

Niranjana Nagarajan

List of Publications by Year in descending order

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Version: 2024-02-01

114
papers

18,231
citations

31976

53
h-index

20358

116
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142
all docs

142
docs citations

142
times ranked

31938
citing authors

#	ARTICLE	IF	CITATIONS
1	SARS-CoV-2 N Gene G29195T Point Mutation May Affect Diagnostic Reverse Transcription-PCR Detection. <i>Microbiology Spectrum</i> , 2022, 10, e0222321.	3.0	13
2	Shared signatures and divergence in skin microbiomes of children with atopic dermatitis and their caregivers. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 150, 894-908.	2.9	14
3	Critical Assessment of Metagenome Interpretation: the second round of challenges. <i>Nature Methods</i> , 2022, 19, 429-440.	19.0	133
4	Metagenomics-enabled microbial surveillance. <i>Nature Microbiology</i> , 2022, 7, 486-496.	13.3	83
5	Emergence of SARS-CoV-2 Spike Mutations during Prolonged Infection in Immunocompromised Hosts. <i>Microbiology Spectrum</i> , 2022, 10, e0079122.	3.0	19
6	Mutual Exclusion of <i>Methanobrevibacter</i> Species in the Human Gut Microbiota Facilitates Directed Cultivation of a <i>Candidatus</i> <i>Methanobrevibacter</i> <i>Intestini</i> Representative. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	6
7	Atopic dermatitis microbiomes stratify into ecologic dermatotypes enabling microbial virulence and disease severity. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 147, 1329-1340.	2.9	26
8	Determination of isoform-specific RNA structure with nanopore long reads. <i>Nature Biotechnology</i> , 2021, 39, 336-346.	17.5	72
9	Household transmission of carbapenemase-producing Enterobacteriaceae: a prospective cohort study. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 1299-1302.	3.0	3
10	Ectopic gut colonization: a metagenomic study of the oral and gut microbiome in Crohn's disease. <i>Gut Pathogens</i> , 2021, 13, 13.	3.4	26
11	COVID-19 drug practices risk antimicrobial resistance evolution. <i>Lancet Microbe</i> , The, 2021, 2, e135-e136.	7.3	47
12	Evaluating the accuracy of <i>Listeria monocytogenes</i> assemblies from quasimetagenomic samples using long and short reads. <i>BMC Genomics</i> , 2021, 22, 389.	2.8	9
13	Stool metagenome analysis of patients with <i>Klebsiella pneumoniae</i> liver abscess and their domestic partners. <i>International Journal of Infectious Diseases</i> , 2021, 107, 1-4.	3.3	4
14	A global metagenomic map of urban microbiomes and antimicrobial resistance. <i>Cell</i> , 2021, 184, 3376-3393.e17.	28.9	164
15	TUGDA: task uncertainty guided domain adaptation for robust generalization of cancer drug response prediction from <i>in vitro</i> to <i>in vivo</i> settings. <i>Bioinformatics</i> , 2021, 37, i76-i83.	4.1	11
16	BEEM-Static: Accurate inference of ecological interactions from cross-sectional microbiome data. <i>PLoS Computational Biology</i> , 2021, 17, e1009343.	3.2	2
17	Extended-Spectrum β -Lactamase-Producing and <i>mcr-1</i> -Positive <i>Escherichia coli</i> from the Gut Microbiota of Healthy Singaporeans. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0048821.	3.1	10
18	CalmBelt: Rapid SARS-CoV-2 Genome Characterization for Outbreak Tracking. <i>Frontiers in Medicine</i> , 2021, 8, 790662.	2.6	8

