

Winston Timp

List of Publications by Year in descending order

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Version: 2024-02-01

81
papers

9,095
citations

109321

35
h-index

64796

79
g-index

118
all docs

118
docs citations

118
times ranked

12255
citing authors

#	ARTICLE	IF	CITATIONS
1	Chromosome-specific telomere lengths and the minimal functional telomere revealed by nanopore sequencing. <i>Genome Research</i> , 2022, 32, 616-628.	5.5	25
2	Epigenetic comparison of CHO hosts and clones reveals divergent methylation and transcription patterns across lineages. <i>Biotechnology and Bioengineering</i> , 2022, 119, 1062-1076.	3.3	6
3	Direct detection of RNA modifications and structure using single-molecule nanopore sequencing. <i>Cell Genomics</i> , 2022, 2, 100097.	6.5	55
4	Assembled and annotated 26.5 Gbp coast redwood genome: a resource for estimating evolutionary adaptive potential and investigating hexaploid origin. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	28
5	Epigenetic patterns in a complete human genome. <i>Science</i> , 2022, 376, eabj5089.	12.6	118
6	Complete genomic and epigenetic maps of human centromeres. <i>Science</i> , 2022, 376, eabl4178.	12.6	204
7	From telomere to telomere: The transcriptional and epigenetic state of human repeat elements. <i>Science</i> , 2022, 376, eabk3112.	12.6	146
8	The complete sequence of a human genome. <i>Science</i> , 2022, 376, 44-53.	12.6	1,222
9	Segmental duplications and their variation in a complete human genome. <i>Science</i> , 2022, 376, eabj6965.	12.6	130
10	Temozolomide-induced guanine mutations create exploitable vulnerabilities of guanine-rich DNA and RNA regions in drug-resistant gliomas. <i>Science Advances</i> , 2022, 8, .	10.3	7
11	Long read mitochondrial genome sequencing using Cas9-guided adaptor ligation. <i>Mitochondrion</i> , 2022, 65, 176-183.	3.4	8
12	Metagenomic next-generation sequencing of rectal swabs for the surveillance of antimicrobial-resistant organisms on the Illumina Miseq and Oxford MinION platforms. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2021, 40, 95-102.	2.9	16
13	Targeted nanopore sequencing by real-time mapping of raw electrical signal with UNCALLED. <i>Nature Biotechnology</i> , 2021, 39, 431-441.	17.5	160
14	Subcloning induces changes in the DNA methylation pattern of outgrowing Chinese hamster ovary cell colonies. <i>Biotechnology Journal</i> , 2021, 16, e2000350.	3.5	11
15	Epigenetically regulated digital signaling defines epithelial innate immunity at the tissue level. <i>Nature Communications</i> , 2021, 12, 1836.	12.8	13
16	Genomic diversity of SARS-CoV-2 during early introduction into the Baltimore-Washington metropolitan area. <i>JCI Insight</i> , 2021, 6, .	5.0	31
17	A plasmid locus associated with <i>Klebsiella</i> clinical infections encodes a microbiome-dependent gut fitness factor. <i>PLoS Pathogens</i> , 2021, 17, e1009537.	4.7	20
18	Genome and transcriptome of a pathogenic yeast, <i>Candida nivariensis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	1

