

Nicholas J Loman

List of Publications by Citations

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

108
papers

14,886
citations

51
h-index

122
g-index

129
ext. papers

20,563
ext. citations

17.2
avg. IF

6.77
L-index

#	Paper	IF	Citations
108	Performance comparison of benchtop high-throughput sequencing platforms. <i>Nature Biotechnology</i> , 2012 , 30, 434-9	44.5	1035
107	Nanopore sequencing and assembly of a human genome with ultra-long reads. <i>Nature Biotechnology</i> , 2018 , 36, 338-345	44.5	968
106	Binning metagenomic contigs by coverage and composition. <i>Nature Methods</i> , 2014 , 11, 1144-6	21.6	872
105	Real-time, portable genome sequencing for Ebola surveillance. <i>Nature</i> , 2016 , 530, 228-232	50.4	845
104	A complete bacterial genome assembled de novo using only nanopore sequencing data. <i>Nature Methods</i> , 2015 , 12, 733-5	21.6	783
103	Shotgun metagenomics, from sampling to analysis. <i>Nature Biotechnology</i> , 2017 , 35, 833-844	44.5	643
102	Genomics and epidemiology of the P.1 SARS-CoV-2 lineage in Manaus, Brazil. <i>Science</i> , 2021 , 372, 815-821	33.3	603
101	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	18.8	529
100	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , 2021 , 184, 64-75.e11	56.2	518
99	Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England. <i>Nature</i> , 2021 , 593, 266-269	50.4	452
98	Open-source genomic analysis of Shiga-toxin-producing E. coli O104:H4. <i>New England Journal of Medicine</i> , 2011 , 365, 718-24	59.2	340
97	High-throughput bacterial genome sequencing: an embarrassment of choice, a world of opportunity. <i>Nature Reviews Microbiology</i> , 2012 , 10, 599-606	22.2	326
96	Poretools: a toolkit for analyzing nanopore sequence data. <i>Bioinformatics</i> , 2014 , 30, 3399-401	7.2	313
95	An amplicon-based sequencing framework for accurately measuring intrahost virus diversity using PrimalSeq and iVar. <i>Genome Biology</i> , 2019 , 20, 8	18.3	308
94	Towards a genomics-informed, real-time, global pathogen surveillance system. <i>Nature Reviews Genetics</i> , 2018 , 19, 9-20	30.1	301
93	Evolution and epidemic spread of SARS-CoV-2 in Brazil. <i>Science</i> , 2020 , 369, 1255-1260	33.3	277
92	Telomere-to-telomere assembly of a complete human X chromosome. <i>Nature</i> , 2020 , 585, 79-84	50.4	269

91	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017 , 544, 309-315	50.4	238
90	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , 2017 , 546, 401-405	50.4	235
89	Coast-to-Coast Spread of SARS-CoV-2 during the Early Epidemic in the United States. <i>Cell</i> , 2020 , 181, 990-996.e5	56.2	235
88	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, 1502-10	27.4	226
87	Rapid draft sequencing and real-time nanopore sequencing in a hospital outbreak of <i>Salmonella</i> . <i>Genome Biology</i> , 2015 , 16, 114	18.3	211
86	Nanopore native RNA sequencing of a human poly(A) transcriptome. <i>Nature Methods</i> , 2019 , 16, 1297-1305	35.6	198
85	Co-infections: potentially lethal and unexplored in COVID-19. <i>Lancet Microbe, The</i> , 2020 , 1, e11	22.2	187
84	Twenty years of bacterial genome sequencing. <i>Nature Reviews Microbiology</i> , 2015 , 13, 787-94	22.2	181
83	A reference bacterial genome dataset generated on the MinION portable single-molecule nanopore sequencer. <i>GigaScience</i> , 2014 , 3, 22	7.6	168
82	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , 2021 , 371, 708-712	33.3	159
81	Changes in symptomatology, reinfection, and transmissibility associated with the SARS-CoV-2 variant B.1.1.7: an ecological study. <i>Lancet Public Health, The</i> , 2021 , 6, e335-e345	22.4	146
80	Defining bacterial species in the genomic era: insights from the genus <i>Acinetobacter</i> . <i>BMC Microbiology</i> , 2012 , 12, 302	4.5	138
79	Identification of novel imidazo[1,2-a]pyridine inhibitors targeting <i>M. tuberculosis</i> QcrB. <i>PLoS ONE</i> , 2012 , 7, e52951	3.7	135
78	Extreme genetic fragility of the HIV-1 capsid. <i>PLoS Pathogens</i> , 2013 , 9, e1003461	7.6	134
77	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	11.6	134
76	Mobile real-time surveillance of Zika virus in Brazil. <i>Genome Medicine</i> , 2016 , 8, 97	14.4	130
75	Improvements to the ARTIC multiplex PCR method for SARS-CoV-2 genome sequencing using nanopore 2020 ,		128
74	Eighteenth-century genomes show that mixed infections were common at time of peak tuberculosis in Europe. <i>Nature Communications</i> , 2015 , 6, 6717	17.4	122

