Niranjan Nagarajan

List of Publications by Year
in descending order

114 papers	18,231 citations	31976 53 h-index	20358 116 g-index
142 all docs	142 docs citations	142 times ranked	31938 citing authors

#	Article	IF	Citations
1	Fast and accurate de novo genome assembly from long uncorrected reads. Genome Research, 2017, 27, 737-746.	5.5	2,071
2	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	28.9	1,670
3	Statistical Methods for Detecting Differentially Abundant Features in Clinical Metagenomic Samples. PLoS Computational Biology, 2009, 5, e1000352.	3.2	1,495
4	LoFreq: a sequence-quality aware, ultra-sensitive variant caller for uncovering cell-population heterogeneity from high-throughput sequencing datasets. Nucleic Acids Research, 2012, 40, 11189-11201.	14.5	1,074
5	The draft genome of the transgenic tropical fruit tree papaya (Carica papaya Linnaeus). Nature, 2008, 452, 991-996.	27.8	964
6	The draft genome of sweet orange (Citrus sinensis). Nature Genetics, 2013, 45, 59-66.	21.4	837
7	Critical Assessment of Metagenome Interpretation—a benchmark of metagenomics software. Nature Methods, 2017, 14, 1063-1071.	19.0	635
8	Genome mapping on nanochannel arrays for structural variation analysis and sequence assembly. Nature Biotechnology, 2012, 30, 771-776.	17.5	586
9	Exome sequencing of gastric adenocarcinoma identifies recurrent somatic mutations in cell adhesion and chromatin remodeling genes. Nature Genetics, 2012, 44, 570-574.	21.4	560
10	A common BIM deletion polymorphism mediates intrinsic resistance and inferior responses to tyrosine kinase inhibitors in cancer. Nature Medicine, 2012, 18, 521-528.	30.7	510
11	Sequence assembly demystified. Nature Reviews Genetics, 2013, 14, 157-167.	16.3	396
12	Fast and sensitive mapping of nanopore sequencing reads with GraphMap. Nature Communications, 2016, 7, 11307.	12.8	331
13	Whole metagenome profiling reveals skin microbiome-dependent susceptibility to atopic dermatitis flare. Nature Microbiology, 2016, 1, 16106.	13.3	298
14	In Vivo Mapping of Eukaryotic RNA Interactomes Reveals Principles of Higher-Order Organization and Regulation. Molecular Cell, 2016, 62, 603-617.	9.7	290
15	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	28.9	272
16	Hybrid metagenomic assembly enables high-resolution analysis of resistance determinants and mobile elements in human microbiomes. Nature Biotechnology, 2019, 37, 937-944.	17.5	216
17	A Randomized, Double-Blind Placebo Controlled Trial of Balapiravir, a Polymerase Inhibitor, in Adult Dengue Patients. Journal of Infectious Diseases, 2013, 207, 1442-1450.	4.0	201
18	Genus-Wide Comparative Genomics of Malassezia Delineates Its Phylogeny, Physiology, and Niche Adaptation on Human Skin. PLoS Genetics, 2015, 11, e1005614.	3.5	198

