

Nicholas J Loman

List of Publications by Year in descending order

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Version: 2024-02-01

95
papers

23,638
citations

31976

53
h-index

39675

94
g-index

129
all docs

129
docs citations

129
times ranked

34515
citing authors

#	ARTICLE	IF	CITATIONS
1	Binning metagenomic contigs by coverage and composition. <i>Nature Methods</i> , 2014, 11, 1144-1146.	19.0	1,709
2	Nanopore sequencing and assembly of a human genome with ultra-long reads. <i>Nature Biotechnology</i> , 2018, 36, 338-345.	17.5	1,443
3	Performance comparison of benchtop high-throughput sequencing platforms. <i>Nature Biotechnology</i> , 2012, 30, 434-439.	17.5	1,226
4	Shotgun metagenomics, from sampling to analysis. <i>Nature Biotechnology</i> , 2017, 35, 833-844.	17.5	1,196
5	Real-time, portable genome sequencing for Ebola surveillance. <i>Nature</i> , 2016, 530, 228-232.	27.8	1,179
6	A complete bacterial genome assembled de novo using only nanopore sequencing data. <i>Nature Methods</i> , 2015, 12, 733-735.	19.0	1,176
7	Genomics and epidemiology of the P.1 SARS-CoV-2 lineage in Manaus, Brazil. <i>Science</i> , 2021, 372, 815-821.	12.6	1,125
8	Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England. <i>Nature</i> , 2021, 593, 266-269.	27.8	1,001
9	Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples. <i>Nature Protocols</i> , 2017, 12, 1261-1276.	12.0	898
10	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
11	An amplicon-based sequencing framework for accurately measuring intrahost virus diversity using PrimalSeq and iVar. <i>Genome Biology</i> , 2019, 20, 8.	8.8	712
12	Telomere-to-telomere assembly of a complete human X chromosome. <i>Nature</i> , 2020, 585, 79-84.	27.8	549
13	Towards a genomics-informed, real-time, global pathogen surveillance system. <i>Nature Reviews Genetics</i> , 2018, 19, 9-20.	16.3	505
14	Evolution and epidemic spread of SARS-CoV-2 in Brazil. <i>Science</i> , 2020, 369, 1255-1260.	12.6	454
15	Nanopore native RNA sequencing of a human poly(A) transcriptome. <i>Nature Methods</i> , 2019, 16, 1297-1305.	19.0	411
16	Poretools: a toolkit for analyzing nanopore sequence data. <i>Bioinformatics</i> , 2014, 30, 3399-3401.	4.1	404
17	Open-Source Genomic Analysis of Shiga-Toxin-Producing <i>E. coli</i> O104:H4. <i>New England Journal of Medicine</i> , 2011, 365, 718-724.	27.0	392
18	High-throughput bacterial genome sequencing: an embarrassment of choice, a world of opportunity. <i>Nature Reviews Microbiology</i> , 2012, 10, 599-606.	28.6	367

