

# Nicholas R Thomson

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/4517839/nicholas-r-thomson-publications-by-year.pdf>

**Version:** 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

211  
papers

13,705  
citations

58  
h-index

114  
g-index

245  
ext. papers

17,153  
ext. citations

9.7  
avg, IF

5.77  
L-index

#	Paper	IF	Citations
211	Population structure analysis and laboratory monitoring of Shigella by core-genome multilocus sequence typing.. <i>Nature Communications</i> , <b>2022</b> , 13, 551	17.4	4
210	Genomic Characteristics of Recently Recognized Vibrio cholerae El Tor Lineages Associated with Cholera in Bangladesh, 1991 to 2017.. <i>Microbiology Spectrum</i> , <b>2022</b> , e0039122	8.9	0
209	Global phylogeny of Treponema pallidum lineages reveals recent expansion and spread of contemporary syphilis. <i>Nature Microbiology</i> , <b>2021</b> , 6, 1549-1560	26.6	2
208	Evolutionary histories and antimicrobial resistance in Shigella flexneri and Shigella sonnei in Southeast Asia. <i>Communications Biology</i> , <b>2021</b> , 4, 353	6.7	3
207	Epidemiologic and Genomic Reidentification of Yaws, Liberia. <i>Emerging Infectious Diseases</i> , <b>2021</b> , 27, 1123-1132	10.2	0
206	Progress towards an inducible, replication-proficient transposon delivery vector for. <i>Wellcome Open Research</i> , <b>2021</b> , 6, 82	4.8	2
205	Global population structure and genotyping framework for genomic surveillance of the major dysentery pathogen, Shigella sonnei. <i>Nature Communications</i> , <b>2021</b> , 12, 2684	17.4	9
204	Ongoing evolution of lymphogranuloma venereum: exploring the genomic diversity of circulating strains. <i>Microbial Genomics</i> , <b>2021</b> , 7,	4.4	1
203	Canine brucellosis in Costa Rica reveals widespread Brucella canis infection and the recent introduction of foreign strains. <i>Veterinary Microbiology</i> , <b>2021</b> , 257, 109072	3.3	1
202	Brucella sp. sequence-type 27 associated with abortion in dwarf sperm whale Kogia sima. <i>European Journal of Wildlife Research</i> , <b>2021</b> , 67, 1	2	3
201	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> , <b>2021</b> , 87, 102990	5.5	2
200	A comprehensive and high-quality collection of genomes and their genes. <i>Microbial Genomics</i> , <b>2021</b> , 7,	4.4	12
199	Different evolutionary trends form the twilight zone of the bacterial pan-genome. <i>Microbial Genomics</i> , <b>2021</b> , 7,	4.4	3
198	Genomics, social media and mobile phone data enable mapping of SARS-CoV-2 lineages to inform health policy in Bangladesh. <i>Nature Microbiology</i> , <b>2021</b> , 6, 1271-1278	26.6	1
197	Linkage of Whole Genome Sequencing, Epidemiological, and Clinical Data to Understand the Genetic Diversity and Clinical Outcomes of Shigella flexneri among Men Who Have Sex with Men in England.. <i>Microbiology Spectrum</i> , <b>2021</b> , e0121321	8.9	0
196	The Nature and Extent of Plasmid Variation in. <i>Microorganisms</i> , <b>2020</b> , 8,	4.9	4
195	Detecting extra-ocular Chlamydia trachomatis In a trachoma-endemic community in Ethiopia: Identifying potential routes of transmission. <i>PLoS Neglected Tropical Diseases</i> , <b>2020</b> , 14, e0008120	4.8	18

