

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	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
2	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission. <i>Nature Communications</i> , 2022, 13, 1012.	12.8	10
3	Gut Dysbiosis in Ocular Mucous Membrane Pemphigoid. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 780354.	3.9	10
4	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
5	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
6	O9-STOP-colitis pilot: prospective, open-label, randomised study comparing nasogastric versus colonic FMT delivery in ulcerative colitis. , 2021, , .		1
7	P136-Immunomodulatory mechanisms of FMT is associated with clinical response in UC - results from STOP-Colitis. , 2021, , .		0
8	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , 2021, 371, 708-712.	12.6	335
9	Evaluation of full-length nanopore 16S sequencing for detection of pathogens in microbial keratitis. <i>PeerJ</i> , 2021, 9, e10778.	2.0	18
10	Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England. <i>Nature</i> , 2021, 593, 266-269.	27.8	1,001
11	Transmission, adaptation and geographical spread of the <i>Pseudomonas aeruginosa</i> Liverpool epidemic strain. <i>Microbial Genomics</i> , 2021, 7, .	2.0	12
12	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
13	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
14	Details of SARS-CoV-2 reinfections at a major UK tertiary centre. <i>Journal of Infection</i> , 2021, 82, e29-e30.	3.3	7
15	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. <i>Science</i> , 2021, 373, 889-895.	12.6	142
16	CLIMB-COVID: continuous integration supporting decentralised sequencing for SARS-CoV-2 genomic surveillance. <i>Genome Biology</i> , 2021, 22, 196.	8.8	53
17	A multi-targeting pre-clinical candidate against drug-resistant tuberculosis. <i>Tuberculosis</i> , 2021, 129, 102104.	1.9	12
18	Generation and transmission of interlineage recombinants in the SARS-CoV-2 pandemic. <i>Cell</i> , 2021, 184, 5179-5188.e8.	28.9	182

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19	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
20	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
21	Evolution and epidemic spread of SARS-CoV-2 in Brazil. <i>Science</i> , 2020, 369, 1255-1260.	12.6	454
22	Telomere-to-telomere assembly of a complete human X chromosome. <i>Nature</i> , 2020, 585, 79-84.	27.8	549
23	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
24	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
25	Anti-tubercular derivatives of rhein require activation by the monoglyceride lipase Rv0183. <i>Cell Surface</i> , 2020, 6, 100040.	3.0	2
26	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. <i>Cell Reports</i> , 2020, 30, 2275-2283.e7.	6.4	37
27	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
28	Co-infections: potentially lethal and unexplored in COVID-19. <i>Lancet Microbe</i> , The, 2020, 1, e11.	7.3	279
29	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
30	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
31	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
32	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
33	Genomic surveillance of Zika virus transmission in the Amazonas State, Brazil. <i>Virus Evolution</i> , 2019, 5, .	4.9	0
34	Reply to "Errors in long-read assemblies can critically affect protein prediction". <i>Nature Biotechnology</i> , 2019, 37, 127-128.	17.5	29
35	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
36	Ultra-deep, long-read nanopore sequencing of mock microbial community standards. <i>GigaScience</i> , 2019, 8, .	6.4	209

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37	Genomic, epidemiological and digital surveillance of Chikungunya virus in the Brazilian Amazon. PLoS Neglected Tropical Diseases, 2019, 13, e0007065.	3.0	75
38	Voices in methods development. Nature Methods, 2019, 16, 945-951.	19.0	5
39	Nanopore native RNA sequencing of a human poly(A) transcriptome. Nature Methods, 2019, 16, 1297-1305.	19.0	411
40	An amplicon-based sequencing framework for accurately measuring intrahost virus diversity using PrimalSeq and iVar. Genome Biology, 2019, 20, 8.	8.8	712
41	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. BMJ Open, 2019, 9, e030659.	1.9	9
42	Nanopore sequencing and assembly of a human genome with ultra-long reads. Nature Biotechnology, 2018, 36, 338-345.	17.5	1,443
43	Towards a genomics-informed, real-time, global pathogen surveillance system. Nature Reviews Genetics, 2018, 19, 9-20.	16.3	505
44	Complete Closed Genome Sequence of Nontoxigenic Invasive Corynebacterium diphtheriae bv. mitis Strain ISS 3319. Genome Announcements, 2018, 6, .	0.8	3
45	Virus genomes reveal factors that spread and sustained the Ebola epidemic. Nature, 2017, 544, 309-315.	27.8	346
46	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. Nature, 2017, 546, 401-405.	27.8	298
47	Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples. Nature Protocols, 2017, 12, 1261-1276.	12.0	898
48	Shotgun metagenomics, from sampling to analysis. Nature Biotechnology, 2017, 35, 833-844.	17.5	1,196
49	Inhibiting mycobacterial tryptophan synthase by targeting the inter-subunit interface. Scientific Reports, 2017, 7, 9430.	3.3	48
50	Sequencing a piece of history: complete genome sequence of the original Escherichia coli strain. Microbial Genomics, 2017, 3, mgen000106.	2.0	33
51	Unusual Ebola Virus Chain of Transmission, Conakry, Guinea, 2014-2015. Emerging Infectious Diseases, 2016, 22, 2149-2152.	4.3	21
52	Mobile real-time surveillance of Zika virus in Brazil. Genome Medicine, 2016, 8, 97.	8.2	182
53	Staphylococcal species heterogeneity in the nasal microbiome following antibiotic prophylaxis revealed by tuf gene deep sequencing. Microbiome, 2016, 4, 63.	11.1	15
54	Ebola Virus Persistence in Breast Milk After No Reported Illness: A Likely Source of Virus Transmission From Mother to Child. Clinical Infectious Diseases, 2016, 64, ciw793.	5.8	70

