Tobias Marschall

List of Publications by Year
in descending order

61	8,601	136950 32	133252 59
papers	citations	h-index	g-index

103	103	103	8669
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The complete sequence of a human genome. Science, 2022, 376, 44-53.	12.6	1,222
2	Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome. Nature Biotechnology, 2019, 37, 1155-1162.	17.5	1,010
3	Eleven grand challenges in single-cell data science. Genome Biology, 2020, 21, 31.	8.8	742
4	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
5	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	12.6	358
6	Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. Nature Biotechnology, 2020, 38, 1044-1053.	17.5	344
7	W<scp>hats</scp>H<scp>ap</scp>: Weighted Haplotype Assembly for Future-Generation Sequencing Reads. Journal of Computational Biology, 2015, 22, 498-509.	1.6	337
8	Mapping and phasing of structural variation in patient genomes using nanopore sequencing. Nature Communications, 2017, 8, 1326.	12.8	315
9	A robust benchmark for detection of germline large deletions and insertions. Nature Biotechnology, 2020, 38, 1347-1355.	17.5	233
10	The Human Pangenome Project: a global resource to map genomic diversity. Nature, 2022, 604, 437-446.	27.8	192
11	Deep sequencing reveals differential expression of microRNAs in favorable versus unfavorable neuroblastoma. Nucleic Acids Research, 2010, 38, 5919-5928.	14.5	183
12	Pangenome Graphs. Annual Review of Genomics and Human Genetics, 2020, 21, 139-162.	6.2	148
13	Fully phased human genome assembly without parental data using single-cell strand sequencing and long reads. Nature Biotechnology, 2021, 39, 302-308.	17.5	127
14	Characteristics of de novo structural changes in the human genome. Genome Research, 2015, 25, 792-801.	5.5	115
15	Chromosome-scale, haplotype-resolved assembly of human genomes. Nature Biotechnology, 2021, 39, 309-312.	17.5	109
16	Negative selection in humans and fruit flies involves synergistic epistasis. Science, 2017, 356, 539-542.	12.6	103
17	CLEVER: clique-enumerating variant finder. Bioinformatics, 2012, 28, 2875-2882.	4.1	101
18	A high-quality human reference panel reveals the complexity and distribution of genomic structural variants. Nature Communications, 2016, 7, 12989.	12.8	99

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19	Viral Quasispecies Assembly via Maximal Clique Enumeration. PLoS Computational Biology, 2014, 10, e1003515.	3.2	93
20	Pangenome-based genome inference allows efficient and accurate genotyping across a wide spectrum of variant classes. Nature Genetics, 2022, 54, 518-525.	21.4	92
21	GraphAligner: rapid and versatile sequence-to-graph alignment. Genome Biology, 2020, 21, 253.	8.8	90
22	Dense and accurate whole-chromosome haplotyping of individual genomes. Nature Communications, 2017, 8, 1293.	12.8	83
23	Benchmarking challenging small variants with linked and long reads. Cell Genomics, 2022, 2, 100128.	6.5	77
24	Expectations and blind spots for structural variation detection from long-read assemblies and short-read genome sequencing technologies. American Journal of Human Genetics, 2021, 108, 919-928.	6.2	72
25	Recurrent inversion polymorphisms in humans associate with genetic instability and genomic disorders. Cell, 2022, 185, 1986-2005.e26.	28.9	67
26	A graph-based approach to diploid genome assembly. Bioinformatics, 2018, 34, i105-i114.	4.1	59
27	Single-cell analysis of structural variations and complex rearrangements with tri-channel processing. Nature Biotechnology, 2020, 38, 343-354.	17.5	59
28	A diploid assembly-based benchmark for variants in the major histocompatibility complex. Nature Communications, 2020, 11, 4794.	12.8	56
29	Bit-parallel sequence-to-graph alignment. Bioinformatics, 2019, 35, 3599-3607.	4.1	50
30	Haplotype threading: accurate polyploid phasing from long reads. Genome Biology, 2020, 21, 252.	8.8	50
31	MBG: Minimizer-based sparse de Bruijn Graph construction. Bioinformatics, 2021, 37, 2476-2478.	4.1	49
32	Efficient exact motif discovery. Bioinformatics, 2009, 25, i356-i364.	4.1	48
33	Discovering motifs that induce sequencing errors. BMC Bioinformatics, 2013, 14, S1.	2.6	47
34	MATE-CLEVER: Mendelian-inheritance-aware discovery and genotyping of midsize and long indels. Bioinformatics, 2013, 29, 3143-3150.	4.1	44
35	Haplotype-aware diplotyping from noisy long reads. Genome Biology, 2019, 20, 116.	8.8	43
36	Read-based phasing of related individuals. Bioinformatics, 2016, 32, i234-i242.	4.1	40