#	Article	IF	Citations
19	Scaffolding and validation of bacterial genome assemblies using optical restriction maps. Bioinformatics, 2008, 24, 1229-1235.	4.1	195
20	Opera: Reconstructing Optimal Genomic Scaffolds with High-Throughput Paired-End Sequences. Journal of Computational Biology, 2011, 18, 1681-1691.	1.6	183
21	Genomic characterization of three unique *Dehalococcoides* that respire on persistent polychlorinated biphenyls. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 12103-12108.	7.1	168
22	A global metagenomic map of urban microbiomes and antimicrobial resistance. Cell, 2021, 184, 3376-3393.e17.	28.9	164
23	Cloning and variation of ground state intestinal stem cells. Nature, 2015, 522, 173-178.	27.8	156
24	The draft genome of tropical fruit durian (Durio zibethinus). Nature Genetics, 2017, 49, 1633-1641.	21.4	150
25	The Opisthorchis viverrini genome provides insights into life in the bile duct. Nature Communications, 2014, 5, 4378.	12.8	144
26	INC-Seq: accurate single molecule reads using nanopore sequencing. GigaScience, 2016, 5, 34.	6.4	133
27	Critical Assessment of Metagenome Interpretation: the second round of challenges. Nature Methods, 2022, 19, 429-440.	19.0	133
28	Cartography of opportunistic pathogens and antibiotic resistance genes in a tertiary hospital environment. Nature Medicine, 2020, 26, 941-951.	30.7	130
29	Whole-genome reconstruction and mutational signatures in gastric cancer. Genome Biology, 2012, 13, R115.	9.6	116
30	Recurrent Fusion Genes in Gastric Cancer: CLDN18-ARHGAP26 Induces Loss of Epithelial Integrity. Cell Reports, 2015, 12, 272-285.	6.4	112
31	Patient-specific driver gene prediction and risk assessment through integrated network analysis of cancer omics profiles. Nucleic Acids Research, 2015, 43, e44-e44.	14.5	111
32	Immunological corollary of the pulmonary mycobiome in bronchiectasis: the CAMEB study. European Respiratory Journal, 2018, 52, 1800766.	6.7	105
33	Structure mapping of dengue and Zika viruses reveals functional long-range interactions. Nature Communications, 2019, 10, 1408.	12.8	104
34	Genomic characterization of the Yersinia genus. Genome Biology, 2010, 11, R1.	9.6	103
35	Predicting Cancer Drug Response using a Recommender System. Bioinformatics, 2018, 34, 3907-3914.	4.1	101
36	Metagenome-wide association analysis identifies microbial determinants of post-antibiotic ecological recovery in the gut. Nature Ecology and Evolution, 2020, 4, 1256-1267.	7.8	98

#	Article	IF	Citations
37	Parametric Complexity of Sequence Assembly: Theory and Applications to Next Generation Sequencing. Journal of Computational Biology, 2009, 16, 897-908.	1.6	96
38	A Min<scp>ION</scp>â„¢â€‘based pipeline for fast and costâ€‘effective <scp>DNA</scp> barcoding. Molecular Ecology Resources, 2018, 18, 1035-1049.	4.8	96
39	Tissue Microbiome Profiling Identifies an Enrichment of Specific Enteric Bacteria in Opisthorchis viverrini Associated Cholangiocarcinoma. EBioMedicine, 2016, 8, 195-202.	6.1	94
40	Species Identification and Profiling of Complex Microbial Communities Using Shotgun Illumina Sequencing of 16S rRNA Amplicon Sequences. PLoS ONE, 2013, 8, e60811.	2.5	93
41	Mammalian Systems Biotechnology Reveals Global Cellular Adaptations in a Recombinant CHO Cell Line. Cell Systems, 2017, 4, 530-542.e6.	6.2	84
42	Gut microbiota changes in children with autism spectrum disorder: a systematic review. Gut Pathogens, 2020, 12, 6.	3.4	83
43	Metagenomics-enabled microbial surveillance. Nature Microbiology, 2022, 7, 486-496.	13.3	83
44	OPERA-LG: efficient and exact scaffolding of large, repeat-rich eukaryotic genomes with performance guarantees. Genome Biology, 2016, 17, 102.	8.8	77
45	The liverâ€“gut microbiota axis modulates hepatotoxicity of tacrine in the rat. Hepatology, 2018, 67, 282-295.	7.3	75
46	Comprehensive long-span paired-end-tag mapping reveals characteristic patterns of structural variations in epithelial cancer genomes. Genome Research, 2011, 21, 665-675.	5.5	74
47	Automatic prediction of protein domains from sequence information using a hybrid learning system. Bioinformatics, 2004, 20, 1335-1360.	4.1	73
48	Determination of isoform-specific RNA structure with nanopore long reads. Nature Biotechnology, 2021, 39, 336-346.	17.5	72
49	Tracking Dengue Virus Intra-host Genetic Diversity during Human-to-Mosquito Transmission. PLoS Neglected Tropical Diseases, 2015, 9, e0004052.	3.0	70
50	<i>In vitro</i> and <i>in vivo</i> correlates of physiological and neoplastic human Fallopian tube stem cells. Journal of Pathology, 2016, 238, 519-530.	4.5	68
51	GiRaF: robust, computational identification of influenza reassortments via graph mining. Nucleic Acids Research, 2011, 39, e34-e34.	14.5	64
52	Alignment and clustering of phylogenetic markers - implications for microbial diversity studies. BMC Bioinformatics, 2010, 11, 152.	2.6	63
53	Mutational spectrum of Barrettâ€™s stem cells suggests paths to initiation of a precancerous lesion. Nature Communications, 2016, 7, 10380.	12.8	57
54	Predicting microbial interactions through computational approaches. Methods, 2016, 102, 12-19.	3.8	49

