

# Nicholas J Loman

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/7106203/nicholas-j-loman-publications-by-year.pdf>

**Version:** 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission.. <i>Nature Communications</i> , <b>2022</b> , 13, 1012	17.4	2
107	Gut Dysbiosis in Ocular Mucous Membrane Pemphigoid.. <i>Frontiers in Cellular and Infection Microbiology</i> , <b>2022</b> , 12, 780354	5.9	0
106	Molecular and genomic investigation of an urban outbreak of dengue virus serotype 2 in Angola, 2017-2019.. <i>PLoS Neglected Tropical Diseases</i> , <b>2022</b> , 16, e0010255	4.8	1
105	Context-specific emergence and growth of the SARS-CoV-2 Delta variant. <b>2021</b> ,		3
104	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. <i>Science</i> , <b>2021</b> , 374, eabl9551	33.3	31
103	Genomics and epidemiology of a novel SARS-CoV-2 lineage in Manaus, Brazil <b>2021</b> ,		53
102	Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England. <i>Nature</i> , <b>2021</b> , 593, 266-269	50.4	452
101	Transmission, adaptation and geographical spread of the Liverpool epidemic strain. <i>Microbial Genomics</i> , <b>2021</b> , 7,	4.4	5
100	Genomics and epidemiology of the P.1 SARS-CoV-2 lineage in Manaus, Brazil. <i>Science</i> , <b>2021</b> , 372, 815-821	33.3	603
99	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> , <b>2021</b> , 6, e335-e345	22.4	146
98	Details of SARS-CoV-2 reinfections at a major UK tertiary centre. <i>Journal of Infection</i> , <b>2021</b> , 82, e29-e30	18.9	4
97	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. <i>Science</i> , <b>2021</b> , 373, 889-895	33.3	41
96	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , <b>2021</b> , 184, 64-75.e11	56.2	518
95	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , <b>2021</b> , 371, 708-712	33.3	159
94	Evaluation of full-length nanopore 16S sequencing for detection of pathogens in microbial keratitis. <i>PeerJ</i> , <b>2021</b> , 9, e10778	3.1	6
93	A multi-targeting pre-clinical candidate against drug-resistant tuberculosis. <i>Tuberculosis</i> , <b>2021</b> , 129, 102104	10.4	2
92	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> , <b>2021</b> ,	9.5	7

91	Generation and transmission of interlineage recombinants in the SARS-CoV-2 pandemic. <i>Cell</i> , <b>2021</b> , 184, 5179-5188.e8	56.2	48
90	Observations of SARS-CoV-2 variant of concern B.1.1.7 at the UK's largest hospital trust. <i>Journal of Infection</i> , <b>2021</b> , 83, e21-e23	18.9	6
89	Context-specific emergence and growth of the SARS-CoV-2 Delta variant. <b>2021</b> ,		2
88	Treatment of COVID-19 with remdesivir in the absence of humoral immunity: a case report. <i>Nature Communications</i> , <b>2020</b> , 11, 6385	17.4	62
87	Coast-to-Coast Spread of SARS-CoV-2 during the Early Epidemic in the United States. <i>Cell</i> , <b>2020</b> , 181, 990-996.e5	56.2	235
86	Anti-tubercular derivatives of rhein require activation by the monoglyceride lipase Rv0183. <i>Cell Surface</i> , <b>2020</b> , 6, 100040	4.8	1
85	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. <i>Cell Reports</i> , <b>2020</b> , 30, 2275-2283.e7	10.6	24
84	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> , <b>2020</b> , 14, 935-947	1.5	36
83	Co-infections: potentially lethal and unexplored in COVID-19. <i>Lancet Microbe, The</i> , <b>2020</b> , 1, e11	22.2	187
82	Genomic detection of a virus lineage replacement event of dengue virus serotype 2 in Brazil, 2019. <i>Memorias Do Instituto Oswaldo Cruz</i> , <b>2020</b> , 115, e190423	2.6	10
81	Importation and early local transmission of COVID-19 in Brazil, 2020. <i>Revista Do Instituto De Medicina Tropical De Sao Paulo</i> , <b>2020</b> , 62, e30	2.2	50
80	Post-acute COVID-19 associated with evidence of bystander T-cell activation and a recurring antibiotic-resistant bacterial pneumonia. <i>ELife</i> , <b>2020</b> , 9,	8.9	14
79	Coast-to-coast spread of SARS-CoV-2 in the United States revealed by genomic epidemiology <b>2020</b> ,		19
78	Improvements to the ARTIC multiplex PCR method for SARS-CoV-2 genome sequencing using nanopore <b>2020</b> ,		128
77	Evolution and epidemic spread of SARS-CoV-2 in Brazil. <i>Science</i> , <b>2020</b> , 369, 1255-1260	33.3	277
76	Telomere-to-telomere assembly of a complete human X chromosome. <i>Nature</i> , <b>2020</b> , 585, 79-84	50.4	269
75	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> , <b>2020</b> , 5, 531	18.8	23
74	Reply to Errors in long-read assemblies can critically affect protein prediction <i>Nature Biotechnology</i> , <b>2019</b> , 37, 127-128	44.5	18