73	xBASE2: a comprehensive resource for comparative bacterial genomics. <i>Nucleic Acids Research</i> , 2008 , 36, D543-6	20.1	113
72	Ultra-deep, long-read nanopore sequencing of mock microbial community standards. <i>GigaScience</i> , 2019 , 8,	7.6	108
71	De novoidentification of DNA Modifications Enabled by Genome-Guided Nanopore Signal Processing		107
70	High-throughput sequencing and clinical microbiology: progress, opportunities and challenges. <i>Current Opinion in Microbiology</i> , 2010 , 13, 625-31	7.9	106
69	CLIMB (the Cloud Infrastructure for Microbial Bioinformatics): an online resource for the medical microbiology community. <i>Microbial Genomics</i> , 2016 , 2, e000086	4.4	105
68	Tetrahydropyrazolo[1,5-a]pyrimidine-3-carboxamide and N-benzyl-6R7Rdihydrospiro[piperidine-4,4Rthieno[3,2-c]pyran] analogues with bactericidal efficacy against <i>Mycobacterium tuberculosis</i> targeting MmpL3. <i>PLoS ONE</i> , 2013 , 8, e60933	3.7	103
67	Successful test launch for nanopore sequencing. <i>Nature Methods</i> , 2015 , 12, 303-4	21.6	99
66	Real-time digital pathogen surveillance - the time is now. <i>Genome Biology</i> , 2015 , 16, 155	18.3	91
65	Parallel evolutionary pathways to antibiotic resistance selected by biocide exposure. <i>Journal of Antimicrobial Chemotherapy</i> , 2015 , 70, 2241-8	5.1	85
64	A32 Genomic surveillance of Zika virus transmission in the Amazonas State, Brazil. <i>Virus Evolution</i> , 2019 , 5,	3.7	78
63	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	3	69
62	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> , 2017 , 64, 513-516	11.6	63
61	Treatment of COVID-19 with remdesivir in the absence of humoral immunity: a case report. <i>Nature Communications</i> , 2020 , 11, 6385	17.4	62
60	An abundance of bacterial ADP-ribosyltransferases--implications for the origin of exotoxins and their human homologues. <i>Trends in Microbiology</i> , 2001 , 9, 302-7; discussion 308	12.4	60
59	Genomics and epidemiology of a novel SARS-CoV-2 lineage in Manaus, Brazil 2021 ,		53
58	Identification of KasA as the cellular target of an anti-tubercular scaffold. <i>Nature Communications</i> , 2016 , 7, 12581	17.4	51
57	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	2.2	50
56	Nanopore native RNA sequencing of a human poly(A) transcriptome		49

55	Generation and transmission of interlineage recombinants in the SARS-CoV-2 pandemic. <i>Cell</i> , 2021 , 184, 5179-5188.e8	56.2	48
54	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	6	45
53	Microbial TIR domains: not necessarily agents of subversion?. <i>Trends in Microbiology</i> , 2009 , 17, 393-8	12.4	45
52	Telomere-to-telomere assembly of a complete human X chromosome		45
51	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. <i>Science</i> , 2021 , 373, 889-895	33.3	41
50	Genomic, epidemiological and digital surveillance of Chikungunya virus in the Brazilian Amazon. <i>PLoS Neglected Tropical Diseases</i> , 2019 , 13, e0007065	4.8	37
49	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 Crohns and Colitis</i> , 2020 , 14, 935-947	1.5	36
48	Inhibiting mycobacterial tryptophan synthase by targeting the inter-subunit interface. <i>Scientific Reports</i> , 2017 , 7, 9430	4.9	34
47	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	3.5	34
46	Mycobacterial dihydrofolate reductase inhibitors identified using chemogenomic methods and in vitro validation. <i>PLoS ONE</i> , 2015 , 10, e0121492	3.7	32
45	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, 911-27	4.1	32
44	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. <i>Science</i> , 2021 , 374, eabl9551	33.3	31
43	Bacterial flagellar diversity and evolution: seek simplicity and distrust it?. <i>Trends in Microbiology</i> , 2009 , 17, 1-5	12.4	28
42	Next-generation sequencing--the promise and perils of charting the great microbial unknown. <i>Microbial Ecology</i> , 2009 , 57, 1-3	4.4	27
41	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. <i>Cell Reports</i> , 2020 , 30, 2275-2283.e7	10.6	24
40	Biochemical and structural characterization of mycobacterial aspartyl-tRNA synthetase AspS, a promising TB drug target. <i>PLoS ONE</i> , 2014 , 9, e113568	3.7	23
39	Sequencing a piece of history: complete genome sequence of the original strain. <i>Microbial Genomics</i> , 2017 , 3, mgen000106	4.4	23
38	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	18.8	23