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19	Predicting heterogeneity in clone-specific therapeutic vulnerabilities using single-cell transcriptomic signatures. <i>Genome Medicine</i> , 2021, 13, 189.	8.2	20
20	Human Tumor-Infiltrating MAIT Cells Display Hallmarks of Bacterial Antigen Recognition in Colorectal Cancer. <i>Cell Reports Medicine</i> , 2020, 1, 100039.	6.5	32
21	Emergence of tigecycline- and eravacycline-resistant Tet(X4)-producing Enterobacteriaceae in the gut microbiota of healthy Singaporeans. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 3480-3484.	3.0	34
22	Duration of Carbapenemase-Producing <i>Enterobacteriaceae</i> Carriage in Hospital Patients. <i>Emerging Infectious Diseases</i> , 2020, 26, 2182-2185.	4.3	13
23	Cartography of opportunistic pathogens and antibiotic resistance genes in a tertiary hospital environment. <i>Nature Medicine</i> , 2020, 26, 941-951.	30.7	130
24	Metagenome-wide association analysis identifies microbial determinants of post-antibiotic ecological recovery in the gut. <i>Nature Ecology and Evolution</i> , 2020, 4, 1256-1267.	7.8	98
25	Gut microbiota changes in children with autism spectrum disorder: a systematic review. <i>Gut Pathogens</i> , 2020, 12, 6.	3.4	83
26	Hybrid metagenomic assembly enables high-resolution analysis of resistance determinants and mobile elements in human microbiomes. <i>Nature Biotechnology</i> , 2019, 37, 937-944.	17.5	216
27	Development and application of a transcriptional sensor for detection of heterologous acrylic acid production in <i>E. coli</i> . <i>Microbial Cell Factories</i> , 2019, 18, 139.	4.0	13
28	Boosting natural history research via metagenomic clean-up of crowdsourced feces. <i>PLoS Biology</i> , 2019, 17, e3000517.	5.6	18
29	An expectation-maximization algorithm enables accurate ecological modeling using longitudinal microbiome sequencing data. <i>Microbiome</i> , 2019, 7, 118.	11.1	28
30	Structure mapping of dengue and Zika viruses reveals functional long-range interactions. <i>Nature Communications</i> , 2019, 10, 1408.	12.8	104
31	A MinION-based pipeline for fast and cost-effective DNA barcoding. <i>Molecular Ecology Resources</i> , 2018, 18, 1035-1049.	4.8	96
32	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18.	28.9	1,670
33	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018, 173, 305-320.e10.	28.9	272
34	ConsensusDriver Improves upon Individual Algorithms for Predicting Driver Alterations in Different Cancer Types and Individual Patients. <i>Cancer Research</i> , 2018, 78, 290-301.	0.9	20
35	Genome-wide identification of natural RNA aptamers in prokaryotes and eukaryotes. <i>Nature Communications</i> , 2018, 9, 1289.	12.8	37
36	The liver-gut microbiota axis modulates hepatotoxicity of tacrine in the rat. <i>Hepatology</i> , 2018, 67, 282-295.	7.3	75