73	Development of a whole-cell high-throughput phenotypic screen to identify inhibitors of mycobacterial amino acid biosynthesis. <i>FASEB BioAdvances</i> , <b>2019</b> , 1, 246-254	2.8	6
72	Ultra-deep, long-read nanopore sequencing of mock microbial community standards. <i>GigaScience</i> , <b>2019</b> , 8,	7.6	108
71	Genomic, epidemiological and digital surveillance of Chikungunya virus in the Brazilian Amazon. <i>PLoS Neglected Tropical Diseases</i> , <b>2019</b> , 13, e0007065	4.8	37
70	A32 Genomic surveillance of Zika virus transmission in the Amazonas State, Brazil. <i>Virus Evolution</i> , <b>2019</b> , 5,	3.7	78
69	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> , <b>2019</b> , 9, e030659	3	6
68	Nanopore native RNA sequencing of a human poly(A) transcriptome. <i>Nature Methods</i> , <b>2019</b> , 16, 1297-1305	5.6	198
67	An amplicon-based sequencing framework for accurately measuring intrahost virus diversity using PrimalSeq and iVar. <i>Genome Biology</i> , <b>2019</b> , 20, 8	18.3	308
66	Nanopore sequencing and assembly of a human genome with ultra-long reads. <i>Nature Biotechnology</i> , <b>2018</b> , 36, 338-345	44.5	968
65	Towards a genomics-informed, real-time, global pathogen surveillance system. <i>Nature Reviews Genetics</i> , <b>2018</b> , 19, 9-20	30.1	301
64	Complete Closed Genome Sequence of Nontoxigenic Invasive <i>bv. mitis</i> Strain ISS 3319. <i>Genome Announcements</i> , <b>2018</b> , 6,		2
63	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , <b>2017</b> , 544, 309-315	50.4	238
62	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , <b>2017</b> , 546, 401-405	50.4	235
61	Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples. <i>Nature Protocols</i> , <b>2017</b> , 12, 1261-1276	18.8	529
60	Shotgun metagenomics, from sampling to analysis. <i>Nature Biotechnology</i> , <b>2017</b> , 35, 833-844	44.5	643
59	Inhibiting mycobacterial tryptophan synthase by targeting the inter-subunit interface. <i>Scientific Reports</i> , <b>2017</b> , 7, 9430	4.9	34
58	Sequencing a piece of history: complete genome sequence of the original strain. <i>Microbial Genomics</i> , <b>2017</b> , 3, mgen000106	4.4	23
57	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> , <b>2017</b> , 64, 513-516	11.6	63
56	Identification of KasA as the cellular target of an anti-tubercular scaffold. <i>Nature Communications</i> , <b>2016</b> , 7, 12581	17.4	51

