Thomas R Connor

List of Publications by Year
in descending order

79 papers	15,252 citations	57758 44 h-index	69250 77 g-index
97 all docs	97 docs citations	97 times ranked	22282 citing authors

#	Article	IF	Citations
1	Combined epidemiological and genomic analysis of nosocomial SARS-CoV-2 infection early in the pandemic and the role of unidentified cases in transmission. Clinical Microbiology and Infection, 2022, 28, 93-100.	6.0	21
2	Hospital admission and emergency care attendance risk for SARS-CoV-2 delta (B.1.617.2) compared with alpha (B.1.1.7) variants of concern: a cohort study. Lancet Infectious Diseases, The, 2022, 22, 35-42.	9.1	612
3	Future-proofing and maximizing the utility of metadata: The PHA4GE SARS-CoV-2 contextual data specification package. GigaScience, 2022, 11, .	6.4	18
4	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission. Nature Communications, 2022, 13, 1012.	12.8	10
5	Phylogenetic and phylodynamic approaches to understanding and combating the early SARS-CoV-2 pandemic. Nature Reviews Genetics, 2022, 23, 547-562.	16.3	70
6	Epidemiological analysis of the first 1000 cases of SARS‐CoV‐2 lineage BA.1 (B.1.1.529, Omicron) compared with co‐circulating Delta in Wales, UK. Influenza and Other Respiratory Viruses, 2022, 16, 986-993.	3.4	13
7	A structure-based nomenclature for Bacillus thuringiensis and other bacteria-derived pesticidal proteins. Journal of Invertebrate Pathology, 2021, 186, 107438.	3.2	177
8	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. Cell, 2021, 184, 64-75.e11.	28.9	843
9	Kill and cure: genomic phylogeny and bioactivity of Burkholderia gladioli bacteria capable of pathogenic and beneficial lifestyles. Microbial Genomics, 2021, 7, .	2.0	24
10	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. Science, 2021, 371, 708-712.	12.6	335
11	SARS-CoV-2 within-host diversity and transmission. Science, 2021, 372, .	12.6	278
12	Genomics reveals the novel species placement of industrial contaminant isolates incorrectly identified as Burkholderia lata. Microbial Genomics, 2021, 7, .	2.0	2
13	Recurrent emergence of SARS-CoV-2 spike deletion H69/V70 and its role in the Alpha variant B.1.1.7. Cell Reports, 2021, 35, 109292.	6.4	375
14	CLIMB-COVID: continuous integration supporting decentralised sequencing for SARS-CoV-2 genomic surveillance. Genome Biology, 2021, 22, 196.	8.8	53
15	Monitoring SARS-CoV-2 in municipal wastewater to evaluate the success of lockdown measures for controlling COVID-19 in the UK. Water Research, 2021, 200, 117214.	11.3	117
16	Discovery of the Pseudomonas Polyyne Protegencin by a Phylogeny-Guided Study of Polyyne Biosynthetic Gene Cluster Diversity. MBio, 2021, 12, e0071521.	4.1	16
17	Generation and transmission of interlineage recombinants in the SARS-CoV-2 pandemic. Cell, 2021, 184, 5179-5188.e8.	28.9	182
18	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. Science, 2021, 374, eabl9551.	12.6	111

