

Miten Jain

List of Publications by Year in descending order

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Version: 2024-02-01

35
papers

8,136
citations

257357

24
h-index

330025

37
g-index

58
all docs

58
docs citations

58
times ranked

8870
citing authors

#	ARTICLE	IF	CITATIONS
1	Nanopore sequencing and assembly of a human genome with ultra-long reads. <i>Nature Biotechnology</i> , 2018, 36, 338-345.	9.4	1,443
2	The complete sequence of a human genome. <i>Science</i> , 2022, 376, 44-53.	6.0	1,222
3	The Oxford Nanopore MinION: delivery of nanopore sequencing to the genomics community. <i>Genome Biology</i> , 2016, 17, 239.	3.8	985
4	Improved data analysis for the MinION nanopore sequencer. <i>Nature Methods</i> , 2015, 12, 351-356.	9.0	557
5	Nanopore native RNA sequencing of a human poly(A) transcriptome. <i>Nature Methods</i> , 2019, 16, 1297-1305.	9.0	411
6	Mapping DNA methylation with high-throughput nanopore sequencing. <i>Nature Methods</i> , 2017, 14, 411-413.	9.0	390
7	Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. <i>Nature Biotechnology</i> , 2020, 38, 1044-1053.	9.4	344
8	Nanopore long-read RNAseq reveals widespread transcriptional variation among the surface receptors of individual B cells. <i>Nature Communications</i> , 2017, 8, 16027.	5.8	329
9	MinION Analysis and Reference Consortium: Phase 1 data release and analysis. <i>F1000Research</i> , 2015, 4, 1075.	0.8	270
10	Linear assembly of a human centromere on the Y chromosome. <i>Nature Biotechnology</i> , 2018, 36, 321-323.	9.4	216
11	Centromere reference models for human chromosomes X and Y satellite arrays. <i>Genome Research</i> , 2014, 24, 697-707.	2.4	210
12	Haplotype-aware variant calling with PEPPER-Margin-DeepVariant enables high accuracy in nanopore long-reads. <i>Nature Methods</i> , 2021, 18, 1322-1332.	9.0	139
13	MinION-based long-read sequencing and assembly extends the <i>Caenorhabditis elegans</i> reference genome. <i>Genome Research</i> , 2018, 28, 266-274.	2.4	132
14	Reading canonical and modified nucleobases in 16S ribosomal RNA using nanopore native RNA sequencing. <i>PLoS ONE</i> , 2019, 14, e0216709.	1.1	130
15	Epigenetic patterns in a complete human genome. <i>Science</i> , 2022, 376, eabj5089.	6.0	118
16	Ultrarapid Nanopore Genome Sequencing in a Critical Care Setting. <i>New England Journal of Medicine</i> , 2022, 386, 700-702.	13.9	116
17	MinION Analysis and Reference Consortium: Phase 2 data release and analysis of R9.0 chemistry. <i>F1000Research</i> , 2017, 6, 760.	0.8	107
18	PrecisionFDA Truth Challenge V2: Calling variants from short and long reads in difficult-to-map regions. <i>Cell Genomics</i> , 2022, 2, 100129.	3.0	72

#	ARTICLE	IF	CITATIONS
19	Direct Nanopore Sequencing of Individual Full Length tRNA Strands. <i>ACS Nano</i> , 2021, 15, 16642-16653.	7.3	57
20	Accelerated identification of disease-causing variants with ultra-rapid nanopore genome sequencing. <i>Nature Biotechnology</i> , 2022, 40, 1035-1041.	9.4	45
21	Off Earth Identification of Bacterial Populations Using 16S rDNA Nanopore Sequencing. <i>Genes</i> , 2020, 11, 76.	1.0	43
22	Real-Time Culture-Independent Microbial Profiling Onboard the International Space Station Using Nanopore Sequencing. <i>Genes</i> , 2021, 12, 106.	1.0	41
23	A Survey of Rare Epigenetic Variation in 23,116 Human Genomes Identifies Disease-Relevant Epivariations and CCG Expansions. <i>American Journal of Human Genetics</i> , 2020, 107, 654-669.	2.6	40
24	Pervasive cis effects of variation in copy number of large tandem repeats on local DNA methylation and gene expression. <i>American Journal of Human Genetics</i> , 2021, 108, 809-824.	2.6	30
25	Inflammation drives alternative first exon usage to regulate immune genes including a novel iron-regulated isoform of Aim2. <i>ELife</i> , 2021, 10, .	2.8	23
26	Resolving the complex <i>Bordetella pertussis</i> genome using barcoded nanopore sequencing. <i>Microbial Genomics</i> , 2018, 4, .	1.0	22
27	Gaussian mixture model-based unsupervised nucleotide modification number detection using nanopore-sequencing readouts. <i>Bioinformatics</i> , 2020, 36, 4928-4934.	1.8	21
28	miRNA-independent function of long noncoding pri-miRNA loci. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	18
29	A community challenge to evaluate RNA-seq, fusion detection, and isoform quantification methods for cancer discovery. <i>Cell Systems</i> , 2021, 12, 827-838.e5.	2.9	15
30	Permutational analysis of <i>Saccharomyces cerevisiae</i> regulatory elements. <i>Synthetic Biology</i> , 2020, 5, ysa007.	1.2	12
31	Synthesis of modified nucleotide polymers by the poly(U) polymerase Cid1: application to direct RNA sequencing on nanopores. <i>Rna</i> , 2021, 27, 1497-1511.	1.6	12
32	Identification of high-confidence human poly(A) RNA isoform scaffolds using nanopore sequencing. <i>Rna</i> , 2022, 28, 162-176.	1.6	12
33	Nanopore ReCappable sequencing maps SARS-CoV-2 5' capping sites and provides new insights into the structure of sgRNAs. <i>Nucleic Acids Research</i> , 2022, 50, 3475-3489.	6.5	12
34	Adaptation of Human Ribosomal RNA for Nanopore Sequencing of Canonical and Modified Nucleotides. <i>Methods in Molecular Biology</i> , 2021, 2298, 53-74.	0.4	6
35	Ultra-Rapid Nanopore Whole Genome Genetic Diagnosis of Dilated Cardiomyopathy in an Adolescent With Cardiogenic Shock. <i>Circulation Genomic and Precision Medicine</i> , 2022, 15, CIRCGEN121003591.	1.6	3