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55	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
56	Identification of KasA as the cellular target of an anti-tubercular scaffold. <i>Nature Communications</i> , 2016, 7, 12581.	12.8	72
57	Real-time, portable genome sequencing for Ebola surveillance. <i>Nature</i> , 2016, 530, 228-232.	27.8	1,179
58	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
59	Real-time digital pathogen surveillance – the time is now. <i>Genome Biology</i> , 2015, 16, 155.	8.8	123
60	Mycobacterial Dihydrofolate Reductase Inhibitors Identified Using Chemogenomic Methods and In Vitro Validation. <i>PLoS ONE</i> , 2015, 10, e0121492.	2.5	40
61	A complete bacterial genome assembled de novo using only nanopore sequencing data. <i>Nature Methods</i> , 2015, 12, 733-735.	19.0	1,176
62	Rapid draft sequencing and real-time nanopore sequencing in a hospital outbreak of Salmonella. <i>Genome Biology</i> , 2015, 16, 114.	8.8	271
63	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
64	Successful test launch for nanopore sequencing. <i>Nature Methods</i> , 2015, 12, 303-304.	19.0	129
65	Parallel evolutionary pathways to antibiotic resistance selected by biocide exposure. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 2241-2248.	3.0	116
66	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
67	Twenty years of bacterial genome sequencing. <i>Nature Reviews Microbiology</i> , 2015, 13, 787-794.	28.6	246
68	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
69	Characterization of mutations in the PAS domain of the EvgS 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
70	Poretools: a toolkit for analyzing nanopore sequence data. <i>Bioinformatics</i> , 2014, 30, 3399-3401.	4.1	404
71	A reference bacterial genome dataset generated on the MinION, a portable single-molecule nanopore sequencer. <i>GigaScience</i> , 2014, 3, 22.	6.4	208
72	Binning metagenomic contigs by coverage and composition. <i>Nature Methods</i> , 2014, 11, 1144-1146.	19.0	1,709

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73	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
74	A Culture-Independent Sequence-Based Metagenomics Approach to the Investigation of an Outbreak of Shiga-Toxicogenic <i>Escherichia coli</i> O104:H4. <i>JAMA - Journal of the American Medical Association</i> , 2013, 309, 1502.	7.4	290
75	Extreme Genetic Fragility of the HIV-1 Capsid. <i>PLoS Pathogens</i> , 2013, 9, e1003461.	4.7	178
76	Clonal Expansion within Pneumococcal Serotype 6C after Use of Seven-Valent Vaccine. <i>PLoS ONE</i> , 2013, 8, e64731.	2.5	21
77	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
78	Identification of Novel Imidazo[1,2-a]pyridine Inhibitors Targeting <i>M. tuberculosis</i> QcrB. <i>PLoS ONE</i> , 2012, 7, e52951.	2.5	162
79	Defining bacterial species in the genomic era: insights from the genus <i>Acinetobacter</i> . <i>BMC Microbiology</i> , 2012, 12, 302.	3.3	188
80	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
81	Performance comparison of benchtop high-throughput sequencing platforms. <i>Nature Biotechnology</i> , 2012, 30, 434-439.	17.5	1,226
82	Are diagnostic and public health bacteriology ready to become branches of genomic medicine?. <i>Genome Medicine</i> , 2011, 3, 53.	8.2	20
83	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
84	Calculating Orthologs in Bacteria and Archaea: A Divide and Conquer Approach. <i>PLoS ONE</i> , 2011, 6, e28388.	2.5	24
85	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
86	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
87	EntrezAJAX: direct web browser access to the Entrez Programming Utilities. <i>Source Code for Biology and Medicine</i> , 2010, 5, 6.	1.7	2
88	High-throughput sequencing and clinical microbiology: progress, opportunities and challenges. <i>Current Opinion in Microbiology</i> , 2010, 13, 625-631.	5.1	135
89	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
90	Next-Generation Sequencing—the Promise and Perils of Charting the Great Microbial Unknown. <i>Microbial Ecology</i> , 2009, 57, 1-3.	2.8	35

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91	Bacterial flagellar diversity and evolution: seek simplicity and distrust it?. Trends in Microbiology, 2009, 17, 1-5.	7.7	34
92	Microbial TIR domains: not necessarily agents of subversion?. Trends in Microbiology, 2009, 17, 393-398.	7.7	49
93	xBASE2: a comprehensive resource for comparative bacterial genomics. Nucleic Acids Research, 2007, 36, D543-D546.	14.5	119
94	An abundance of bacterial ADP-ribosyltransferases â€” implications for the origin of exotoxins and their human homologues. Trends in Microbiology, 2001, 9, 302-307.	7.7	64
95	Rapid viral metagenomics using SMART-9N amplification and nanopore sequencing. Wellcome Open Research, 0, 6, 241.	1.8	10