging Infectious Diseases</i> , 2015, 21, 847-851.	4.3	29
130	Novel R Pipeline for Analyzing Biolog Phenotypic Microarray Data. <i>PLoS ONE</i> , 2015, 10, e0118392.	2.5	29
131	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.	3.0	26
132	Species-wide whole genome sequencing reveals historical global spread and recent local persistence in <i>Shigella flexneri</i> . <i>ELife</i> , 2015, 4, e07335.	6.0	94
133	Draft genomes of <i>Shigella</i> strains used by the STOPENTERICS consortium. <i>Gut Pathogens</i> , 2015, 7, 14.	3.4	7
134	Whole genome analysis to detect potential vaccine-induced changes on <i>Shigella sonnei</i> genome. <i>Vaccine</i> , 2015, 33, 2978-2983.	3.8	2
135	A putative, novel coli surface antigen 8B (CS8B) of enterotoxigenic <i>Escherichia coli</i> . <i>Pathogens and Disease</i> , 2015, 73, ftv047.	2.0	2
136	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.	2.2	72
137	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
138	Genomic Investigations Unmask <i>Mycoplasma amphoriforme</i> , a New Respiratory Pathogen. <i>Clinical Infectious Diseases</i> , 2015, 60, 381-388.	5.8	10
139	An O Antigen Capsule Modulates Bacterial Pathogenesis in <i>Shigella sonnei</i> . <i>PLoS Pathogens</i> , 2015, 11, e1004749.	4.7	92
140	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.	7.1	942
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