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19	The American lobster genome reveals insights on longevity, neural, and immune adaptations. <i>Science Advances</i> , 2021, 7, .	10.3	27
20	Chemical and photochemical error rates in light-directed synthesis of complex DNA libraries. <i>Nucleic Acids Research</i> , 2021, 49, 6687-6701.	14.5	20
21	PRINCESS: comprehensive detection of haplotype resolved SNVs, SVs, and methylation. <i>Genome Biology</i> , 2021, 22, 268.	8.8	28
22	<i>De novo</i> genome assembly of the tobacco hornworm moth (<i>Manduca sexta</i>). <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	20
23	Plasma virome and the risk of blood-borne infection in persons with substance use disorder. <i>Nature Communications</i> , 2021, 12, 6909.	12.8	8
24	Cell-Cycle-Dependent ERK Signaling Dynamics Direct Fate Specification in the Mammalian Preimplantation Embryo. <i>Developmental Cell</i> , 2020, 55, 328-340.e5.	7.0	66
25	Simultaneous profiling of chromatin accessibility and methylation on human cell lines with nanopore sequencing. <i>Nature Methods</i> , 2020, 17, 1191-1199.	19.0	133
26	Multi-ancestry fine mapping of interferon lambda and the outcome of acute hepatitis C virus infection. <i>Genes and Immunity</i> , 2020, 21, 348-359.	4.1	5
27	Comprehensive analysis of structural variants in breast cancer genomes using single-molecule sequencing. <i>Genome Research</i> , 2020, 30, 1258-1273.	5.5	72
28	A Reference Genome Sequence for Giant Sequoia. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3907-3919.	1.8	67
29	Telomere-to-telomere assembly of a complete human X chromosome. <i>Nature</i> , 2020, 585, 79-84.	27.8	549
30	Identification of Essential Genes and Fluconazole Susceptibility Genes in <i>Candida glabrata</i> by Profiling <i>Hermes</i> Transposon Insertions. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3859-3870.	1.8	27
31	High-quality chromosome-scale assembly of the walnut (<i>Juglans regia</i> L.) reference genome. <i>GigaScience</i> , 2020, 9, .	6.4	83
32	Characterization of Allele-Specific Regulation of Telomerase Reverse Transcriptase in Promoter Mutant Thyroid Cancer Cell Lines. <i>Thyroid</i> , 2020, 30, 1470-1481.	4.5	14
33	A framework for assessing 16S rRNA marker-gene survey data analysis methods using mixtures.. <i>Microbiome</i> , 2020, 8, 35.	11.1	2
34	The full-length transcriptome of <i>C. elegans</i> using direct RNA sequencing. <i>Genome Research</i> , 2020, 30, 299-312.	5.5	77
35	Targeted nanopore sequencing with Cas9-guided adapter ligation. <i>Nature Biotechnology</i> , 2020, 38, 433-438.	17.5	286
36	Beyond mass spectrometry, the next step in proteomics. <i>Science Advances</i> , 2020, 6, eaax8978.	10.3	208

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37	Characterization of human telomerase reverse transcriptase promoter methylation and transcription factor binding in differentiated thyroid cancer cell lines. <i>Genes Chromosomes and Cancer</i> , 2019, 58, 530-540.	2.8	21
38	Epigenetic Changes Induced by <i>Bacteroides fragilis</i> Toxin. <i>Infection and Immunity</i> , 2019, 87, .	2.2	43
39	Current State of and Future Opportunities for Prediction in Microbiome Research: Report from the Mid-Atlantic Microbiome Meet-up in Baltimore on 9 January 2019. <i>MSystems</i> , 2019, 4, .	3.8	6
40	Nanopore native RNA sequencing of a human poly(A) transcriptome. <i>Nature Methods</i> , 2019, 16, 1297-1305.	19.0	411
41	Applying Rapid Whole-Genome Sequencing To Predict Phenotypic Antimicrobial Susceptibility Testing Results among Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Clinical Isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	62
42	MiR-203a is differentially expressed during branching morphogenesis and EMT in breast progenitor cells and is a repressor of peroxidase. <i>Mechanisms of Development</i> , 2019, 155, 34-47.	1.7	13
43	Transmission and clearance of potential procarcinogenic bacteria during fecal microbiota transplantation for recurrent <i>Clostridioides difficile</i> . <i>JCI Insight</i> , 2019, 4, .	5.0	32
44	Single-molecule, full-length transcript sequencing provides insight into the extreme metabolism of the ruby-throated hummingbird <i>Archilochus colubris</i> . <i>GigaScience</i> , 2018, 7, 1-12.	6.4	67
45	Antibiotic pressure on the acquisition and loss of antibiotic resistance genes in <i>Klebsiella pneumoniae</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 1796-1803.	3.0	44
46	Successful Treatment of Persistent <i>Burkholderia cepacia</i> Complex Bacteremia with Ceftazidime-Avibactam. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	28
47	Protein engineering strategies for improving the selective methylation of target CpG sites by a dCas9-directed cytosine methyltransferase in bacteria. <i>PLoS ONE</i> , 2018, 13, e0209408.	2.5	9
48	A Loss of Epigenetic Control Can Promote Cell Death through Reversing the Balance of Pathways in a Signaling Network. <i>Molecular Cell</i> , 2018, 72, 60-70.e3.	9.7	10
49	Detecting DNA cytosine methylation using nanopore sequencing. <i>Nature Methods</i> , 2017, 14, 407-410.	19.0	820
50	First Draft Genome Sequence of the Pathogenic Fungus <i>Lomentospora prolificans</i> (Formerly) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i>	1.8	11
51	Whole genome DNA methylation sequencing of the chicken retina, cornea and brain. <i>Scientific Data</i> , 2017, 4, 170148.	5.3	29
52	Multiplexed analysis of fixed tissue RNA using Ligation in situ Hybridization. <i>Nucleic Acids Research</i> , 2017, 45, e128-e128.	14.5	7
53	Targeted DNA methylation in human cells using engineered dCas9-methyltransferases. <i>Scientific Reports</i> , 2017, 7, 6732.	3.3	73
54	Presence of Human Hepatitis B Virus in a Cohort of People Who Inject Drugs. <i>Annals of Internal Medicine</i> , 2017, 167, 1.	3.9	28