194	Genomic surveillance for hypervirulence and multi-drug resistance in invasive <i>Klebsiella pneumoniae</i> from South and Southeast Asia. <i>Genome Medicine</i> , <b>2020</b> , 12, 11	14.4	74
193	Novel Subclone of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Sequence Type 11 with Enhanced Virulence and Transmissibility, China. <i>Emerging Infectious Diseases</i> , <b>2020</b> , 26, 289-297	10.2	52
192	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> , <b>2020</b> , 48, 4357-4370	20.1	10
191	Genetic Markers in Paratyphi C Reveal Primary Adaptation to Pigs. <i>Microorganisms</i> , <b>2020</b> , 8,	4.9	2
190	Community evolution- laboratory strains and pedigrees in the age of genomics. <i>Microbiology (United Kingdom)</i> , <b>2020</b> , 166, 233-238	2.9	4
189	Emergence of carbapenemase-producing Enterobacteriaceae in Malawi. <i>Journal of Global Antimicrobial Resistance</i> , <b>2020</b> , 20, 225-227	3.4	1
188	Genomics of the Argentinian cholera epidemic elucidate the contrasting dynamics of epidemic and endemic <i>Vibrio cholerae</i> . <i>Nature Communications</i> , <b>2020</b> , 11, 4918	17.4	4
187	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> , <b>2020</b> , 14, e0008449	4.8	9
186	Yaws re-emergence and bacterial drug resistance selection after mass administration of azithromycin: a genomic epidemiology investigation.. <i>Lancet Microbe, The</i> , <b>2020</b> , 1, e263-e271	22.2	7
185	Network Rewiring: Physiological Consequences of Reciprocally Exchanging the Physical Locations and Growth-Phase-Dependent Expression Patterns of the and Genes. <i>MBio</i> , <b>2020</b> , 11,	7.8	5
184	Fine capsule variation affects bacteriophage susceptibility in <i>Klebsiella pneumoniae</i> ST258. <i>FASEB Journal</i> , <b>2020</b> , 34, 10801-10817	0.9	8
183	Persistence of <i>Brucella abortus</i> lineages revealed by genomic characterization and phylodynamic analysis. <i>PLoS Neglected Tropical Diseases</i> , <b>2020</b> , 14, e0008235	4.8	6
182	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> , <b>2019</b> , 20, 184	18.3	12
181	Whole genome sequence of <i>Vibrio cholerae</i> directly from dried spotted filter paper. <i>PLoS Neglected Tropical Diseases</i> , <b>2019</b> , 13, e0007330	4.8	3
180	Antimicrobial Resistance Diversity Suggestive of Distinct Typhimurium Sources or Selective Pressures in Food-Production Animals. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 708	5.7	15
179	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> , <b>2019</b> , 286, 20182025	4.4	8
178	High quality reference genomes for toxigenic and non-toxigenic <i>Vibrio cholerae</i> serogroup O139. <i>Scientific Reports</i> , <b>2019</b> , 9, 5865	4.9	7
177	Genetic and Phenotypic Characterization of the Etiological Agent of Canine Orchiepididymitis Smooth sp. BCCN84.3. <i>Frontiers in Veterinary Science</i> , <b>2019</b> , 6, 175	3.1	9

176	Genomic epidemiology of syphilis reveals independent emergence of macrolide resistance across multiple circulating lineages. <i>Nature Communications</i> , <b>2019</b> , 10, 3255	17.4	31
175	Type III secretion system confers enhanced virulence in clinical non-O1/non-O139 <i>Vibrio cholerae</i> . <i>Microbial Pathogenesis</i> , <b>2019</b> , 135, 103645	3.8	8
174	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> , <b>2019</b> , 19, 148	4.5	12
173	Dissecting the molecular evolution of fluoroquinolone-resistant <i>Shigella sonnei</i> . <i>Nature Communications</i> , <b>2019</b> , 10, 4828	17.4	17
172	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> , <b>2019</b> , 1,	1	1
171	Clinical and laboratory-induced colistin-resistance mechanisms in <i>Acinetobacter baumannii</i> . <i>Microbial Genomics</i> , <b>2019</b> , 5,	4.4	12
170	rPinecone: Define sub-lineages of a clonal expansion via a phylogenetic tree. <i>Microbial Genomics</i> , <b>2019</b> , 5,	4.4	7
169	Caribbean multi-centre study of <i>Klebsiella pneumoniae</i> : whole-genome sequencing, antimicrobial resistance and virulence factors. <i>Microbial Genomics</i> , <b>2019</b> , 5,	4.4	9
168	The speciation and hybridization history of the genus. <i>Microbial Genomics</i> , <b>2019</b> , 5,	4.4	9
167	Use of whole-genome sequencing to identify clusters of associated with sexual transmission in men who have sex with men in England: a validation study using linked behavioural data. <i>Microbial Genomics</i> , <b>2019</b> , 5,	4.4	6
166	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> , <b>2019</b> , 74, 1223-1232	5.1	19
165	Genomic insights into the 2016-2017 cholera epidemic in Yemen. <i>Nature</i> , <b>2019</b> , 565, 230-233	50.4	92
164	The Hidden Genomics of <i>Chlamydia trachomatis</i> . <i>Current Topics in Microbiology and Immunology</i> , <b>2018</b> , 412, 107-131	3.3	3
163	Horizontal antimicrobial resistance transfer drives epidemics of multiple <i>Shigella</i> species. <i>Nature Communications</i> , <b>2018</b> , 9, 1462	17.4	57
162	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> , <b>2018</b> , 67, 161-170	11.6	57
161	Diagnostics for Yaws Eradication: Insights From Direct Next-Generation Sequencing of Cutaneous Strains of <i>Treponema pallidum</i> . <i>Clinical Infectious Diseases</i> , <b>2018</b> , 66, 818-824	11.6	20
160	Morphological, genomic and transcriptomic responses of <i>Klebsiella pneumoniae</i> to the last-line antibiotic colistin. <i>Scientific Reports</i> , <b>2018</b> , 8, 9868	4.9	11
159	Microevolution and Patterns of Transmission of <i>Shigella sonnei</i> within Cyclic Outbreaks Shigellosis, Israel. <i>Emerging Infectious Diseases</i> , <b>2018</b> , 24, 1335-1339	10.2	4

