Benedict Paten

List of Publications by Year
in descending order

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82 papers	20,752 citations	53939 47 h-index	64407 83 g-index
115 all docs	115 docs citations	115 times ranked	29881 citing authors

#	Article	IF	Citations
1	Inverting the model of genomics data sharing with the NHGRI Genomic Data Science Analysis, Visualization, and Informatics Lab-space. Cell Genomics, 2022, 2, 100085.	3.0	59
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	Chasing perfection: validation and polishing strategies for telomere-to-telomere genome assemblies. Nature Methods, 2022, 19, 687-695.	9.0	42
5	Accelerated identification of disease-causing variants with ultra-rapid nanopore genome sequencing. Nature Biotechnology, 2022, 40, 1035-1041.	9.4	45
6	Complete genomic and epigenetic maps of human centromeres. Science, 2022, 376, eabl4178.	6.0	204
7	Concerted modification of nucleotides at functional centers of the ribosome revealed by single-molecule RNA modification profiling. ELife, 2022, 11, .	2.8	17
8	A complete reference genome improves analysis of human genetic variation. Science, 2022, 376, eabl3533.	6.0	144
9	The complete sequence of a human genome. Science, 2022, 376, 44-53.	6.0	1,222
10	The Human Pangenome Project: a global resource to map genomic diversity. Nature, 2022, 604, 437-446.	13.7	192
11	PrecisionFDA Truth Challenge V2: Calling variants from short and long reads in difficult-to-map regions. Cell Genomics, 2022, 2, 100129.	3.0	72
12	A complete pedigree-based graph workflow for rare candidate variant analysis. Genome Research, 2022, , .	2.4	1
13	Efficient dynamic variation graphs. Bioinformatics, 2021, 36, 5139-5144.	1.8	18
14	Fully phased human genome assembly without parental data using single-cell strand sequencing and long reads. Nature Biotechnology, 2021, 39, 302-308.	9.4	127
15	GENCODE 2021. Nucleic Acids Research, 2021, 49, D916-D923.	6.5	633
16	Walk-Preserving Transformation of Overlapped Sequence Graphs into Blunt Sequence Graphs with GetBlunted. Lecture Notes in Computer Science, 2021, , 169-177.	1.0	6
17	Towards complete and error-free genome assemblies of all vertebrate species. Nature, 2021, 592, 737-746.	13.7	1,139
18	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

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19	A high-quality bonobo genome refines the analysis of hominid evolution. Nature, 2021, 594, 77-81.	13.7	39
20	Positive selection in noncoding genomic regions of vocal learning birds is associated with genes implicated in vocal learning and speech functions in humans. Genome Research, 2021, 31, 2035-2049.	2.4	16
21	Haplotype-aware variant calling with PEPPER-Margin-DeepVariant enables high accuracy in nanopore long-reads. Nature Methods, 2021, 18, 1322-1332.	9.0	139
22	Towards inferring nanopore sequencing ionic currents from nucleotide chemical structures. Nature Communications, 2021, 12, 6545.	5.8	3
23	Pangenomics enables genotyping of known structural variants in 5202 diverse genomes. Science, 2021, 374, abg8871.	6.0	132
24	Haplotype-aware graph indexes. Bioinformatics, 2020, 36, 400-407.	1.8	59
25	Distance indexing and seed clustering in sequence graphs. Bioinformatics, 2020, 36, i146-i153.	1.8	10
26	ProTECTâ€"Prediction of T-Cell Epitopes for Cancer Therapy. Frontiers in Immunology, 2020, 11, 483296.	2.2	14
27	Progressive Cactus is a multiple-genome aligner for the thousand-genome era. Nature, 2020, 587, 246-251.	13.7	256
28	Dense sampling of bird diversity increases power of comparative genomics. Nature, 2020, 587, 252-257.	13.7	251
29	Telomere-to-telomere assembly of a complete human X chromosome. Nature, 2020, 585, 79-84.	13.7	549
30	Sequence diversity analyses of an improved rhesus macaque genome enhance its biomedical utility. Science, 2020, 370, .	6.0	105
31	Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. Nature Biotechnology, 2020, 38, 1044-1053.	9.4	344
32	Pangenome Graphs. Annual Review of Genomics and Human Genetics, 2020, 21, 139-162.	2.5	148
33	Gaussian mixture model-based unsupervised nucleotide modification number detection using nanopore-sequencing readouts. Bioinformatics, 2020, 36, 4928-4934.	1.8	21
34	Genotyping structural variants in pangenome graphs using the vg toolkit. Genome Biology, 2020, 21, 35.	3.8	150
35	SegAlign: A Scalable GPU-Based Whole Genome Aligner. , 2020, , .		8
36	Sequence tube maps: making graph genomes intuitive to commuters. Bioinformatics, 2019, 35, 5318-5320.	1.8	28