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19	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017, 544, 309-315.	27.8	346
20	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , 2021, 371, 708-712.	12.6	335
21	Coast-to-Coast Spread of SARS-CoV-2 during the Early Epidemic in the United States. <i>Cell</i> , 2020, 181, 990-996.e5.	28.9	321
22	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , 2017, 546, 401-405.	27.8	298
23	A Culture-Independent Sequence-Based Metagenomics Approach to the Investigation of an Outbreak of Shiga-Toxigenic <i>Escherichia coli</i> O104:H4. <i>JAMA - Journal of the American Medical Association</i> , 2013, 309, 1502.	7.4	290
24	Co-infections: potentially lethal and unexplored in COVID-19. <i>Lancet Microbe</i> , The, 2020, 1, e11.	7.3	279
25	Rapid draft sequencing and real-time nanopore sequencing in a hospital outbreak of <i>Salmonella</i> . <i>Genome Biology</i> , 2015, 16, 114.	8.8	271
26	Changes in symptomatology, reinfection, and transmissibility associated with the SARS-CoV-2 variant B.1.1.7: an ecological study. <i>Lancet Public Health</i> , The, 2021, 6, e335-e345.	10.0	269
27	Twenty years of bacterial genome sequencing. <i>Nature Reviews Microbiology</i> , 2015, 13, 787-794.	28.6	246
28	Ultra-deep, long-read nanopore sequencing of mock microbial community standards. <i>GigaScience</i> , 2019, 8, .	6.4	209
29	A reference bacterial genome dataset generated on the MinION, a portable single-molecule nanopore sequencer. <i>GigaScience</i> , 2014, 3, 22.	6.4	208
30	Resurgence of Ebola Virus Disease in Guinea Linked to a Survivor With Virus Persistence in Seminal Fluid for More Than 500 Days. <i>Clinical Infectious Diseases</i> , 2016, 63, 1353-1356.	5.8	201
31	Defining bacterial species in the genomic era: insights from the genus <i>Acinetobacter</i> . <i>BMC Microbiology</i> , 2012, 12, 302.	3.3	188
32	Mobile real-time surveillance of Zika virus in Brazil. <i>Genome Medicine</i> , 2016, 8, 97.	8.2	182
33	Generation and transmission of interlineage recombinants in the SARS-CoV-2 pandemic. <i>Cell</i> , 2021, 184, 5179-5188.e8.	28.9	182
34	Extreme Genetic Fragility of the HIV-1 Capsid. <i>PLoS Pathogens</i> , 2013, 9, e1003461.	4.7	178
35	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
36	Eighteenth-century genomes show that mixed infections were common at time of peak tuberculosis in Europe. <i>Nature Communications</i> , 2015, 6, 6717.	12.8	165

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37	Identification of Novel Imidazo[1,2-a]pyridine Inhibitors Targeting M. tuberculosis QcrB. <i>PLoS ONE</i> , 2012, 7, e52951.	2.5	162
38	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. <i>Science</i> , 2021, 373, 889-895.	12.6	142
39	High-throughput sequencing and clinical microbiology: progress, opportunities and challenges. <i>Current Opinion in Microbiology</i> , 2010, 13, 625-631.	5.1	135
40	Successful test launch for nanopore sequencing. <i>Nature Methods</i> , 2015, 12, 303-304.	19.0	129
41	Real-time digital pathogen surveillance – the time is now. <i>Genome Biology</i> , 2015, 16, 155.	8.8	123
42	Tetrahydropyrazolo[1,5-a]Pyrimidine-3-Carboxamide and N-Benzyl-6,7-Dihydrospiro[Piperidine-4,4-Thieno[3,2-c]Pyran] Analogues with Bactericidal Efficacy against <i>Mycobacterium tuberculosis</i> Targeting MmpL3. <i>PLoS ONE</i> , 2013, 8, e60933.	2.5	123
43	xBASE2: a comprehensive resource for comparative bacterial genomics. <i>Nucleic Acids Research</i> , 2007, 36, D543-D546.	14.5	119
44	Parallel evolutionary pathways to antibiotic resistance selected by biocide exposure. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 2241-2248.	3.0	116
45	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
46	Seeking the source of <i>Pseudomonas aeruginosa</i> infections in a recently opened hospital: an observational study using whole-genome sequencing. <i>BMJ Open</i> , 2014, 4, e006278.	1.9	104
47	Treatment of COVID-19 with remdesivir in the absence of humoral immunity: a case report. <i>Nature Communications</i> , 2020, 11, 6385.	12.8	103
48	A Pilot Integrative Analysis of Colonic Gene Expression, Gut Microbiota, and Immune Infiltration in Primary Sclerosing Cholangitis-Inflammatory Bowel Disease: Association of Disease With Bile Acid Pathways. <i>Journal of Crohn's and Colitis</i> , 2020, 14, 935-947.	1.3	81
49	Importation and early local transmission of COVID-19 in Brazil, 2020. <i>Revista Do Instituto De Medicina Tropical De Sao Paulo</i> , 2020, 62, e30.	1.1	80
50	Genomic, epidemiological and digital surveillance of Chikungunya virus in the Brazilian Amazon. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007065.	3.0	75
51	Identification of KasA as the cellular target of an anti-tubercular scaffold. <i>Nature Communications</i> , 2016, 7, 12581.	12.8	72
52	Ebola Virus Persistence in Breast Milk After No Reported Illness: A Likely Source of Virus Transmission From Mother to Child. <i>Clinical Infectious Diseases</i> , 2016, 64, ciw793.	5.8	70
53	An abundance of bacterial ADP-ribosyltransferases – implications for the origin of exotoxins and their human homologues. <i>Trends in Microbiology</i> , 2001, 9, 302-307.	7.7	64
54	CLIMB-COVID: continuous integration supporting decentralised sequencing for SARS-CoV-2 genomic surveillance. <i>Genome Biology</i> , 2021, 22, 196.	8.8	53

