

Thomas R Connor

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8327433/publications.pdf>

Version: 2024-02-01

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	Rapid phylogenetic analysis of large samples of recombinant bacterial whole genome sequences using Gubbins. <i>Nucleic Acids Research</i> , 2015, 43, e15-e15.	14.5	1,834
2	A tale of three next generation sequencing platforms: comparison of Ion torrent, pacific biosciences and illumina MiSeq sequencers. <i>BMC Genomics</i> , 2012, 13, 341.	2.8	1,601
3	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
4	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , 2021, 184, 64-75.e11.	28.9	843
5	Emergence and global spread of epidemic healthcare-associated <i>Clostridium difficile</i> . <i>Nature Genetics</i> , 2013, 45, 109-113.	21.4	669
6	Evidence for several waves of global transmission in the seventh cholera pandemic. <i>Nature</i> , 2011, 477, 462-465.	27.8	649
7	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. <i>Lancet Infectious Diseases</i> , The, 2022, 22, 35-42.	9.1	612
8	Hierarchical and Spatially Explicit Clustering of DNA Sequences with BAPS Software. <i>Molecular Biology and Evolution</i> , 2013, 30, 1224-1228.	8.9	568
9	Targeted Restoration of the Intestinal Microbiota with a Simple, Defined Bacteriotherapy Resolves Relapsing <i>Clostridium difficile</i> Disease in Mice. <i>PLoS Pathogens</i> , 2012, 8, e1002995.	4.7	504
10	Recurrent emergence of SARS-CoV-2 spike deletion H69/V70 and its role in the Alpha variant B.1.1.7. <i>Cell Reports</i> , 2021, 35, 109292.	6.4	375
11	Intracontinental spread of human invasive <i>Salmonella</i> Typhimurium pathovariants in sub-Saharan Africa. <i>Nature Genetics</i> , 2012, 44, 1215-1221.	21.4	370
12	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , 2021, 371, 708-712.	12.6	335
13	Distinguishable Epidemics of Multidrug-Resistant <i>Salmonella</i> Typhimurium DT104 in Different Hosts. <i>Science</i> , 2013, 341, 1514-1517.	12.6	310
14	Genome Sequencing and Analysis of the Tasmanian Devil and Its Transmissible Cancer. <i>Cell</i> , 2012, 148, 780-791.	28.9	300
15	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. <i>Science of the Total Environment</i> , 2020, 749, 141364.	8.0	293
16	SARS-CoV-2 within-host diversity and transmission. <i>Science</i> , 2021, 372, .	12.6	278
17	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
18	Intercontinental dissemination of azithromycin-resistant shigellosis through sexual transmission: a cross-sectional study. <i>Lancet Infectious Diseases</i> , The, 2015, 15, 913-921.	9.1	204