#	Article	IF	Citations
55	Sequencing and Genome Assembly Using Next-Generation Technologies. Methods in Molecular Biology, 2010, 673, 1-17.	0.9	47
56	Analysis of Dengue Virus Genetic Diversity during Human and Mosquito Infection Reveals Genetic Constraints. PLoS Neglected Tropical Diseases, 2015, 9, e0004044.	3.0	47
57	Understanding the microbial basis of body odor in pre-pubescent children and teenagers. Microbiome, 2018, 6, 213.	11.1	47
58	COVID-19 drug practices risk antimicrobial resistance evolution. Lancet Microbe, The, 2021, 2, e135-e136.	7.3	47
59	Finishing genomes with limited resources: lessons from an ensemble of microbial genomes. BMC Genomics, 2010, 11, 242.	2.8	46
60	BAsE-Seq: a method for obtaining long viral haplotypes from short sequence reads. Genome Biology, 2014, 15, 517.	8.8	45
61	Comparative genomics of Cryptococcus neoformans var. grubii associated with meningitis in HIV infected and uninfected patients in Vietnam. PLoS Neglected Tropical Diseases, 2017, 11, e0005628.	3.0	45
62	High-depth sequencing of over 750 genes supports linear progression of primary tumors and metastases in most patients with liver-limited metastatic colorectal cancer. Genome Biology, 2015, 16, 32.	8.8	42
63	Genome-wide identification of natural RNA aptamers in prokaryotes and eukaryotes. Nature Communications, 2018, 9, 1289.	12.8	37
64	Computing the P-value of the information content from an alignment of multiple sequences. Bioinformatics, 2005, 21, i311-i318.	4.1	34
65	Emergence of tigecycline- and eravacycline-resistant Tet(X4)-producing Enterobacteriaceae in the gut microbiota of healthy Singaporeans. Journal of Antimicrobial Chemotherapy, 2020, 75, 3480-3484.	3.0	34
66	Transcriptomics Analysis Reveals Putative Genes Involved in Biofilm Formation and Biofilm-associated Drug Resistance of Enterococcus faecalis. Journal of Endodontics, 2017, 43, 949-955.	3.1	33
67	Systems consequences of amplicon formation in human breast cancer. Genome Research, 2014, 24, 1559-1571.	5.5	32
68	Human Tumor-Infiltrating MAIT Cells Display Hallmarks of Bacterial Antigen Recognition in Colorectal Cancer. Cell Reports Medicine, 2020, 1, 100039.	6.5	32
69	2009 Swine-Origin Influenza A (H1N1) Resembles Previous Influenza Isolates. PLoS ONE, 2009, 4, e6402.	2.5	31
70	@MInter: automated text-mining of microbial interactions. Bioinformatics, 2016, 32, 2981-2987.	4.1	30
71	Direct whole-genome deep-sequencing of human respiratory syncytial virus A and B from Vietnamese children identifies distinct patterns of inter- and intra-host evolution. Journal of General Virology, 2015, 96, 3470-3483.	2.9	30
72	Finding Biologically Accurate Clusterings in Hierarchical Tree Decompositions Using the Variation of Information. Journal of Computational Biology, 2010, 17, 503-516.	1.6	29