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55	The Complete Genome and Proteome of <i>Laribacter hongkongensis</i> Reveal Potential Mechanisms for Adaptations to Different Temperatures and Habitats. <i>PLoS Genetics</i> , 2009, 5, e1000416.	3.5	52
56	Complete Genome Sequence of the Crohn's Disease-Associated Adherent-Invasive <i>Escherichia coli</i> Strain HM605. <i>Journal of Bacteriology</i> , 2011, 193, 4540-4540.	2.2	50
57	Microbial TIR domains: not necessarily agents of subversion?. <i>Trends in Microbiology</i> , 2009, 17, 393-398.	7.7	49
58	Characterization of mutations in the <i>PAS</i> domain of the <i>EvgS</i> sensor kinase selected by laboratory evolution for acid resistance in <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2014, 93, 911-927.	2.5	48
59	Inhibiting mycobacterial tryptophan synthase by targeting the inter-subunit interface. <i>Scientific Reports</i> , 2017, 7, 9430.	3.3	48
60	Mycobacterial Dihydrofolate Reductase Inhibitors Identified Using Chemogenomic Methods and In Vitro Validation. <i>PLoS ONE</i> , 2015, 10, e0121492.	2.5	40
61	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. <i>Cell Reports</i> , 2020, 30, 2275-2283.e7.	6.4	37
62	Next-Generation Sequencing—the Promise and Perils of Charting the Great Microbial Unknown. <i>Microbial Ecology</i> , 2009, 57, 1-3.	2.8	35
63	Bacterial flagellar diversity and evolution: seek simplicity and distrust it?. <i>Trends in Microbiology</i> , 2009, 17, 1-5.	7.7	34
64	Sequencing a piece of history: complete genome sequence of the original <i>Escherichia coli</i> strain. <i>Microbial Genomics</i> , 2017, 3, mgen000106.	2.0	33
65	Deletions in a ribosomal protein-coding gene are associated with tigecycline resistance in <i>Enterococcus faecium</i> . <i>International Journal of Antimicrobial Agents</i> , 2015, 46, 572-575.	2.5	32
66	Biochemical and Structural Characterization of Mycobacterial Aspartyl-tRNA Synthetase AspS, a Promising TB Drug Target. <i>PLoS ONE</i> , 2014, 9, e113568.	2.5	31
67	Genomic detection of a virus lineage replacement event of dengue virus serotype 2 in Brazil, 2019. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2020, 115, e190423.	1.6	30
68	Reply to “Errors in long-read assemblies can critically affect protein prediction”. <i>Nature Biotechnology</i> , 2019, 37, 127-128.	17.5	29
69	Screening faecal microbiota transplant donors for SARS-CoV-2 by molecular testing of stool is the safest way forward. <i>The Lancet Gastroenterology and Hepatology</i> , 2020, 5, 531.	8.1	29
70	Genome Sequences of Three <i>Acinetobacter baumannii</i> Strains Assigned to the Multilocus Sequence Typing Genotypes ST2, ST25, and ST78. <i>Journal of Bacteriology</i> , 2011, 193, 2359-2360.	2.2	28
71	Post-acute COVID-19 associated with evidence of bystander T-cell activation and a recurring antibiotic-resistant bacterial pneumonia. <i>ELife</i> , 2020, 9, .	6.0	26
72	Calculating Orthologs in Bacteria and Archaea: A Divide and Conquer Approach. <i>PLoS ONE</i> , 2011, 6, e28388.	2.5	24