55	Real-time, portable genome sequencing for Ebola surveillance. <i>Nature</i> , <b>2016</b> , 530, 228-232	50.4	845
54	CLIMB (the Cloud Infrastructure for Microbial Bioinformatics): an online resource for the medical microbiology community. <i>Microbial Genomics</i> , <b>2016</b> , 2, e000086	4.4	105
53	Unusual Ebola Virus Chain of Transmission, Conakry, Guinea, 2014-2015. <i>Emerging Infectious Diseases</i> , <b>2016</b> , 22, 2149-2152	10.2	17
52	Mobile real-time surveillance of Zika virus in Brazil. <i>Genome Medicine</i> , <b>2016</b> , 8, 97	14.4	130
51	Staphylococcal species heterogeneity in the nasal microbiome following antibiotic prophylaxis revealed by tuf gene deep sequencing. <i>Microbiome</i> , <b>2016</b> , 4, 63	16.6	12
50	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> , <b>2016</b> , 63, 1353-1356	11.6	134
49	A complete bacterial genome assembled de novo using only nanopore sequencing data. <i>Nature Methods</i> , <b>2015</b> , 12, 733-5	21.6	783
48	Rapid draft sequencing and real-time nanopore sequencing in a hospital outbreak of Salmonella. <i>Genome Biology</i> , <b>2015</b> , 16, 114	18.3	211
47	Eighteenth-century genomes show that mixed infections were common at time of peak tuberculosis in Europe. <i>Nature Communications</i> , <b>2015</b> , 6, 6717	17.4	122
46	Successful test launch for nanopore sequencing. <i>Nature Methods</i> , <b>2015</b> , 12, 303-4	21.6	99
45	Parallel evolutionary pathways to antibiotic resistance selected by biocide exposure. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2015</b> , 70, 2241-8	5.1	85
44	Deletions in a ribosomal protein-coding gene are associated with tigecycline resistance in <i>Enterococcus faecium</i> . <i>International Journal of Antimicrobial Agents</i> , <b>2015</b> , 46, 572-5	14.3	20
43	Twenty years of bacterial genome sequencing. <i>Nature Reviews Microbiology</i> , <b>2015</b> , 13, 787-94	22.2	181
42	Real-time digital pathogen surveillance - the time is now. <i>Genome Biology</i> , <b>2015</b> , 16, 155	18.3	91
41	Mycobacterial dihydrofolate reductase inhibitors identified using chemogenomic methods and in vitro validation. <i>PLoS ONE</i> , <b>2015</b> , 10, e0121492	3.7	32
40	Binning metagenomic contigs by coverage and composition. <i>Nature Methods</i> , <b>2014</b> , 11, 1144-6	21.6	872
39	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> , <b>2014</b> , 4, e006278	3	69
38	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> , <b>2014</b> , 93, 911-27	4.1	32