#	ARTICLE	IF	CITATIONS
19	Identification of enterotoxigenic <i>Escherichia coli</i> (ETEC) clades with long-term global distribution. <i>Nature Genetics</i> , 2014, 46, 1321-1326.	21.4	192
20	Whole genome sequencing reveals potential spread of <i>Clostridium difficile</i> between humans and farm animals in the Netherlands, 2002 to 2011. <i>Eurosurveillance</i> , 2014, 19, 20954.	7.0	188
21	Geographical and temporal distribution of SARS-CoV-2 clades in the WHO European Region, January to June 2020. <i>Eurosurveillance</i> , 2020, 25, .	7.0	186
22	Generation and transmission of interlineage recombinants in the SARS-CoV-2 pandemic. <i>Cell</i> , 2021, 184, 5179-5188.e8.	28.9	182
23	Detection of recombination events in bacterial genomes from large population samples. <i>Nucleic Acids Research</i> , 2012, 40, e6-e6.	14.5	179
24	A structure-based nomenclature for <i>Bacillus thuringiensis</i> and other bacteria-derived pesticidal proteins. <i>Journal of Invertebrate Pathology</i> , 2021, 186, 107438.	3.2	177
25	CLIMB (the Cloud Infrastructure for Microbial Bioinformatics): an online resource for the medical microbiology community. <i>Microbial Genomics</i> , 2016, 2, e000086.	2.0	176
26	<i>Salmonella bongori</i> Provides Insights into the Evolution of the Salmonellae. <i>PLoS Pathogens</i> , 2011, 7, e1002191.	4.7	171
27	Hyper-Recombination, Diversity, and Antibiotic Resistance in <i>Pneumococcus</i> . <i>Science</i> , 2009, 324, 1454-1457.	12.6	164
28	Microevolution of Monophasic <i>Salmonella</i> Typhimurium during Epidemic, United Kingdom, 2005-2010. <i>Emerging Infectious Diseases</i> , 2016, 22, 617-624.	4.3	158
29	Parallel independent evolution of pathogenicity within the genus <i>Yersinia</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6768-6773.	7.1	154
30	An extended genotyping framework for <i>Salmonella enterica</i> serovar Typhi, the cause of human typhoid. <i>Nature Communications</i> , 2016, 7, 12827.	12.8	145
31	Cryptic ecology among host generalist <i>Campylobacter jejuni</i> in domestic animals. <i>Molecular Ecology</i> , 2014, 23, 2442-2451.	3.9	131
32	Assessing the reliability of eBURST using simulated populations with known ancestry. <i>BMC Microbiology</i> , 2007, 7, 30.	3.3	123
33	Monitoring SARS-CoV-2 in municipal wastewater to evaluate the success of lockdown measures for controlling COVID-19 in the UK. <i>Water Research</i> , 2021, 200, 117214.	11.3	117
34	Signatures of Adaptation in Human Invasive <i>Salmonella</i> Typhimurium ST313 Populations from Sub-Saharan Africa. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003611.	3.0	116
35	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. <i>Science</i> , 2021, 374, eabl9551.	12.6	111
36	Genome mining identifies cepacin as a plant-protective metabolite of the biopesticidal bacterium <i>Burkholderia ambifaria</i> . <i>Nature Microbiology</i> , 2019, 4, 996-1005.	13.3	106

#	ARTICLE	IF	CITATIONS
37	Zoonotic Transfer of <i>Clostridium difficile</i> Harboring Antimicrobial Resistance between Farm Animals and Humans. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	102
38	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
39	Peptideâ€MHC Class I Tetramers Can Fail To Detect Relevant Functional T Cell Clonotypes and Underestimate Antigen-Reactive T Cell Populations. <i>Journal of Immunology</i> , 2018, 200, 2263-2279.	0.8	87
40	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.	2.2	82
41	Phylogenetic and phylodynamic approaches to understanding and combating the early SARS-CoV-2 pandemic. <i>Nature Reviews Genetics</i> , 2022, 23, 547-562.	16.3	70
42	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.	4.1	57
43	Historical Zoonoses and Other Changes in Host Tropism of <i>Staphylococcus aureus</i> , Identified by Phylogenetic Analysis of a Population Dataset. <i>PLoS ONE</i> , 2013, 8, e62369.	2.5	55
44	Characterization of Plasmids in Extensively Drug-Resistant <i>Acinetobacter</i> Strains Isolated in India and Pakistan. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 923-929.	3.2	54
45	CLIMB-COVID: continuous integration supporting decentralised sequencing for SARS-CoV-2 genomic surveillance. <i>Genome Biology</i> , 2021, 22, 196.	8.8	53
46	Emergence of a New Epidemic <i>Neisseria meningitidis</i> Serogroup A Clone in the African Meningitis Belt: High-Resolution Picture of Genomic Changes That Mediate Immune Evasion. <i>MBio</i> , 2014, 5, e01974-14.	4.1	51
47	Understanding and responding to COVID-19 in Wales: protocol for a privacy-protecting data platform for enhanced epidemiology and evaluation of interventions. <i>BMJ Open</i> , 2020, 10, e043010.	1.9	50
48	Molecular Surveillance Identifies Multiple Transmissions of Typhoid in West Africa. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004781.	3.0	46
49	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.	3.9	45
50	Retrospective analysis of whole genome sequencing compared to prospective typing data in further informing the epidemiological investigation of an outbreak of <i>Shigella sonnei</i> in the UK. <i>Epidemiology and Infection</i> , 2013, 141, 2568-2575.	2.1	42
51	Whole genome sequencing of <i>Shigella sonnei</i> through PulseNet Latin America and Caribbean: advancing global surveillance of foodborne illnesses. <i>Clinical Microbiology and Infection</i> , 2017, 23, 845-853.	6.0	37
52	Population structure in the <i>Neisseria</i> , and the biological significance of fuzzy species. <i>Journal of the Royal Society Interface</i> , 2012, 9, 1208-1215.	3.4	33
53	Novel R Pipeline for Analyzing Biolog Phenotypic Microarray Data. <i>PLoS ONE</i> , 2015, 10, e0118392.	2.5	29
54	Whatâ€™s in a Name? Species-Wide Whole-Genome Sequencing Resolves Invasive and Noninvasive Lineages of <i>Salmonella enterica</i> Serotype Paratyphi B. <i>MBio</i> , 2016, 7, .	4.1	29