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37	Recurrent inversion toggling and great ape genome evolution. Nature Genetics, 2020, 52, 849-858.	21.4	40
38	Nextâ€generation RNA sequencing reveals differential expression of MYCN target genes and suggests the mTOR pathway as a promising therapy target in MYCNâ€amplified neuroblastoma. International Journal of Cancer, 2013, 132, E106-15.	5.1	26
39	Strand-seq enables reliable separation of long reads by chromosome via expectation maximization. Bioinformatics, 2018, 34, i115-i123.	4.1	24
40	SNP and indel frequencies at transcription start sites and at canonical and alternative translation initiation sites in the human genome. PLoS ONE, 2019, 14, e0214816.	2.5	24
41	Detecting horizontal gene transfer by mapping sequencing reads across species boundaries. Bioinformatics, 2016, 32, i595-i604.	4.1	23
42	Repeat- and error-aware comparison of deletions. Bioinformatics, 2015, 31, 2947-2954.	4.1	16
43	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	1.6	14
44	K2P18.1 translates T cell receptor signals into thymic regulatory T cell development. Cell Research, 2022, 32, 72-88.	12.0	14
45	Genotyping inversions and tandem duplications. Bioinformatics, 2017, 33, 4015-4023.	4.1	12
46	Fully-sensitive seed finding in sequence graphs using a hybrid index. Bioinformatics, 2019, 35, i81-i89.	4.1	12
47	Varlociraptor: enhancing sensitivity and controlling false discovery rate in somatic indel discovery. Genome Biology, 2020, 21, 98.	8.8	12
48	Probabilistic Arithmetic Automata and Their Applications. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1737-1750.	3.0	11
49	PWHATSHAP: efficient haplotyping for future generation sequencing. BMC Bioinformatics, 2016, 17, 342.	2.6	11
50	Identifying transcriptional miRNA biomarkers by integrating high-throughput sequencing and real-time PCR data. Methods, 2013, 59, 154-163.	3.8	10
51	A multi-platform reference for somatic structural variation detection. Cell Genomics, 2022, 2, 100139.	6.5	10
52	ASHLEYS: automated quality control for single-cell Strand-seq data. Bioinformatics, 2021, 37, 3356-3357.	4.1	9
53	Genome sequence analysis with MonetDB. Datenbank-Spektrum, 2015, 15, 185-191.	1.3	7
54	SV-AUTOPILOT: optimized, automated construction of structural variation discovery and benchmarking pipelines. BMC Genomics, 2015, 16, 238.	2.8	5

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55	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	1.6	5
56	An Algorithm to Compute the Character Access Count Distribution for Pattern Matching Algorithms. Algorithms, 2011, 4, 285-306.	2.1	3
57	A Guided Tour to Computational Haplotyping. Lecture Notes in Computer Science, 2017, , 50-63.	1.3	3
58	Genetic polyploid phasing from low-depth progeny samples. IScience, 2022, 25, 104461.	4.1	1
59	BubbleGun: enumerating bubbles and superbubbles in genome graphs. Bioinformatics, 2022, 38, 4217-4219.	4.1	1
60	Chromatyping: Reconstructing Nucleosome Profiles from NOMe Sequencing Data. Journal of Computational Biology, 2020, 27, 330-341.	1.6	0
61	Chromatyping: Reconstructing Nucleosome Profiles from NOMe Sequencing Data. Lecture Notes in Computer Science, 2018, , 21-36.	1.3	0