37	Poretools: a toolkit for analyzing nanopore sequence data. <i>Bioinformatics</i> , <b>2014</b> , 30, 3399-401	7.2	313
36	A reference bacterial genome dataset generated on the MinION portable single-molecule nanopore sequencer. <i>GigaScience</i> , <b>2014</b> , 3, 22	7.6	168
35	Biochemical and structural characterization of mycobacterial aspartyl-tRNA synthetase AspS, a promising TB drug target. <i>PLoS ONE</i> , <b>2014</b> , 9, e113568	3.7	23
34	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> , <b>2013</b> , 309, 1502-10	27.4	226
33	Extreme genetic fragility of the HIV-1 capsid. <i>PLoS Pathogens</i> , <b>2013</b> , 9, e1003461	7.6	134
32	Clonal expansion within pneumococcal serotype 6C after use of seven-valent vaccine. <i>PLoS ONE</i> , <b>2013</b> , 8, e64731	3.7	20
31	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> , <b>2013</b> , 8, e60933	3.7	103
30	Defining bacterial species in the genomic era: insights from the genus <i>Acinetobacter</i> . <i>BMC Microbiology</i> , <b>2012</b> , 12, 302	4.5	138
29	High-throughput bacterial genome sequencing: an embarrassment of choice, a world of opportunity. <i>Nature Reviews Microbiology</i> , <b>2012</b> , 10, 599-606	22.2	326
28	Performance comparison of benchtop high-throughput sequencing platforms. <i>Nature Biotechnology</i> , <b>2012</b> , 30, 434-9	44.5	1035
27	Identification of novel imidazo[1,2-a]pyridine inhibitors targeting <i>M. tuberculosis</i> QcrB. <i>PLoS ONE</i> , <b>2012</b> , 7, e52951	3.7	135
26	Open-source genomic analysis of Shiga-toxin-producing <i>E. coli</i> O104:H4. <i>New England Journal of Medicine</i> , <b>2011</b> , 365, 718-24	59.2	340
25	Calculating orthologs in bacteria and Archaea: a divide and conquer approach. <i>PLoS ONE</i> , <b>2011</b> , 6, e28388	3.7	9
24	Are diagnostic and public health bacteriology ready to become branches of genomic medicine?. <i>Genome Medicine</i> , <b>2011</b> , 3, 53	14.4	17
23	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> , <b>2011</b> , 193, 2359-60	3.5	16
22	Complete genome sequence of the Crohn's disease-associated adherent-invasive <i>Escherichia coli</i> strain HM605. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 4540	3.5	34
21	High-throughput sequencing and clinical microbiology: progress, opportunities and challenges. <i>Current Opinion in Microbiology</i> , <b>2010</b> , 13, 625-31	7.9	106
20	EntrezAJAX: direct web browser access to the Entrez Programming Utilities. <i>Source Code for Biology and Medicine</i> , <b>2010</b> , 5, 6	1.9	0

19	The complete genome and proteome of <i>Laribacter hongkongensis</i> reveal potential mechanisms for adaptations to different temperatures and habitats. <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000416	6	45
18	Next-generation sequencing--the promise and perils of charting the great microbial unknown. <i>Microbial Ecology</i> , <b>2009</b> , 57, 1-3	4.4	27
17	Bacterial flagellar diversity and evolution: seek simplicity and distrust it?. <i>Trends in Microbiology</i> , <b>2009</b> , 17, 1-5	12.4	28
16	Microbial TIR domains: not necessarily agents of subversion?. <i>Trends in Microbiology</i> , <b>2009</b> , 17, 393-8	12.4	45
15	xBASE2: a comprehensive resource for comparative bacterial genomics. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D543-6	20.1	113
14	An abundance of bacterial ADP-ribosyltransferases--implications for the origin of exotoxins and their human homologues. <i>Trends in Microbiology</i> , <b>2001</b> , 9, 302-7; discussion 308	12.4	60
13	CLIMB (the Cloud Infrastructure for Microbial Bioinformatics): an online resource for the medical microbiology community		4
12	De novoidentification of DNA Modifications Enabled by Genome-Guided Nanopore Signal Processing		107
11	Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples		6
10	Evolution and epidemic spread of SARS-CoV-2 in Brazil		6
9	MAJORA: Continuous integration supporting decentralised sequencing for SARS-CoV-2 genomic surveillance		11
8	Establishment & lineage dynamics of the SARS-CoV-2 epidemic in the UK		9
7	An amplicon-based sequencing framework for accurately measuring intrahost virus diversity using PrimalSeq and iVar		7
6	Nanopore native RNA sequencing of a human poly(A) transcriptome		49
5	Ultra-deep, long-read nanopore sequencing of mock microbial community standards		5
4	Telomere-to-telomere assembly of a complete human X chromosome		45
3	Virus genomes reveal the factors that spread and sustained the West African Ebola epidemic		2
2	Rapid viral metagenomics using SMART-9N amplification and nanopore sequencing. <i>Wellcome Open Research</i> , <b>6</b> , 241	4.8	2

1 The origins and molecular evolution of SARS-CoV-2 lineage B.1.1.7 in the UK

2