#	ARTICLE	IF	CITATIONS
55	Not all <i>Pseudomonas aeruginosa</i> are equal: strains from industrial sources possess uniquely large multireplicon genomes. <i>Microbial Genomics</i> , 2019, 5, .	2.0	26
56	Kill and cure: genomic phylogeny and bioactivity of <i>Burkholderia gladioli</i> bacteria capable of pathogenic and beneficial lifestyles. <i>Microbial Genomics</i> , 2021, 7, .	2.0	24
57	Population subdivision and the detection of recombination in non-typable <i>Haemophilus influenzae</i> . <i>Microbiology (United Kingdom)</i> , 2012, 158, 2958-2964.	1.8	24
58	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
59	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
60	HIGH-FREQUENCY failure of combination antiretroviral therapy in paediatric HIV infection is associated with unmet maternal needs causing maternal NON-ADHERENCE. <i>EClinicalMedicine</i> , 2020, 22, 100344.	7.1	23
61	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. <i>Journal of Immunology</i> , 2016, 197, 971-982.	0.8	21
62	Combined epidemiological and genomic analysis of nosocomial SARS-CoV-2 infection early in the pandemic and the role of unidentified cases in transmission. <i>Clinical Microbiology and Infection</i> , 2022, 28, 93-100.	6.0	21
63	Future-proofing and maximizing the utility of metadata: The PHA4GE SARS-CoV-2 contextual data specification package. <i>GigaScience</i> , 2022, 11, .	6.4	18
64	Bayesian semi-supervised classification of bacterial samples using MLST databases. <i>BMC Bioinformatics</i> , 2011, 12, 302.	2.6	17
65	Discovery of the <i>Pseudomonas</i> Polyene Protegencin by a Phylogeny-Guided Study of Polyene Biosynthetic Gene Cluster Diversity. <i>MBio</i> , 2021, 12, e0071521.	4.1	16
66	Epidemiological analysis of the first 1000 cases of SARS-CoV-2 lineage BA.1 (B.1.1.529, Omicron) compared with circulating Delta in Wales, UK. <i>Influenza and Other Respiratory Viruses</i> , 2022, 16, 986-993.	3.4	13
67	Evaluation of methods for detecting human reads in microbial sequencing datasets. <i>Microbial Genomics</i> , 2020, 6, .	2.0	11
68	The consistent differential expression of genetic pathways following exposure of an industrial <i>Pseudomonas aeruginosa</i> strain to preservatives and a laundry detergent formulation. <i>FEMS Microbiology Letters</i> , 2018, 365, .	1.8	10
69	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission. <i>Nature Communications</i> , 2022, 13, 1012.	12.8	10
70	Genomic Assemblies of Members of <i>Burkholderia</i> and Related Genera as a Resource for Natural Product Discovery. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	9
71	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
72	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

#	ARTICLE	IF	CITATIONS
73	The Genome Sequences of Three <i>Paraburkholderia</i> sp. Strains Isolated from Wood-Decay Fungi Reveal Them as Novel Species with Antimicrobial Biosynthetic Potential. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	3
74	Influenza classification from short reads with VAPOR facilitates robust mapping pipelines and zoonotic strain detection for routine surveillance applications. <i>Bioinformatics</i> , 2020, 36, 1681-1688.	4.1	3
75	Automated Cloud Brokerage Based Upon Continuous Real-Time Benchmarking. , 2015, , .		3
76	Genomics reveals the novel species placement of industrial contaminant isolates incorrectly identified as <i>Burkholderia lata</i> . <i>Microbial Genomics</i> , 2021, 7, .	2.0	2
77	Genome Sequence of <i>Pluralibacter gergoviae</i> ECO77, a Multireplicon Isolate of Industrial Origin. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	2
78	Scalable Pathogen Pipeline Platform (SP ³): Enabling Unified Genomic Data Analysis with Elastic Cloud Computing. , 2019, , .		1
79	Multilocus Models of Bacterial Population Genetics. , 0, , 93-104.		0