37	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, 572-5	14.3	20
36	Clonal expansion within pneumococcal serotype 6C after use of seven-valent vaccine. <i>PLoS ONE</i> , 2013 , 8, e64731	3.7	20
35	Coast-to-coast spread of SARS-CoV-2 in the United States revealed by genomic epidemiology 2020 ,		19
34	Reply to Errors in long-read assemblies can critically affect protein prediction <i>Nature Biotechnology</i> , 2019 , 37, 127-128	44.5	18
33	Are diagnostic and public health bacteriology ready to become branches of genomic medicine?. <i>Genome Medicine</i> , 2011 , 3, 53	14.4	17
32	Unusual Ebola Virus Chain of Transmission, Conakry, Guinea, 2014-2015. <i>Emerging Infectious Diseases</i> , 2016 , 22, 2149-2152	10.2	17
31	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, 2359-60	3.5	16
30	Post-acute COVID-19 associated with evidence of bystander T-cell activation and a recurring antibiotic-resistant bacterial pneumonia. <i>ELife</i> , 2020 , 9,	8.9	14
29	Staphylococcal species heterogeneity in the nasal microbiome following antibiotic prophylaxis revealed by <i>tuf</i> gene deep sequencing. <i>Microbiome</i> , 2016 , 4, 63	16.6	12
28	MAJORA: Continuous integration supporting decentralised sequencing for SARS-CoV-2 genomic surveillance		11
27	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	2.6	10
26	Calculating orthologs in bacteria and Archaea: a divide and conquer approach. <i>PLoS ONE</i> , 2011 , 6, e28388	3.7	9
25	Establishment & lineage dynamics of the SARS-CoV-2 epidemic in the UK		9
24	An amplicon-based sequencing framework for accurately measuring intrahost virus diversity using PrimalSeq and iVar		7
23	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> , 2021 ,	9.5	7
22	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	2.8	6
21	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	3	6
20	Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples		6

19	Evolution and epidemic spread of SARS-CoV-2 in Brazil		6
18	Evaluation of full-length nanopore 16S sequencing for detection of pathogens in microbial keratitis. <i>PeerJ</i> , 2021 , 9, e10778	3.1	6
17	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	18.9	6
16	Ultra-deep, long-read nanopore sequencing of mock microbial community standards		5
15	Transmission, adaptation and geographical spread of the Liverpool epidemic strain. <i>Microbial Genomics</i> , 2021 , 7,	4.4	5
14	CLIMB (the Cloud Infrastructure for Microbial Bioinformatics): an online resource for the medical microbiology community		4
13	Details of SARS-CoV-2 reinfections at a major UK tertiary centre. <i>Journal of Infection</i> , 2021 , 82, e29-e30	18.9	4
12	Context-specific emergence and growth of the SARS-CoV-2 Delta variant. 2021 ,		3
11	Virus genomes reveal the factors that spread and sustained the West African Ebola epidemic		2
10	Complete Closed Genome Sequence of Nontoxigenic Invasive <i>bv. mitis</i> Strain ISS 3319. <i>Genome Announcements</i> , 2018 , 6,		2
9	A multi-targeting pre-clinical candidate against drug-resistant tuberculosis. <i>Tuberculosis</i> , 2021 , 129, 102104	10.4	2
8	Rapid viral metagenomics using SMART-9N amplification and nanopore sequencing. <i>Wellcome Open Research</i> , 6 , 241	4.8	2
7	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission.. <i>Nature Communications</i> , 2022 , 13, 1012	17.4	2
6	The origins and molecular evolution of SARS-CoV-2 lineage B.1.1.7 in the UK		2
5	Context-specific emergence and growth of the SARS-CoV-2 Delta variant. 2021 ,		2
4	Anti-tubercular derivatives of rhein require activation by the monoglyceride lipase Rv0183. <i>Cell Surface</i> , 2020 , 6, 100040	4.8	1
3	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	4.8	1
2	EntrezAJAX: direct web browser access to the Entrez Programming Utilities. <i>Source Code for Biology and Medicine</i> , 2010 , 5, 6	1.9	0

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