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37	Understanding the microbial basis of body odor in pre-pubescent children and teenagers. <i>Microbiome</i> , 2018, 6, 213.	11.1	47
38	Predicting Cancer Drug Response using a Recommender System. <i>Bioinformatics</i> , 2018, 34, 3907-3914.	4.1	101
39	Immunological corollary of the pulmonary mycobiome in bronchiectasis: the CAMEB study. <i>European Respiratory Journal</i> , 2018, 52, 1800766.	6.7	105
40	Fast and accurate de novo genome assembly from long uncorrected reads. <i>Genome Research</i> , 2017, 27, 737-746.	5.5	2,071
41	Development of a genetically programmed vanillin-sensing bacterium for high-throughput screening of lignin-degrading enzyme libraries. <i>Biotechnology for Biofuels</i> , 2017, 10, 32.	6.2	28
42	Transcriptomics Analysis Reveals Putative Genes Involved in Biofilm Formation and Biofilm-associated Drug Resistance of <i>Enterococcus faecalis</i> . <i>Journal of Endodontics</i> , 2017, 43, 949-955.	3.1	33
43	Mammalian Systems Biotechnology Reveals Global Cellular Adaptations in a Recombinant CHO Cell Line. <i>Cell Systems</i> , 2017, 4, 530-542.e6.	6.2	84
44	Critical Assessment of Metagenome Interpretationâ€”a benchmark of metagenomics software. <i>Nature Methods</i> , 2017, 14, 1063-1071.	19.0	635
45	The draft genome of tropical fruit durian (<i>Durio zibethinus</i>). <i>Nature Genetics</i> , 2017, 49, 1633-1641.	21.4	150
46	Mapping RNA-RNA Interactions Globally Using Biotinylated Psoralen. <i>Journal of Visualized Experiments</i> , 2017, , .	0.3	12
47	Single-virion sequencing of lamivudine-treated HBV populations reveal population evolution dynamics and demographic history. <i>BMC Genomics</i> , 2017, 18, 829.	2.8	6
48	Comparative genomics of <i>Cryptococcus neoformans</i> var. <i>grubii</i> associated with meningitis in HIV infected and uninfected patients in Vietnam. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005628.	3.0	45
49	Measurement of fetal fraction in cell-free DNA from maternal plasma using a panel of insertion/deletion polymorphisms. <i>PLoS ONE</i> , 2017, 12, e0186771.	2.5	21
50	<i>In vitro</i> and <i>in vivo</i> correlates of physiological and neoplastic human Fallopian tube stem cells. <i>Journal of Pathology</i> , 2016, 238, 519-530.	4.5	68
51	Fast and sensitive mapping of nanopore sequencing reads with GraphMap. <i>Nature Communications</i> , 2016, 7, 11307.	12.8	331
52	Predicting microbial interactions through computational approaches. <i>Methods</i> , 2016, 102, 12-19.	3.8	49
53	Tissue Microbiome Profiling Identifies an Enrichment of Specific Enteric Bacteria in <i>Opisthorchis viverrini</i> Associated Cholangiocarcinoma. <i>EBioMedicine</i> , 2016, 8, 195-202.	6.1	94
54	<i>In Vivo</i> Mapping of Eukaryotic RNA Interactomes Reveals Principles of Higher-Order Organization and Regulation. <i>Molecular Cell</i> , 2016, 62, 603-617.	9.7	290

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55	Whole metagenome profiling reveals skin microbiome-dependent susceptibility to atopic dermatitis flare. <i>Nature Microbiology</i> , 2016, 1, 16106.	13.3	298
56	INC-Seq: accurate single molecule reads using nanopore sequencing. <i>GigaScience</i> , 2016, 5, 34.	6.4	133
57	@MInter: automated text-mining of microbial interactions. <i>Bioinformatics</i> , 2016, 32, 2981-2987.	4.1	30
58	OPERA-LG: efficient and exact scaffolding of large, repeat-rich eukaryotic genomes with performance guarantees. <i>Genome Biology</i> , 2016, 17, 102.	8.8	77
59	OPTIMA: sensitive and accurate whole-genome alignment of error-prone genomic maps by combinatorial indexing and technology-agnostic statistical analysis. <i>GigaScience</i> , 2016, 5, 2.	6.4	12
60	Mutational spectrum of Barrett's stem cells suggests paths to initiation of a precancerous lesion. <i>Nature Communications</i> , 2016, 7, 10380.	12.8	57
61	Single-molecule optical genome mapping of a human HapMap and a colorectal cancer cell line. <i>GigaScience</i> , 2015, 4, 65.	6.4	7
62	Genus-Wide Comparative Genomics of <i>Malassezia</i> Delineates Its Phylogeny, Physiology, and Niche Adaptation on Human Skin. <i>PLoS Genetics</i> , 2015, 11, e1005614.	3.5	198
63	Analysis of Dengue Virus Genetic Diversity during Human and Mosquito Infection Reveals Genetic Constraints. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0004044.	3.0	47
64	Tracking Dengue Virus Intra-host Genetic Diversity during Human-to-Mosquito Transmission. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0004052.	3.0	70
65	Cloning and variation of ground state intestinal stem cells. <i>Nature</i> , 2015, 522, 173-178.	27.8	156
66	Recurrent Fusion Genes in Gastric Cancer: CLDN18-ARHGAP26 Induces Loss of Epithelial Integrity. <i>Cell Reports</i> , 2015, 12, 272-285.	6.4	112
67	Patient-specific driver gene prediction and risk assessment through integrated network analysis of cancer omics profiles. <i>Nucleic Acids Research</i> , 2015, 43, e44-e44.	14.5	111
68	High-depth sequencing of over 750 genes supports linear progression of primary tumors and metastases in most patients with liver-limited metastatic colorectal cancer. <i>Genome Biology</i> , 2015, 16, 32.	8.8	42
69	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. <i>Journal of General Virology</i> , 2015, 96, 3470-3483.	2.9	30
70	BAE-Seq: a method for obtaining long viral haplotypes from short sequence reads. <i>Genome Biology</i> , 2014, 15, 517.	8.8	45
71	The importance of study design for detecting differentially abundant features in high-throughput experiments. <i>Genome Biology</i> , 2014, 15, 527.	8.8	13
72	The <i>Opisthorchis viverrini</i> genome provides insights into life in the bile duct. <i>Nature Communications</i> , 2014, 5, 4378.	12.8	144