158	Dynamics of cholera epidemics from Benin to Mauritania. <i>PLoS Neglected Tropical Diseases</i> , <b>2018</b> , 12, e0006379	4.8	14
157	Pan-genome Analysis of Ancient and Modern Salmonella enterica Demonstrates Genomic Stability of the Invasive Para C Lineage for Millennia. <i>Current Biology</i> , <b>2018</b> , 28, 2420-2428.e10	6.3	44
156	Population-based analysis of ocular Chlamydia trachomatis in trachoma-endemic West African communities identifies genomic markers of disease severity. <i>Genome Medicine</i> , <b>2018</b> , 10, 15	14.4	8
155	Genomic epidemiology of Shigella in the United Kingdom shows transmission of pathogen sublineages and determinants of antimicrobial resistance. <i>Scientific Reports</i> , <b>2018</b> , 8, 7389	4.9	35
154	The role of intra-NAPL diffusion on mass transfer from MGP residuals. <i>Journal of Contaminant Hydrology</i> , <b>2018</b> , 213, 49-61	3.9	4
153	Long-Lasting Geomagnetically Induced Currents and Harmonic Distortion Observed in New Zealand During the 78 September 2017 Disturbed Period. <i>Space Weather</i> , <b>2018</b> , 16, 704-717	3.7	28
152	The plasmid revisited : new insights into growth kinetics. <i>Wellcome Open Research</i> , <b>2018</b> , 3, 25	4.8	8
151	PlasmidTron: assembling the cause of phenotypes and genotypes from NGS data. <i>Microbial Genomics</i> , <b>2018</b> , 4,	4.4	4
150	Whole-genome sequencing revealed concurrent outbreaks of shigellosis in the English Orthodox Jewish Community caused by multiple importations of Shigella sonnei from Israel. <i>Microbial Genomics</i> , <b>2018</b> , 4,	4.4	8
149	An outbreak of a rare Shiga-toxin-producing Escherichia coli serotype (O117:H7) among men who have sex with men. <i>Microbial Genomics</i> , <b>2018</b> , 4,	4.4	8
148	Assessing gut microbiota perturbations during the early phase of infectious diarrhea in Vietnamese children. <i>Gut Microbes</i> , <b>2018</b> , 9, 38-54	8.8	41
147	Complement Susceptibility in Relation to Genome Sequence of Recent Klebsiella pneumoniae Isolates from Thai Hospitals. <i>MSphere</i> , <b>2018</b> , 3,	5	9
146	New Variant of Multidrug-Resistant Serovar Typhimurium Associated with Invasive Disease in Immunocompromised Patients in Vietnam. <i>MBio</i> , <b>2018</b> , 9,	7.8	26
145	Direct Whole-Genome Sequencing of Cutaneous Strains of Haemophilus ducreyi. <i>Emerging Infectious Diseases</i> , <b>2018</b> , 24, 786-789	10.2	4
144	Genomic insights into the emergence and spread of antimicrobial-resistant bacterial pathogens. <i>Science</i> , <b>2018</b> , 360, 733-738	33.3	146
143	Genomic evidence that the live Chlamydia abortus vaccine strain 1B is not attenuated and has the potential to cause disease. <i>Vaccine</i> , <b>2018</b> , 36, 3593-3598	4.1	13
142	Defining endemic cholera at three levels of spatiotemporal resolution within Bangladesh. <i>Nature Genetics</i> , <b>2018</b> , 50, 951-955	36.3	22
141	Identification and initial characterisation of a protein involved in Campylobacter jejuni cell shape. <i>Microbial Pathogenesis</i> , <b>2017</b> , 104, 202-211	3.8	8

