Miten Jain

List of Publications by Year in descending order

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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	Identification of high-confidence human poly(A) RNA isoform scaffolds using nanopore sequencing. Rna, 2022, 28, 162-176.	1.6	12
2	Ultrarapid Nanopore Genome Sequencing in a Critical Care Setting. New England Journal of Medicine, 2022, 386, 700-702.	13.9	116
3	Ultra-Rapid Nanopore Whole Genome Genetic Diagnosis of Dilated Cardiomyopathy in an Adolescent With Cardiogenic Shock. Circulation Genomic and Precision Medicine, 2022, 15, CIRCGEN121003591.	1.6	3
4	Accelerated identification of disease-causing variants with ultra-rapid nanopore genome sequencing. Nature Biotechnology, 2022, 40, 1035-1041.	9.4	45
5	Nanopore ReCappable sequencing maps SARS-CoV-2 5â€² capping sites and provides new insights into the structure of sgRNAs. Nucleic Acids Research, 2022, 50, 3475-3489.	6.5	12
6	Epigenetic patterns in a complete human genome. Science, 2022, 376, eabj5089.	6.0	118
7	The complete sequence of a human genome. Science, 2022, 376, 44-53.	6.0	1,222
8	PrecisionFDA Truth Challenge V2: Calling variants from short and long reads in difficult-to-map regions. Cell Genomics, 2022, 2, 100129.	3.0	72
9	Adaptation of Human Ribosomal RNA for Nanopore Sequencing of Canonical and Modified Nucleotides. Methods in Molecular Biology, 2021, 2298, 53-74.	0.4	6
10	miRNA-independent function of long noncoding pri-miRNA loci. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	18
11	Pervasive cis effects of variation in copy number of large tandem repeats on local DNA methylation and gene expression. American Journal of Human Genetics, 2021, 108, 809-824.	2.6	30
12	Inflammation drives alternative first exon usage to regulate immune genes including a novel iron-regulated isoform of Aim2. ELife, 2021, 10, .	2.8	23
13	A community challenge to evaluate RNA-seq, fusion detection, and isoform quantification methods for cancer discovery. Cell Systems, 2021, 12, 827-838.e5.	2.9	15
14	Synthesis of modified nucleotide polymers by the poly(U) polymerase Cid1: application to direct RNA sequencing on nanopores. Rna, 2021, 27, 1497-1511.	1.6	12
15	Real-Time Culture-Independent Microbial Profiling Onboard the International Space Station Using Nanopore Sequencing. Genes, 2021, 12, 106.	1.0	41
16	Direct Nanopore Sequencing of Individual Full Length tRNA Strands. ACS Nano, 2021, 15, 16642-16653.	7.3	57
17	Haplotype-aware variant calling with PEPPER-Margin-DeepVariant enables high accuracy in nanopore long-reads. Nature Methods, 2021, 18, 1322-1332.	9.0	139
18	Permutational analysis of Saccharomyces cerevisiae regulatory elements. Synthetic Biology, 2020, 5, ysaa007.	1.2	12

#	Article	IF	Citations
19	A Survey of Rare Epigenetic Variation in 23,116 Human Genomes Identifies Disease-Relevant Epivariations and CGG Expansions. American Journal of Human Genetics, 2020, 107, 654-669.	2.6	40
20	Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. Nature Biotechnology, 2020, 38, 1044-1053.	9.4	344
21	Gaussian mixture model-based unsupervised nucleotide modification number detection using nanopore-sequencing readouts. Bioinformatics, 2020, 36, 4928-4934.	1.8	21
22	Off Earth Identification of Bacterial Populations Using 16S rDNA Nanopore Sequencing. Genes, 2020, 11, 76.	1.0	43
23	Reading canonical and modified nucleobases in 16S ribosomal RNA using nanopore native RNA sequencing. PLoS ONE, 2019, 14, e0216709.	1.1	130
24	Nanopore native RNA sequencing of a human poly(A) transcriptome. Nature Methods, 2019, 16, 1297-1305.	9.0	411
25	Nanopore sequencing and assembly of a human genome with ultra-long reads. Nature Biotechnology, 2018, 36, 338-345.	9.4	1,443
26	MinION-based long-read sequencing and assembly extends the Caenorhabditis elegans reference genome. Genome Research, 2018, 28, 266-274.	2.4	132
27	Linear assembly of a human centromere on the Y chromosome. Nature Biotechnology, 2018, 36, 321-323.	9.4	216
28	Resolving the complex Bordetella pertussis genome using barcoded nanopore sequencing. Microbial Genomics, 2018, 4, .	1.0	22
29	Mapping DNA methylation with high-throughput nanopore sequencing. Nature Methods, 2017, 14, 411-413.	9.0	390
30	Nanopore long-read RNAseq reveals widespread transcriptional variation among the surface receptors of individual B cells. Nature Communications, 2017, 8, 16027.	5.8	329
31	MinION Analysis and Reference Consortium: Phase 2 data release and analysis of R9.0 chemistry. F1000Research, 2017, 6, 760.	0.8	107
32	The Oxford Nanopore MinION: delivery of nanopore sequencing to the genomics community. Genome Biology, 2016, 17, 239.	3.8	985
33	MinION Analysis and Reference Consortium: Phase 1 data release and analysis. F1000Research, 2015, 4, 1075.	0.8	270
34	Improved data analysis for the MinION nanopore sequencer. Nature Methods, 2015, 12, 351-356.	9.0	557
35	Centromere reference models for human chromosomes X and Y satellite arrays. Genome Research, 2014, 24, 697-707.	2.4	210