#	Article	IF	Citations
73	Complete Genome Sequence of *Aggregatibacter* (*Haemophilus*) *aphrophilus* NJ8700. Journal of Bacteriology, 2009, 191, 4693-4694.	2.2	28
74	Development of a genetically programed vanillin-sensing bacterium for high-throughput screening of lignin-degrading enzyme libraries. Biotechnology for Biofuels, 2017, 10, 32.	6.2	28
75	An expectation-maximization algorithm enables accurate ecological modeling using longitudinal microbiome sequencing data. Microbiome, 2019, 7, 118.	11.1	28
76	Atopic dermatitis microbiomes stratify into ecologic dermotypes enabling microbial virulence and disease severity. Journal of Allergy and Clinical Immunology, 2021, 147, 1329-1340.	2.9	26
77	Ectopic gut colonization: a metagenomic study of the oral and gut microbiome in Crohn's disease. Gut Pathogens, 2021, 13, 13.	3.4	26
78	Genome-Wide Analysis of Repetitive Elements in Papaya. Tropical Plant Biology, 2008, 1, 191-201.	1.9	24
79	Measurement of fetal fraction in cell-free DNA from maternal plasma using a panel of insertion/deletion polymorphisms. PLoS ONE, 2017, 12, e0186771.	2.5	21
80	FinIS: Improved in silico Finishing Using an Exact Quadratic Programming Formulation. Lecture Notes in Computer Science, 2012, , 314-325.	1.3	20
81	ConsensusDriver Improves upon Individual Algorithms for Predicting Driver Alterations in Different Cancer Types and Individual Patients. Cancer Research, 2018, 78, 290-301.	0.9	20
82	Predicting heterogeneity in clone-specific therapeutic vulnerabilities using single-cell transcriptomic signatures. Genome Medicine, 2021, 13, 189.	8.2	20
83	Emergence of SARS-CoV-2 Spike Mutations during Prolonged Infection in Immunocompromised Hosts. Microbiology Spectrum, 2022, 10, e0079122.	3.0	19
84	Boosting natural history research via metagenomic clean-up of crowdsourced feces. PLoS Biology, 2019, 17, e3000517.	5.6	18
85	Uncovering Genomic Reassortments among Influenza Strains by Enumerating Maximal Bicliques. , 2008, , .		17
86	Genome Sequencing of Four Strains of Rickettsia prowazekii, the Causative Agent of Epidemic Typhus, Including One Flying Squirrel Isolate. Genome Announcements, 2013, 1, .	0.8	17
87	Next-Generation Whole Genome Sequencing of Dengue Virus. Methods in Molecular Biology, 2014, 1138, 175-195.	0.9	14
88	Shared signatures and divergence in skin microbiomes of children with atopic dermatitis and their caregivers. Journal of Allergy and Clinical Immunology, 2022, 150, 894-908.	2.9	14
89	Long Span DNA Paired-End-Tag (DNA-PET) Sequencing Strategy for the Interrogation of Genomic Structural Mutations and Fusion-Point-Guided Reconstruction of Amplicons. PLoS ONE, 2012, 7, e46152.	2.5	13
90	The importance of study design for detecting differentially abundant features in high-throughput experiments. Genome Biology, 2014, 15, 527.	8.8	13