140	Genomic landscape of extended-spectrum $\beta$ -lactamase resistance in <i>Escherichia coli</i> from an urban African setting. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2017</b> , 72, 1602-1609	5.1	27
139	European <i>Chlamydia abortus</i> livestock isolate genomes reveal unusual stability and limited diversity, reflected in geographical signatures. <i>BMC Genomics</i> , <b>2017</b> , 18, 344	4.5	19
138	Comprehensive global genome dynamics of show ancient diversification followed by contemporary mixing and recent lineage expansion. <i>Genome Research</i> , <b>2017</b> , 27, 1220-1229	9.7	65
137	Annotation of plasmid genes. <i>Plasmid</i> , <b>2017</b> , 91, 61-67	3.3	28
136	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> , <b>2017</b> , 23, 845-853	9.5	22
135	Common determinants of antimicrobial resistance in sequential episodes of sexually transmitted shigellosis in men who have sex with men: a cross-sectional study. <i>Lancet, The</i> , <b>2017</b> , 389, S24	4.0	2
134	Gastrointestinal Carriage Is a Major Reservoir of <i>Klebsiella pneumoniae</i> Infection in Intensive Care Patients. <i>Clinical Infectious Diseases</i> , <b>2017</b> , 65, 208-215	11.6	193
133	<i>Brucella neotomae</i> Infection in Humans, Costa Rica. <i>Emerging Infectious Diseases</i> , <b>2017</b> , 23, 997-1000	10.2	28
132	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> , <b>2017</b> , 11, e0005671	4.8	22
131	<i>Mycoplasma genitalium</i> : whole genome sequence analysis, recombination and population structure. <i>BMC Genomics</i> , <b>2017</b> , 18, 993	4.5	22
130	Concern regarding the alleged spread of hypervirulent lymphogranuloma venereum <i>Chlamydia trachomatis</i> strain in Europe. <i>Eurosurveillance</i> , <b>2017</b> , 22,	19.8	5
129	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> , <b>2017</b> , 7, 9634	4.9	8
128	<i>Galleria mellonella</i> is low cost and suitable surrogate host for studying virulence of human pathogenic <i>Vibrio cholerae</i> . <i>Gene</i> , <b>2017</b> , 628, 1-7	3.8	9
127	<i>Brucella</i> Genetic Variability in Wildlife Marine Mammals Populations Relates to Host Preference and Ocean Distribution. <i>Genome Biology and Evolution</i> , <b>2017</b> , 9, 1901-1912	3.9	19
126	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> , <b>2017</b> , 307, 422-429	3.7	33
125	Genomic history of the seventh pandemic of cholera in Africa. <i>Science</i> , <b>2017</b> , 358, 785-789	33.3	157
124	Integrated view of in the Americas. <i>Science</i> , <b>2017</b> , 358, 789-793	33.3	79
123	Transcriptome and proteome analysis of <i>Salmonella enterica</i> serovar Typhimurium systemic infection of wild type and immune-deficient mice. <i>PLoS ONE</i> , <b>2017</b> , 12, e0181365	3.7	6

122	An untypeable enterotoxigenic represents one of the dominant types causing human disease. <i>Microbial Genomics</i> , <b>2017</b> , 3, e000121	4.4	10
121	Distinct Salmonella Enteritidis lineages associated with enterocolitis in high-income settings and invasive disease in low-income settings. <i>Nature Genetics</i> , <b>2016</b> , 48, 1211-1217	36.3	116
120	A genomic island in Vibrio cholerae with VPI-1 site-specific recombination characteristics contains CRISPR-Cas and type VI secretion modules. <i>Scientific Reports</i> , <b>2016</b> , 6, 36891	4.9	28
119	Global phylogeography and evolutionary history of Shigella dysenteriae type 1. <i>Nature Microbiology</i> , <b>2016</b> , 1, 16027	26.6	47
118	The Type III Secretion System Effector SeoC of Salmonella enterica subsp. salamae and S. enterica subsp. arizonae ADP-Ribosylates Src and Inhibits Opsonophagocytosis. <i>Infection and Immunity</i> , <b>2016</b> , 84, 3618-3628	3.7	5
117	Add, stir and reduce Yersinia spp. as model bacteria for pathogen evolution. <i>Nature Reviews Microbiology</i> , <b>2016</b> , 14, 177-90	22.2	95
116	Emerging pathogens of gilthead seabream: characterisation and genomic analysis of novel intracellular E-proteobacteria. <i>ISME Journal</i> , <b>2016</b> , 10, 1791-803	11.9	21
115	The genomic signatures of Shigella evolution, adaptation and geographical spread. <i>Nature Reviews Microbiology</i> , <b>2016</b> , 14, 235-50	22.2	88
114	Quantitative proteomic analysis of Shigella flexneri and Shigella sonnei Generalized Modules for Membrane Antigens (GMMA) reveals highly pure preparations. <i>International Journal of Medical Microbiology</i> , <b>2016</b> , 306, 99-108	3.7	13
113	Quantitative Proteomics of the Infectious and Replicative Forms of Chlamydia trachomatis. <i>PLoS ONE</i> , <b>2016</b> , 11, e0149011	3.7	23
112	Molecular characterisation of the Chlamydia pecorum plasmid from porcine, ovine, bovine, and koala strains indicates plasmid-strain co-evolution. <i>PeerJ</i> , <b>2016</b> , 4, e1661	3.1	8
111	Travel- and Community-Based Transmission of Multidrug-Resistant Shigella sonnei Lineage among International Orthodox Jewish Communities. <i>Emerging Infectious Diseases</i> , <b>2016</b> , 22, 1545-1553	10.2	
110	Travel- and Community-Based Transmission of Multidrug-Resistant Shigella sonnei Lineage among International Orthodox Jewish Communities. <i>Emerging Infectious Diseases</i> , <b>2016</b> , 22, 1545-53	10.2	14
109	The diversity of surface polysaccharides. <i>Microbial Genomics</i> , <b>2016</b> , 2, e000073	4.4	101
108	Identification of capsule synthesis loci from whole genome data. <i>Microbial Genomics</i> , <b>2016</b> , 2, e000102	4.4	216
107	Salmonella Enteritidis Isolate Harboring Multiple Efflux Pumps and Pathogenicity Factors, Shows Absence of O Antigen Polymerase Gene. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 1130	5.7	1
106	Strain 2308 Wisconsin Genome: Importance of the Definition of Reference Strains. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 1557	5.7	16
105	Retrospective Analysis of Serotype Switching of Vibrio cholerae O1 in a Cholera Endemic Region Shows It Is a Non-random Process. <i>PLoS Neglected Tropical Diseases</i> , <b>2016</b> , 10, e0005044	4.8	12