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73	Draft Genome Sequence of Polychlorinated Biphenyl-Dechlorinating <i>Dehalococcoides mccartyi</i> Strain SG1, Which Carries a Circular Putative Plasmid. <i>Genome Announcements</i> , 2014, 2, .	0.8	6
74	Systems consequences of amplicon formation in human breast cancer. <i>Genome Research</i> , 2014, 24, 1559-1571.	5.5	32
75	Papaya Repeat Database. , 2014, , 225-240.		1
76	Genomic characterization of three unique <i>Dehalococcoides</i> that respire on persistent polychlorinated biphenyls. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 12103-12108.	7.1	168
77	Next-Generation Whole Genome Sequencing of Dengue Virus. <i>Methods in Molecular Biology</i> , 2014, 1138, 175-195.	0.9	14
78	Sequence assembly demystified. <i>Nature Reviews Genetics</i> , 2013, 14, 157-167.	16.3	396
79	The draft genome of sweet orange (<i>Citrus sinensis</i>). <i>Nature Genetics</i> , 2013, 45, 59-66.	21.4	837
80	Species Identification and Profiling of Complex Microbial Communities Using Shotgun Illumina Sequencing of 16S rRNA Amplicon Sequences. <i>PLoS ONE</i> , 2013, 8, e60811.	2.5	93
81	A Randomized, Double-Blind Placebo Controlled Trial of Balapiravir, a Polymerase Inhibitor, in Adult Dengue Patients. <i>Journal of Infectious Diseases</i> , 2013, 207, 1442-1450.	4.0	201
82	Genome Sequencing of Four Strains of <i>Rickettsia prowazekii</i> , the Causative Agent of Epidemic Typhus, Including One Flying Squirrel Isolate. <i>Genome Announcements</i> , 2013, 1, .	0.8	17
83	A common BIM deletion polymorphism mediates intrinsic resistance and inferior responses to tyrosine kinase inhibitors in cancer. <i>Nature Medicine</i> , 2012, 18, 521-528.	30.7	510
84	LoFreq: a sequence-quality aware, ultra-sensitive variant caller for uncovering cell-population heterogeneity from high-throughput sequencing datasets. <i>Nucleic Acids Research</i> , 2012, 40, 11189-11201.	14.5	1,074
85	Exome sequencing of gastric adenocarcinoma identifies recurrent somatic mutations in cell adhesion and chromatin remodeling genes. <i>Nature Genetics</i> , 2012, 44, 570-574.	21.4	560
86	FinIS: Improved in silico Finishing Using an Exact Quadratic Programming Formulation. <i>Lecture Notes in Computer Science</i> , 2012, , 314-325.	1.3	20
87	Whole-genome reconstruction and mutational signatures in gastric cancer. <i>Genome Biology</i> , 2012, 13, R115.	9.6	116
88	Long Span DNA Paired-End-Tag (DNA-PET) Sequencing Strategy for the Interrogation of Genomic Structural Mutations and Fusion-Point-Guided Reconstruction of Amplicons. <i>PLoS ONE</i> , 2012, 7, e46152.	2.5	13
89	Genome mapping on nanochannel arrays for structural variation analysis and sequence assembly. <i>Nature Biotechnology</i> , 2012, 30, 771-776.	17.5	586
90	Comprehensive long-span paired-end-tag mapping reveals characteristic patterns of structural variations in epithelial cancer genomes. <i>Genome Research</i> , 2011, 21, 665-675.	5.5	74