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19	Shedding of SARS-CoV-2 in feces and urine and its potential role in person-to-person transmission and the environment-based spread of COVID-19. Science of the Total Environment, 2020, 749, 141364.	8.0	293
20	Influenza classification from short reads with VAPOR facilitates robust mapping pipelines and zoonotic strain detection for routine surveillance applications. Bioinformatics, 2020, 36, 1681-1688.	4.1	3
21	Evaluation of methods for detecting human reads in microbial sequencing datasets. Microbial Genomics, 2020, 6, .	2.0	11
22	Genomic Assemblies of Members of <i>Burkholderia</i> and Related Genera as a Resource for Natural Product Discovery. Microbiology Resource Announcements, 2020, 9, .	0.6	9
23	HIGH-FREQUENCY failure of combination antiretroviral therapy in paediatric HIV infection is associated with unmet maternal needs causing maternal NON-ADHERENCE. EClinicalMedicine, 2020, 22, 100344.	7.1	23
24	Understanding and responding to COVID-19 in Wales: protocol for a privacy-protecting data platform for enhanced epidemiology and evaluation of interventions. BMJ Open, 2020, 10, e043010.	1.9	50
25	Geographical and temporal distribution of SARS-CoV-2 clades in the WHO European Region, January to June 2020. Eurosurveillance, 2020, 25, .	7.0	186
26	Genome Sequence of Pluralibacter gergoviae ECO77, a Multireplicon Isolate of Industrial Origin. Microbiology Resource Announcements, 2020, 9, .	0.6	2
27	The Genome Sequences of Three <i>Paraburkholderia</i> sp. Strains Isolated from Wood-Decay Fungi Reveal Them as Novel Species with Antimicrobial Biosynthetic Potential. Microbiology Resource Announcements, 2019, 8, .	0.6	3
28	Scalable Pathogen Pipeline Platform (SP^3): Enabling Unified Genomic Data Analysis with Elastic Cloud Computing. , 2019, , .		1
29	Genome mining identifies cepacin as a plant-protective metabolite of the biopesticidal bacterium Burkholderia ambifaria. Nature Microbiology, 2019, 4, 996-1005.	13.3	106
30	Not all Pseudomonas aeruginosa are equal: strains from industrial sources possess uniquely large multireplicon genomes. Microbial Genomics, 2019, 5, .	2.0	26
31	Peptide–MHC Class I Tetramers Can Fail To Detect Relevant Functional T Cell Clonotypes and Underestimate Antigen-Reactive T Cell Populations. Journal of Immunology, 2018, 200, 2263-2279.	0.8	87
32	Zoonotic Transfer of Clostridium difficile Harboring Antimicrobial Resistance between Farm Animals and Humans. Journal of Clinical Microbiology, 2018, 56, .	3.9	102
33	The consistent differential expression of genetic pathways following exposure of an industrial Pseudomonas aeruginosa strain to preservatives and a laundry detergent formulation. FEMS Microbiology Letters, 2018, 365, .	1.8	10
34	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
35	Travel- and Community-Based Transmission of Multidrug-ResistantShigellasonneiLineage among International Orthodox Jewish Communities. Emerging Infectious Diseases, 2016, 22, 1545-1553.	4.3	23
36	Microevolution of Monophasic<i>Salmonella</i>Typhimurium during Epidemic, United Kingdom, 2005–2010. Emerging Infectious Diseases, 2016, 22, 617-624.	4.3	158

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37	Retrospective Analysis of Serotype Switching of Vibrio cholerae O1 in a Cholera Endemic Region Shows It Is a Non-random Process. PLoS Neglected Tropical Diseases, 2016, 10, e0005044.	3.0	23
38	Molecular Surveillance Identifies Multiple Transmissions of Typhoid in West Africa. PLoS Neglected Tropical Diseases, 2016, 10, e0004781.	3.0	46
39	What's in a Name? Species-Wide Whole-Genome Sequencing Resolves Invasive and Noninvasive Lineages of Salmonella enterica Serotype Paratyphi B. MBio, 2016, 7, .	4.1	29
40	An extended genotyping framework for Salmonella enterica serovar Typhi, the cause of human typhoid. Nature Communications, 2016, 7, 12827.	12.8	145
41	The Type III Secretion System Effector SeoC of Salmonella enterica subsp. salamae and S. enterica subsp. arizonae ADP-Ribosylates Src and Inhibits Opsonophagocytosis. Infection and Immunity, 2016, 84, 3618-3628.	2.2	7
42	Engineering of Isogenic Cells Deficient for MR1 with a CRISPR/Cas9 Lentiviral System: Tools To Study Microbial Antigen Processing and Presentation to Human MR1-Restricted T Cells. Journal of Immunology, 2016, 197, 971-982.	0.8	21
43	CLIMB (the Cloud Infrastructure for Microbial Bioinformatics): an online resource for the medical microbiology community. Microbial Genomics, 2016, 2, e000086.	2.0	176
44	Travel- and Community-Based Transmission of Multidrug-ResistantShigellasonneiLineage among International Orthodox Jewish Communities. Emerging Infectious Diseases, 2016, 22, 1545-1553.	4.3	5
45	Novel R Pipeline for Analyzing Biolog Phenotypic Microarray Data. PLoS ONE, 2015, 10, e0118392.	2.5	29
46	Species-wide whole genome sequencing reveals historical global spread and recent local persistence in Shigella flexneri. ELife, 2015, 4, e07335.	6.0	94
47	Patterns of genome evolution that have accompanied host adaptation in <i>Salmonella</i>. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 863-868.	7.1	213
48	Signatures of Adaptation in Human Invasive Salmonella Typhimurium ST313 Populations from Sub-Saharan Africa. PLoS Neglected Tropical Diseases, 2015, 9, e0003611.	3.0	116
49	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.	7.1	942
50	Intercontinental dissemination of azithromycin-resistant shigellosis through sexual transmission: a cross-sectional study. Lancet Infectious Diseases, The, 2015, 15, 913-921.	9.1	204
51	Rapid phylogenetic analysis of large samples of recombinant bacterial whole genome sequences using Gubbins. Nucleic Acids Research, 2015, 43, e15-e15.	14.5	1,834
52	Characterization of Plasmids in Extensively Drug-Resistant Acinetobacter Strains Isolated in India and Pakistan. Antimicrobial Agents and Chemotherapy, 2015, 59, 923-929.	3.2	54
53	Use of Whole-Genus Genome Sequence Data To Develop a Multilocus Sequence Typing Tool That Accurately Identifies Yersinia Isolates to the Species and Subspecies Levels. Journal of Clinical Microbiology, 2015, 53, 35-42.	3.9	45
54	Automated Cloud Brokerage Based Upon Continuous Real-Time Benchmarking. , 2015, , .		3