104	South Asia as a Reservoir for the Global Spread of Ciprofloxacin-Resistant <i>Shigella sonnei</i> : A Cross-Sectional Study. <i>PLoS Medicine</i> , <b>2016</b> , 13, e1002055	11.6	56
103	<i>Chlamydia trachomatis</i> from Australian Aboriginal people with trachoma are polyphyletic composed of multiple distinctive lineages. <i>Nature Communications</i> , <b>2016</b> , 7, 10688	17.4	30
102	Genomic variations leading to alterations in cell morphology of <i>Campylobacter</i> spp. <i>Scientific Reports</i> , <b>2016</b> , 6, 38303	4.9	17
101	Genomic Analysis of <i>Salmonella enterica</i> Serovar Typhimurium from Wild Passerines in England and Wales. <i>Applied and Environmental Microbiology</i> , <b>2016</b> , 82, 6728-6735	4.8	32
100	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> , <b>2015</b> , 112, 863-8	11.5	154
99	Genomic Investigations unmask <i>Mycoplasma amphoriforme</i> , a new respiratory pathogen. <i>Clinical Infectious Diseases</i> , <b>2015</b> , 60, 381-8	11.6	4
98	An O antigen capsule modulates bacterial pathogenesis in <i>Shigella sonnei</i> . <i>PLoS Pathogens</i> , <b>2015</b> , 11, e1004749	7.6	64
97	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> , <b>2015</b> , 112, E3574-81	11.5	588
96	Intercontinental dissemination of azithromycin-resistant shigellosis through sexual transmission: a cross-sectional study. <i>Lancet Infectious Diseases</i> , <b>2015</b> , 15, 913-21	25.5	139
95	Phylogeographical analysis of the dominant multidrug-resistant H58 clade of <i>Salmonella</i> Typhi identifies inter- and intracontinental transmission events. <i>Nature Genetics</i> , <b>2015</b> , 47, 632-9	36.3	305
94	Co-cultivation and transcriptome sequencing of two co-existing fish pathogens <i>Moritella viscosa</i> and <i>Aliivibrio wodanis</i> . <i>BMC Genomics</i> , <b>2015</b> , 16, 447	4.5	21
93	A complete view of the genetic diversity of the <i>Escherichia coli</i> O-antigen biosynthesis gene cluster. <i>DNA Research</i> , <b>2015</b> , 22, 101-7	4.5	108
92	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> , <b>2015</b> , 53, 35-42	9.7	32
91	A high-resolution genomic analysis of multidrug-resistant hospital outbreaks of <i>Klebsiella pneumoniae</i> . <i>EMBO Molecular Medicine</i> , <b>2015</b> , 7, 227-39	12	67
90	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> , <b>2015</b> , 5, 17609	4.9	38
89	The Murray collection of pre-antibiotic era Enterobacteriaceae: a unique research resource. <i>Genome Medicine</i> , <b>2015</b> , 7, 97	14.4	23
88	Draft Genome Sequence of 24570, the Type Strain of <i>Shigella flexneri</i> . <i>Genome Announcements</i> , <b>2015</b> , 3,		2
87	Antimicrobial Drug Resistance of <i>Vibrio cholerae</i> , Democratic Republic of the Congo. <i>Emerging Infectious Diseases</i> , <b>2015</b> , 21, 847-51	10.2	21