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73	Clonal Expansion within Pneumococcal Serotype 6C after Use of Seven-Valent Vaccine. <i>PLoS ONE</i> , 2013, 8, e64731.	2.5	21
74	Unusual Ebola Virus Chain of Transmission, Conakry, Guinea, 2014–2015. <i>Emerging Infectious Diseases</i> , 2016, 22, 2149-2152.	4.3	21
75	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
76	Are diagnostic and public health bacteriology ready to become branches of genomic medicine?. <i>Genome Medicine</i> , 2011, 3, 53.	8.2	20
77	Evaluation of full-length nanopore 16S sequencing for detection of pathogens in microbial keratitis. <i>PeerJ</i> , 2021, 9, e10778.	2.0	18
78	Staphylococcal species heterogeneity in the nasal microbiome following antibiotic prophylaxis revealed by tuf gene deep sequencing. <i>Microbiome</i> , 2016, 4, 63.	11.1	15
79	Transmission, adaptation and geographical spread of the <i>Pseudomonas aeruginosa</i> Liverpool epidemic strain. <i>Microbial Genomics</i> , 2021, 7, .	2.0	12
80	A multi-targeting pre-clinical candidate against drug-resistant tuberculosis. <i>Tuberculosis</i> , 2021, 129, 102104.	1.9	12
81	Observations of SARS-CoV-2 variant of concern B.1.1.7 at the UK's largest hospital trust. <i>Journal of Infection</i> , 2021, 83, e21-e23.	3.3	12
82	Rapid viral metagenomics using SMART-9N amplification and nanopore sequencing. <i>Wellcome Open Research</i> , 0, 6, 241.	1.8	10
83	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission. <i>Nature Communications</i> , 2022, 13, 1012.	12.8	10
84	Gut Dysbiosis in Ocular Mucous Membrane Pemphigoid. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 780354.	3.9	10
85	STOP-Colitis pilot trial protocol: a prospective, open-label, randomised pilot study to assess two possible routes of faecal microbiota transplant delivery in patients with ulcerative colitis. <i>BMJ Open</i> , 2019, 9, e030659.	1.9	9
86	Molecular and genomic investigation of an urban outbreak of dengue virus serotype 2 in Angola, 2017–2019. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010255.	3.0	9
87	Development of a whole-cell high-throughput phenotypic screen to identify inhibitors of mycobacterial amino acid biosynthesis. <i>FASEB BioAdvances</i> , 2019, 1, 246-254.	2.4	7
88	Details of SARS-CoV-2 reinfections at a major UK tertiary centre. <i>Journal of Infection</i> , 2021, 82, e29-e30.	3.3	7
89	Voices in methods development. <i>Nature Methods</i> , 2019, 16, 945-951.	19.0	5
90	Complete Closed Genome Sequence of Nontoxigenic Invasive <i>Corynebacterium diphtheriae</i> bv. mitis Strain ISS 3319. <i>Genome Announcements</i> , 2018, 6, .	0.8	3

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91	EntrezAJAX: direct web browser access to the Entrez Programming Utilities. Source Code for Biology and Medicine, 2010, 5, 6.	1.7	2
92	Anti-tubercular derivatives of rhein require activation by the monoglyceride lipase Rv0183. Cell Surface, 2020, 6, 100040.	3.0	2
93	O9â€¦STOP-colitis pilot: prospective, open-label, randomised study comparing nasogastric versus colonic FMT delivery in ulcerative colitis. , 2021, , .		1
94	A32â€¦Genomic surveillance of Zika virus transmission in the Amazonas State, Brazil. Virus Evolution, 2019, 5, .	4.9	0
95	P136â€¦Immunomodulatory mechanisms of FMT is associated with clinical response in UC â€œ results from STOP-Colitis. , 2021, , .		0