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55	Emergence of a New Epidemic Neisseria meningitidis Serogroup A Clone in the African Meningitis Belt: High-Resolution Picture of Genomic Changes That Mediate Immune Evasion. MBio, 2014, 5, e01974-14.	4.1	51
56	Cryptic ecology among host generalist *Campylobacter jejuni* in domestic animals. Molecular Ecology, 2014, 23, 2442-2451.	3.9	131
57	Identification of enterotoxigenic Escherichia coli (ETEC) clades with long-term global distribution. Nature Genetics, 2014, 46, 1321-1326.	21.4	192
58	Parallel independent evolution of pathogenicity within the genus *Yersinia*. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6768-6773.	7.1	154
59	Whole genome sequencing reveals potential spread of Clostridium difficile between humans and farm animals in the Netherlands, 2002 to 2011. Eurosurveillance, 2014, 19, 20954.	7.0	188
60	Distinguishable Epidemics of Multidrug-Resistant *Salmonella* Typhimurium DT104 in Different Hosts. Science, 2013, 341, 1514-1517.	12.6	310
61	Emergence and global spread of epidemic healthcare-associated Clostridium difficile. Nature Genetics, 2013, 45, 109-113.	21.4	669
62	Genome and Transcriptome Adaptation Accompanying Emergence of the Definitive Type 2 Host-Restricted Salmonella enterica Serovar Typhimurium Pathovar. MBio, 2013, 4, e00565-13.	4.1	57
63	Sequencing and Functional Annotation of Avian Pathogenic Escherichia coli Serogroup O78 Strains Reveal the Evolution of E. coli Lineages Pathogenic for Poultry via Distinct Mechanisms. Infection and Immunity, 2013, 81, 838-849.	2.2	82
64	Retrospective analysis of whole genome sequencing compared to prospective typing data in further informing the epidemiological investigation of an outbreak of *Shigella sonnei* in the UK. Epidemiology and Infection, 2013, 141, 2568-2575.	2.1	42
65	Hierarchical and Spatially Explicit Clustering of DNA Sequences with BAPS Software. Molecular Biology and Evolution, 2013, 30, 1224-1228.	8.9	568
66	Historical Zoonoses and Other Changes in Host Tropism of Staphylococcus aureus, Identified by Phylogenetic Analysis of a Population Dataset. PLoS ONE, 2013, 8, e62369.	2.5	55
67	Targeted Restoration of the Intestinal Microbiota with a Simple, Defined Bacteriotherapy Resolves Relapsing Clostridium difficile Disease in Mice. PLoS Pathogens, 2012, 8, e1002995.	4.7	504
68	Population structure in the *Neisseria*, and the biological significance of fuzzy species. Journal of the Royal Society Interface, 2012, 9, 1208-1215.	3.4	33
69	Detection of recombination events in bacterial genomes from large population samples. Nucleic Acids Research, 2012, 40, e6-e6.	14.5	179
70	Intracontinental spread of human invasive Salmonella Typhimurium pathovariants in sub-Saharan Africa. Nature Genetics, 2012, 44, 1215-1221.	21.4	370
71	Genome Sequencing and Analysis of the Tasmanian Devil and Its Transmissible Cancer. Cell, 2012, 148, 780-791.	28.9	300
72	A tale of three next generation sequencing platforms: comparison of Ion torrent, pacific biosciences and illumina MiSeq sequencers. BMC Genomics, 2012, 13, 341.	2.8	1,601

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73	Population subdivision and the detection of recombination in non-typable Haemophilus influenzae. Microbiology (United Kingdom), 2012, 158, 2958-2964.	1.8	24
74	Evidence for several waves of global transmission in the seventh cholera pandemic. Nature, 2011, 477, 462-465.	27.8	649
75	Bayesian semi-supervised classification of bacterial samples using MLST databases. BMC Bioinformatics, 2011, 12, 302.	2.6	17
76	Salmonella bongori Provides Insights into the Evolution of the Salmonellae. PLoS Pathogens, 2011, 7, e1002191.	4.7	171
77	Hyper-Recombination, Diversity, and Antibiotic Resistance in Pneumococcus. Science, 2009, 324, 1454-1457.	12.6	164
78	Assessing the reliability of eBURST using simulated populations with known ancestry. BMC Microbiology, 2007, 7, 30.	3.3	123
79	Multilocus Models of Bacterial Population Genetics. , 0, , 93-104.		0