86	Novel R pipeline for analyzing Biolog Phenotypic MicroArray data. <i>PLoS ONE</i> , <b>2015</b> , 10, e0118392	3.7	18
85	Relationship between Distinct African Cholera Epidemics Revealed via MLVA Haplotyping of 337 <i>Vibrio cholerae</i> Isolates. <i>PLoS Neglected Tropical Diseases</i> , <b>2015</b> , 9, e0003817	4.8	20
84	Species-wide whole genome sequencing reveals historical global spread and recent local persistence in <i>Shigella flexneri</i> . <i>ELife</i> , <b>2015</b> , 4, e07335	8.9	65
83	Draft genomes of <i>Shigella</i> strains used by the STOPENTERICS consortium. <i>Gut Pathogens</i> , <b>2015</b> , 7, 14	5.4	6
82	Whole genome analysis to detect potential vaccine-induced changes on <i>Shigella sonnei</i> genome. <i>Vaccine</i> , <b>2015</b> , 33, 2978-83	4.1	2
81	A putative, novel coli surface antigen 8B (CS8B) of enterotoxigenic <i>Escherichia coli</i> . <i>Pathogens and Disease</i> , <b>2015</b> , 73,	4.2	1
80	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> , <b>2015</b> , 83, 1778-88	3.7	44
79	<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> , <b>2015</b> , 9, e0004183	4.8	29
78	Genetic characterization of three qnrS1-harboring multidrug-resistance plasmids and qnrS1-containing transposons circulating in Ho Chi Minh City, Vietnam. <i>Journal of Medical Microbiology</i> , <b>2015</b> , 64, 869-878	3.2	8
77	Directional gene flow and ecological separation in. <i>Microbial Genomics</i> , <b>2015</b> , 1, e000030	4.4	15
76	Introduction and establishment of fluoroquinolone-resistant into Bhutan. <i>Microbial Genomics</i> , <b>2015</b> , 1, e000042	4.4	8
75	The <i>Yersinia pseudotuberculosis</i> complex: characterization and delineation of a new species, <i>Yersinia wautersii</i> . <i>International Journal of Medical Microbiology</i> , <b>2014</b> , 304, 452-63	3.7	38
74	Bacillary dysentery from World War 1 and NCTC1, the first bacterial isolate in the National Collection. <i>Lancet, The</i> , <b>2014</b> , 384, 1720	4.0	10
73	Identification of enterotoxigenic <i>Escherichia coli</i> (ETEC) clades with long-term global distribution. <i>Nature Genetics</i> , <b>2014</b> , 46, 1321-6	36.3	134
72	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> , <b>2014</b> , 111, 6768-73	11.5	114
71	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> , <b>2014</b> , 6, 7	5.4	13
70	Genomic epidemiology of <i>Vibrio cholerae</i> O1 associated with floods, Pakistan, 2010. <i>Emerging Infectious Diseases</i> , <b>2014</b> , 20, 13-20	10.2	30
69	The population structure of <i>Vibrio cholerae</i> from the Chandigarh Region of Northern India. <i>PLoS Neglected Tropical Diseases</i> , <b>2014</b> , 8, e2981	4.8	20

68	The genetic basis of plasmid tropism between <i>Chlamydia trachomatis</i> and <i>Chlamydia muridarum</i> . <i>Pathogens and Disease</i> , <b>2014</b> , 72, 19-23	4.2	18
67	Genomic Epidemiology of <i>Vibrio cholerae</i> O1 Associated with Floods, Pakistan, 2010. <i>Emerging Infectious Diseases</i> , <b>2014</b> , 20, 13-20	10.2	29
66	RNA-seq analysis of the influence of anaerobiosis and FNR on <i>Shigella flexneri</i> . <i>BMC Genomics</i> , <b>2014</b> , 15, 438	4.5	20
65	Genome evolution and plasticity of <i>Serratia marcescens</i> , an important multidrug-resistant nosocomial pathogen. <i>Genome Biology and Evolution</i> , <b>2014</b> , 6, 2096-110	3.9	114
64	The extant World War 1 dysentery bacillus NCTC1: a genomic analysis. <i>Lancet, The</i> , <b>2014</b> , 384, 1691-7	4.0	21
63	Plasmid deficiency in urogenital isolates of <i>Chlamydia trachomatis</i> reduces infectivity and virulence in a mouse model. <i>Pathogens and Disease</i> , <b>2014</b> , 70, 61-9	4.2	43
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> , <b>2013</b> , 51, 232-7	9.7	67
61	Generating whole bacterial genome sequences of low-abundance species from complex samples with IMS-MDA. <i>Nature Protocols</i> , <b>2013</b> , 8, 2404-12	18.8	32
60	Whole-genome sequences of <i>Chlamydia trachomatis</i> directly from clinical samples without culture. <i>Genome Research</i> , <b>2013</b> , 23, 855-66	9.7	95
59	Genome Sequence of <i>Chlamydia psittaci</i> Strain 01DC12 Originating from Swine. <i>Genome Announcements</i> , <b>2013</b> , 1,		7
58	Genome Sequence of <i>Klebsiella pneumoniae</i> Ecl8, a Reference Strain for Targeted Genetic Manipulation. <i>Genome Announcements</i> , <b>2013</b> , 1,		11
57	Genome and transcriptome adaptation accompanying emergence of the definitive type 2 host-restricted <i>Salmonella enterica</i> serovar Typhimurium pathovar. <i>MBio</i> , <b>2013</b> , 4, e00565-13	7.8	47
56	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> , <b>2013</b> , 7, e2557	4.8	18
55	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> , <b>2013</b> , 81, 838-49	3.7	64
54	Whole-genome sequencing of bacterial sexually transmitted infections: implications for clinicians. <i>Current Opinion in Infectious Diseases</i> , <b>2013</b> , 26, 90-8	5.4	10
53	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> , <b>2013</b> , 51, 303-5	9.7	16
52	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> , <b>2013</b> , 110, 17522-7	11.5	89
51	A study on the geophylogeny of clinical and environmental <i>Vibrio cholerae</i> in Kenya. <i>PLoS ONE</i> , <b>2013</b> , 8, e74829	3.7	27