#	ARTICLE	IF	CITATIONS
91	Development and application of a transcriptional sensor for detection of heterologous acrylic acid production in E. coli. Microbial Cell Factories, 2019, 18, 139.	4.0	13
92	Duration of Carbapenemase-Producing *Enterobacteriaceae* Carriage in Hospital Patients. Emerging Infectious Diseases, 2020, 26, 2182-2185.	4.3	13
93	SARS-CoV-2 N Gene G29195T Point Mutation May Affect Diagnostic Reverse Transcription-PCR Detection. Microbiology Spectrum, 2022, 10, e0222321.	3.0	13
94	OPTIMA: sensitive and accurate whole-genome alignment of error-prone genomic maps by combinatorial indexing and technology-agnostic statistical analysis. GigaScience, 2016, 5, 2.	6.4	12
95	Mapping RNA-RNA Interactions Globally Using Biotinylated Psoralen. Journal of Visualized Experiments, 2017, , .	0.3	12
96	Opera: Reconstructing Optimal Genomic Scaffolds with High-Throughput Paired-End Sequences. Lecture Notes in Computer Science, 2011, , 437-451.	1.3	12
97	A Fast and Numerically Robust Method for Exact Multinomial Goodness-of-Fit Test. Journal of Computational and Graphical Statistics, 2006, 15, 779-802.	1.7	11
98	TUGDA: task uncertainty guided domain adaptation for robust generalization of cancer drug response prediction from *in vitro* to *in vivo* settings. Bioinformatics, 2021, 37, i76-i83.	4.1	11
99	Reliability and efficiency of algorithms for computing the significance of the Mann–Whitney test. Computational Statistics, 2009, 24, 605-622.	1.5	10
100	Extended-Spectrum β-Lactamase-Producing and *mcr-1*-Positive Escherichia coli from the Gut Microbiota of Healthy Singaporeans. Applied and Environmental Microbiology, 2021, 87, e0048821.	3.1	10
101	Finding Biologically Accurate Clusterings in Hierarchical Tree Decompositions Using the Variation of Information. Lecture Notes in Computer Science, 2009, , 400-417.	1.3	10
102	Evaluating the accuracy of Listeria monocytogenes assemblies from quasimetagenomic samples using long and short reads. BMC Genomics, 2021, 22, 389.	2.8	9
103	Apples to apples: improving the performance of motif finders and their significance analysis in the Twilight Zone. Bioinformatics, 2006, 22, e393-e401.	4.1	8
104	CalmBelt: Rapid SARS-CoV-2 Genome Characterization for Outbreak Tracking. Frontiers in Medicine, 2021, 8, 790662.	2.6	8
105	FAST: Fourier transform based algorithms for significance testing of ungapped multiple alignments. Bioinformatics, 2008, 24, 577-578.	4.1	7
106	Single-molecule optical genome mapping of a human HapMap and a colorectal cancer cell line. GigaScience, 2015, 4, 65.	6.4	7
107	Draft Genome Sequence of Polychlorinated Biphenyl-Dechlorinating Dehalococcoides mccartyi Strain SG1, Which Carries a Circular Putative Plasmid. Genome Announcements, 2014, 2, .	0.8	6
108	Single-virion sequencing of lamivudine-treated HBV populations reveal population evolution dynamics and demographic history. BMC Genomics, 2017, 18, 829.	2.8	6

#	Article	IF	Citations
109	Mutual Exclusion of *Methanobrevibacter* Species in the Human Gut Microbiota Facilitates Directed Cultivation of a *Candidatus* Methanobrevibacter Intestini Representative. Microbiology Spectrum, 2022, 10, .	3.0	6
110	Stool metagenome analysis of patients with Klebsiella pneumoniae liver abscess and their domestic partners. International Journal of Infectious Diseases, 2021, 107, 1-4.	3.3	4
111	Household transmission of carbapenemase-producing Enterobacteriaceae: a prospective cohort study. Journal of Antimicrobial Chemotherapy, 2021, 76, 1299-1302.	3.0	3
112	BEEM-Static: Accurate inference of ecological interactions from cross-sectional microbiome data. PLoS Computational Biology, 2021, 17, e1009343.	3.2	2
113	A multi-expert system for the automatic detection of protein domains from sequence information. , 2003, , .		2
114	Papaya Repeat Database. , 2014, , 225-240.		1