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91	Opera: Reconstructing Optimal Genomic Scaffolds with High-Throughput Paired-End Sequences. <i>Journal of Computational Biology</i> , 2011, 18, 1681-1691.	1.6	183
92	GiRaF: robust, computational identification of influenza reassortments via graph mining. <i>Nucleic Acids Research</i> , 2011, 39, e34-e34.	14.5	64
93	Opera: Reconstructing Optimal Genomic Scaffolds with High-Throughput Paired-End Sequences. <i>Lecture Notes in Computer Science</i> , 2011, , 437-451.	1.3	12
94	Alignment and clustering of phylogenetic markers - implications for microbial diversity studies. <i>BMC Bioinformatics</i> , 2010, 11, 152.	2.6	63
95	Finishing genomes with limited resources: lessons from an ensemble of microbial genomes. <i>BMC Genomics</i> , 2010, 11, 242.	2.8	46
96	Finding Biologically Accurate Clusterings in Hierarchical Tree Decompositions Using the Variation of Information. <i>Journal of Computational Biology</i> , 2010, 17, 503-516.	1.6	29
97	Sequencing and Genome Assembly Using Next-Generation Technologies. <i>Methods in Molecular Biology</i> , 2010, 673, 1-17.	0.9	47
98	Genomic characterization of the <i>Yersinia</i> genus. <i>Genome Biology</i> , 2010, 11, R1.	9.6	103
99	2009 Swine-Origin Influenza A (H1N1) Resembles Previous Influenza Isolates. <i>PLoS ONE</i> , 2009, 4, e6402.	2.5	31
100	Statistical Methods for Detecting Differentially Abundant Features in Clinical Metagenomic Samples. <i>PLoS Computational Biology</i> , 2009, 5, e1000352.	3.2	1,495
101	Complete Genome Sequence of <i>Aggregatibacter</i> (<i>Haemophilus</i>) <i>aphrophilus</i> NJ8700. <i>Journal of Bacteriology</i> , 2009, 191, 4693-4694.	2.2	28
102	Reliability and efficiency of algorithms for computing the significance of the Mann-Whitney test. <i>Computational Statistics</i> , 2009, 24, 605-622.	1.5	10
103	Parametric Complexity of Sequence Assembly: Theory and Applications to Next Generation Sequencing. <i>Journal of Computational Biology</i> , 2009, 16, 897-908.	1.6	96
104	Finding Biologically Accurate Clusterings in Hierarchical Tree Decompositions Using the Variation of Information. <i>Lecture Notes in Computer Science</i> , 2009, , 400-417.	1.3	10
105	Genome-Wide Analysis of Repetitive Elements in Papaya. <i>Tropical Plant Biology</i> , 2008, 1, 191-201.	1.9	24
106	The draft genome of the transgenic tropical fruit tree papaya (<i>Carica papaya</i> Linnaeus). <i>Nature</i> , 2008, 452, 991-996.	27.8	964
107	Uncovering Genomic Reassortments among Influenza Strains by Enumerating Maximal Bicliques. , 2008, , .		17
108	FAST: Fourier transform based algorithms for significance testing of ungapped multiple alignments. <i>Bioinformatics</i> , 2008, 24, 577-578.	4.1	7

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109	Scaffolding and validation of bacterial genome assemblies using optical restriction maps. <i>Bioinformatics</i> , 2008, 24, 1229-1235.	4.1	195
110	Apples to apples: improving the performance of motif finders and their significance analysis in the Twilight Zone. <i>Bioinformatics</i> , 2006, 22, e393-e401.	4.1	8
111	A Fast and Numerically Robust Method for Exact Multinomial Goodness-of-Fit Test. <i>Journal of Computational and Graphical Statistics</i> , 2006, 15, 779-802.	1.7	11
112	Computing the P-value of the information content from an alignment of multiple sequences. <i>Bioinformatics</i> , 2005, 21, i311-i318.	4.1	34
113	Automatic prediction of protein domains from sequence information using a hybrid learning system. <i>Bioinformatics</i> , 2004, 20, 1335-1360.	4.1	73
114	A multi-expert system for the automatic detection of protein domains from sequence information. , 2003, , .		2