50	Shigella sonnei genome sequencing and phylogenetic analysis indicate recent global dissemination from Europe. <i>Nature Genetics</i> , <b>2012</b> , 44, 1056-9	36.3	203
49	Whole-genome analysis of diverse Chlamydia trachomatis strains identifies phylogenetic relationships masked by current clinical typing. <i>Nature Genetics</i> , <b>2012</b> , 44, 413-9, S1	36.3	222
48	New insights into the bacterial fitness-associated mechanisms revealed by the characterization of large plasmids of an avian pathogenic E. coli. <i>PLoS ONE</i> , <b>2012</b> , 7, e29481	3.7	19
47	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> , <b>2012</b> , 109, 1269-74	11.5	277
46	The transcriptional landscape and small RNAs of Salmonella enterica serovar Typhimurium. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, E1277-86	11.5	294
45	Evidence for several waves of global transmission in the seventh cholera pandemic. <i>Nature</i> , <b>2011</b> , 477, 462-5	50.4	492
44	Differential phenotypic and genotypic characteristics of qnrS1-harboring plasmids carried by hospital and community commensal enterobacteria. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2011</b> , 55, 1798-802	5.9	10
43	Salmonella bongori provides insights into the evolution of the Salmonellae. <i>PLoS Pathogens</i> , <b>2011</b> , 7, e1002191	7.6	123
42	Yersinia pestis genome sequencing identifies patterns of global phylogenetic diversity. <i>Nature Genetics</i> , <b>2010</b> , 42, 1140-3	36.3	393
41	The Swedish new variant of Chlamydia trachomatis: genome sequence, morphology, cell tropism and phenotypic characterization. <i>Microbiology (United Kingdom)</i> , <b>2010</b> , 156, 1394-1404	2.9	67
40	The sudden dominance of blaCTX-M harbouring plasmids in Shigella spp. Circulating in Southern Vietnam. <i>PLoS Neglected Tropical Diseases</i> , <b>2010</b> , 4, e702	4.8	45
39	Chlamydia trachomatis: small genome, big challenges. <i>Future Microbiology</i> , <b>2010</b> , 5, 555-61	2.9	16
38	A commensal gone bad: complete genome sequence of the prototypical enterotoxigenic Escherichia coli strain H10407. <i>Journal of Bacteriology</i> , <b>2010</b> , 192, 5822-31	3.5	141
37	The genome of Burkholderia cenocepacia J2315, an epidemic pathogen of cystic fibrosis patients. <i>Journal of Bacteriology</i> , <b>2009</b> , 191, 261-77	3.5	270
36	Epidemic multiple drug resistant Salmonella Typhimurium causing invasive disease in sub-Saharan Africa have a distinct genotype. <i>Genome Research</i> , <b>2009</b> , 19, 2279-87	9.7	374
35	A simple method for directional transcriptome sequencing using Illumina technology. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, e148	20.1	77
34	Variation in Salmonella enterica serovar typhi IncHI1 plasmids during the global spread of resistant typhoid fever. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2009</b> , 53, 716-27	5.9	73
33	Co-evolution of genomes and plasmids within Chlamydia trachomatis and the emergence in Sweden of a new variant strain. <i>BMC Genomics</i> , <b>2009</b> , 10, 239	4.5	99