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55	Nanopore sequencing detects structural variants in cancer. <i>Cancer Biology and Therapy</i> , 2016, 17, 246-253.	3.4	130
56	Ecology of a Simple Synthetic Biofilm. <i>Biological and Medical Physics Series</i> , 2015, , 205-226.	0.4	1
57	Think Small: Nanopores for Sensing and Synthesis. <i>IEEE Access</i> , 2014, 2, 1396-1408.	4.2	18
58	Large hypomethylated blocks as a universal defining epigenetic alteration in human solid tumors. <i>Genome Medicine</i> , 2014, 6, 61.	8.2	170
59	Nanopore Sequencing using a Hidden Markov Model for Base-Calling. <i>Biophysical Journal</i> , 2013, 104, 211a.	0.5	0
60	Epigenetic Memory Emerging from Integrated Transcription Bursts. <i>Biophysical Journal</i> , 2013, 105, 1526-1532.	0.5	7
61	Cancer as a dysregulated epigenome allowing cellular growth advantage at the expense of the host. <i>Nature Reviews Cancer</i> , 2013, 13, 497-510.	28.4	490
62	Using a nanopore for single molecule detection and single cell transfection. <i>Analyst, The</i> , 2012, 137, 3020.	3.5	23
63	DNA Base-Calling from a Nanopore Using a Viterbi Algorithm. <i>Biophysical Journal</i> , 2012, 102, L37-L39.	0.5	75
64	Increased methylation variation in epigenetic domains across cancer types. <i>Nature Genetics</i> , 2011, 43, 768-775.	21.4	968
65	Genome-scale epigenetic reprogramming during epithelial-to-mesenchymal transition. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 867-874.	8.2	340
66	Third Generation DNA Sequencing with a Nanopore. , 2011, , 287-311.		0
67	Molecular diagnostics for personal medicine using a nanopore. <i>Wiley Interdisciplinary Reviews: Nanomedicine and Nanobiotechnology</i> , 2010, 2, 367-381.	6.1	18
68	Nanopore Sequencing: Electrical Measurements of the Code of Life. <i>IEEE Nanotechnology Magazine</i> , 2010, 9, 281-294.	2.0	81
69	Discriminating Bases by Stretching Double-Stranded DNA in a Nanopore. <i>Biophysical Journal</i> , 2010, 98, 599a.	0.5	0
70	A new link between epigenetic progenitor lesions in cancer and the dynamics of signal transduction. <i>Cell Cycle</i> , 2009, 8, 383-390.	2.6	33
71	Nanoelectromechanics of Methylated DNA in a Synthetic Nanopore. <i>Biophysical Journal</i> , 2009, 96, L32-L34.	0.5	54
72	Jamming prokaryotic cell-to-cell communications in a model biofilm. <i>Lab on A Chip</i> , 2009, 9, 925-934.	6.0	31

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73	Optimal optical trap for bacterial viability. <i>Physical Review E</i> , 2008, 78, 021910.	2.1	73
74	Live cell lithography: Using optical tweezers to create synthetic tissue. <i>Lab on A Chip</i> , 2008, 8, 2174.	6.0	89
75	Chapter 14 Electron Microscopy of Hydrated Samples. <i>Methods in Cell Biology</i> , 2008, 89, 391-407.	1.1	13
76	Enhanced sensitivity to IGF-II signaling links loss of imprinting of <i>IGF2</i> to increased cell proliferation and tumor risk. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 20926-20931.	7.1	97
77	Nucleic acid and protein mass mapping by live-cell deep-ultraviolet microscopy. <i>Nature Methods</i> , 2007, 4, 567-569.	19.0	144
78	Laser-Guided Assembly of Heterotypic Three-Dimensional Living Cell Microarrays. <i>Biophysical Journal</i> , 2006, 91, 3465-3473.	0.5	99
79	Wet electron microscopy with quantum dots. <i>BioTechniques</i> , 2006, 41, 295-298.	1.8	11
80	The relentless march of the MOSFET gate oxide thickness to zero. <i>Microelectronics Reliability</i> , 2000, 40, 557-562.	1.7	27
81	Electrical simulation of scanning capacitance microscopy imaging of the pn junction with semiconductor probe tips. <i>Applied Physics Letters</i> , 1999, 74, 3672-3674.	3.3	24