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37	Haplotype-aware diplotyping from noisy long reads. Genome Biology, 2019, 20, 116.	3.8	43
38	The Genome of C57BL/6J â€œEveâ€ the Mother of the Laboratory Mouse Genome Reference Strain. G3: Genes, Genomes, Genetics, 2019, 9, 1795-1805.	0.8	49
39	Nanopore native RNA sequencing of a human poly(A) transcriptome. Nature Methods, 2019, 16, 1297-1305.	9.0	411
40	GENCODE reference annotation for the human and mouse genomes. Nucleic Acids Research, 2019, 47, D766-D773.	6.5	2,350
41	Whole-Genome Alignment and Comparative Annotation. Annual Review of Animal Biosciences, 2019, 7, 41-64.	3.6	62
42	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	0.8	5
43	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	0.8	14
44	Superbubbles, Ultrabubbles, and Cacti. Journal of Computational Biology, 2018, 25, 649-663.	0.8	46
45	Nanopore sequencing and assembly of a human genome with ultra-long reads. Nature Biotechnology, 2018, 36, 338-345.	9.4	1,443
46	Repeat associated mechanisms of genome evolution and function revealed by the Mus caroli and Mus pahari genomes. Genome Research, 2018, 28, 448-459.	2.4	99
47	Linear assembly of a human centromere on the Y chromosome. Nature Biotechnology, 2018, 36, 321-323.	9.4	216
48	BRCA Challenge: BRCA Exchange as a global resource for variants in BRCA1 and BRCA2. PLoS Genetics, 2018, 14, e1007752.	1.5	148
49	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. Nature Genetics, 2018, 50, 1574-1583.	9.4	169
50	Chromosome assembly of large and complex genomes using multiple references. Genome Research, 2018, 28, 1720-1732.	2.4	94
51	Evaluating recovery potential of the northern white rhinoceros from cryopreserved somatic cells. Genome Research, 2018, 28, 780-788.	2.4	39
52	Variation graph toolkit improves read mapping by representing genetic variation in the reference. Nature Biotechnology, 2018, 36, 875-879.	9.4	435
53	High-resolution comparative analysis of great ape genomes. Science, 2018, 360, .	6.0	304
54	Comparative Annotation Toolkit (CAT)â€”simultaneous clade and personal genome annotation. Genome Research, 2018, 28, 1029-1038.	2.4	86

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55	Improved genome assembly of American alligator genome reveals conserved architecture of estrogen signaling. Genome Research, 2017, 27, 686-696.	2.4	38
56	Mapping DNA methylation with high-throughput nanopore sequencing. Nature Methods, 2017, 14, 411-413.	9.0	390
57	Toil enables reproducible, open source, big biomedical data analyses. Nature Biotechnology, 2017, 35, 314-316.	9.4	873
58	Genome graphs and the evolution of genome inference. Genome Research, 2017, 27, 665-676.	2.4	264
59	Modelling haplotypes with respect to reference cohort variation graphs. Bioinformatics, 2017, 33, i118-i123.	1.8	12
60	A graph extension of the positional Burrowsâ€“Wheeler transform and its applications. Algorithms for Molecular Biology, 2017, 12, 18.	0.3	33
61	Long-read sequence assembly of the gorilla genome. Science, 2016, 352, aae0344.	6.0	368
62	The Oxford Nanopore MinION: delivery of nanopore sequencing to the genomics community. Genome Biology, 2016, 17, 239.	3.8	985
63	A Graph Extension of the Positional Burrows-Wheeler Transform and Its Applications. Lecture Notes in Computer Science, 2016, , 246-256.	1.0	9
64	Representing and decomposing genomic structural variants as balanced integer flows on sequence graphs. BMC Bioinformatics, 2016, 17, 400.	1.2	6
65	Improved data analysis for the MinION nanopore sequencer. Nature Methods, 2015, 12, 351-356.	9.0	557
66	Building a Pan-Genome Reference for a Population. Journal of Computational Biology, 2015, 22, 387-401.	0.8	48
67	The Genome 10K Project: A Way Forward. Annual Review of Animal Biosciences, 2015, 3, 57-111.	3.6	294
68	Canonical, stable, general mapping using context schemes. Bioinformatics, 2015, 31, btv435.	1.8	5
69	The UCSC Genome Browser database: 2015 update. Nucleic Acids Research, 2015, 43, D670-D681.	6.5	891
70	Track data hubs enable visualization of user-defined genome-wide annotations on the UCSC Genome Browser. Bioinformatics, 2014, 30, 1003-1005.	1.8	375
71	Alignathon: a competitive assessment of whole-genome alignment methods. Genome Research, 2014, 24, 2077-2089.	2.4	102
72	Three crocodilian genomes reveal ancestral patterns of evolution among archosaurs. Science, 2014, 346, 1254449.	6.0	300

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73	Ragoutâ€"a reference-assisted assembly tool for bacterial genomes. Bioinformatics, 2014, 30, i302-i309.	1.8	169
74	Comparative assembly hubs: Web-accessible browsers for comparative genomics. Bioinformatics, 2014, 30, 3293-3301.	1.8	33
75	An evolutionary arms race between KRAB zinc-finger genes ZNF91/93 and SVA/L1 retrotransposons. Nature, 2014, 516, 242-245.	13.7	396
76	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. GigaScience, 2013, 2, 10.	3.3	582
77	HAL: a hierarchical format for storing and analyzing multiple genome alignments. Bioinformatics, 2013, 29, 1341-1342.	1.8	164
78	Cactus Graphs for Genome Comparisons. Journal of Computational Biology, 2011, 18, 469-481.	0.8	93
79	Cactus: Algorithms for genome multiple sequence alignment. Genome Research, 2011, 21, 1512-1528.	2.4	245
80	Sequence progressive alignment, a framework for practical large-scale probabilistic consistency alignment. Bioinformatics, 2009, 25, 295-301.	1.8	47
81	Genome-wide nucleotide-level mammalian ancestor reconstruction. Genome Research, 2008, 18, 1829-1843.	2.4	164
82	Enredo and Pecan: Genome-wide mammalian consistency-based multiple alignment with paralogs. Genome Research, 2008, 18, 1814-1828.	2.4	249