32	Pseudogene accumulation in the evolutionary histories of <i>Salmonella enterica</i> serovars Paratyphi A and Typhi. <i>BMC Genomics</i> , <b>2009</b> , 10, 36	4.5	120
31	Genomic and phenotypic variation in epidemic-spanning <i>Salmonella enterica</i> serovar Enteritidis isolates. <i>BMC Microbiology</i> , <b>2009</b> , 9, 237	4.5	34
30	A strand-specific RNA-Seq analysis of the transcriptome of the typhoid bacillus <i>Salmonella typhi</i> . <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000569	6	188
29	The genome sequence of the fish pathogen <i>Aliivibrio salmonicida</i> strain LFI1238 shows extensive evidence of gene decay. <i>BMC Genomics</i> , <b>2008</b> , 9, 616	4.5	77
28	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> , <b>2008</b> , 190, 6881-93	3.5	607
27	Comparative genome analysis of <i>Salmonella Enteritidis</i> PT4 and <i>Salmonella Gallinarum</i> 287/91 provides insights into evolutionary and host adaptation pathways. <i>Genome Research</i> , <b>2008</b> , 18, 1624-37	9.7	320
26	<i>Chlamydia trachomatis</i> : genome sequence analysis of lymphogranuloma venereum isolates. <i>Genome Research</i> , <b>2008</b> , 18, 161-71	9.7	154
25	A bimodal pattern of relatedness between the <i>Salmonella Paratyphi A</i> and Typhi genomes: convergence or divergence by homologous recombination?. <i>Genome Research</i> , <b>2007</b> , 17, 61-8	9.7	98
24	Multidrug-resistant <i>Salmonella enterica</i> serovar paratyphi A harbors IncHI1 plasmids similar to those found in serovar typhi. <i>Journal of Bacteriology</i> , <b>2007</b> , 189, 4257-64	3.5	64
23	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> , <b>2007</b> , 45, 2590-8	9.7	44
22	The complete genome sequence and comparative genome analysis of the high pathogenicity <i>Yersinia enterocolitica</i> strain 8081. <i>PLoS Genetics</i> , <b>2006</b> , 2, e206	6	192
21	<i>Escherichia coli</i> K-12: a cooperatively developed annotation snapshot--2005. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, 1-9	20.1	525
20	Proteomic and microarray characterization of the AggR regulon identifies a pheU pathogenicity island in enteroaggregative <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , <b>2006</b> , 61, 1267-82	4.1	185
19	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> , <b>2005</b> , 102, 838-43	11.5	139
18	The <i>Chlamydomonas abortus</i> genome sequence reveals an array of variable proteins that contribute to interspecies variation. <i>Genome Research</i> , <b>2005</b> , 15, 629-40	9.7	144
17	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> , <b>2004</b> , 101, 14240-5	11.5	569
16	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> , <b>2004</b> , 150, 2289-2300	2.9	42
15	The role of prophage-like elements in the diversity of <i>Salmonella enterica</i> serovars. <i>Journal of Molecular Biology</i> , <b>2004</b> , 339, 279-300	6.5	102

14	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> , <b>2004</b> , 101, 17837-42	11.5	404
13	Comparative analysis of the genome sequences of <i>Bordetella pertussis</i> , <i>Bordetella parapertussis</i> and <i>Bordetella bronchiseptica</i> . <i>Nature Genetics</i> , <b>2003</b> , 35, 32-40	36.3	787
12	Fitting the niche by genomic adaptation. <i>Nature Reviews Microbiology</i> , <b>2003</b> , 1, 92-3	22.2	6
11	Genomic epidemiology of syphilis reveals independent emergence of macrolide resistance across multiple circulating lineages		1
10	Caribbean multi-centre study of <i>Klebsiella pneumoniae</i> : whole genome sequencing, antimicrobial resistance and virulence factors		1
9	Identification of <i>Klebsiella</i> capsule synthesis loci from whole genome data		3
8	Millennia of genomic stability within the invasive Para C Lineage of <i>Salmonella enterica</i>		9
7	A comprehensive and high-quality collection of <i>E. coli</i> genomes and their genes		2
6	Antimicrobial resistant <i>Klebsiella pneumoniae</i> carriage and infection in specialized geriatric care wards linked to acquisition in the referring hospital		3
5	rPinecone: Define sub-lineages of a clonal expansion via a phylogenetic tree		2
4	Genomic surveillance for hypervirulence and multi-drug resistance in invasive <i>Klebsiella pneumoniae</i> from south and southeast Asia		3
3	<i>K. pneumoniae</i> ST258 genomic variability and bacteriophage susceptibility		2
2	Exploring bacterial diversity via a curated and searchable snapshot of archived DNA sequences		1
1	Contemporary syphilis is characterised by rapid global spread of pandemic <i>Treponema pallidum</i> lineages		1