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	K2P18.1 translates T cell receptor signals into thymic regulatory T cell development. Cell Research, 2022, 32, 72-88.	12.0	14
2	The complete sequence of a human genome. Science, 2022, 376, 44-53.	12.6	1,222
3	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
4	The Human Pangenome Project: a global resource to map genomic diversity. Nature, 2022, 604, 437-446.	27.8	192
5	Recurrent inversion polymorphisms in humans associate with genetic instability and genomic disorders. Cell, 2022, 185, 1986-2005.e26.	28.9	67
6	Benchmarking challenging small variants with linked and long reads. Cell Genomics, 2022, 2, 100128.	6.5	77
7	Genetic polyploid phasing from low-depth progeny samples. IScience, 2022, 25, 104461.	4.1	1
8	A multi-platform reference for somatic structural variation detection. Cell Genomics, 2022, 2, 100139.	6.5	10
9	BubbleGun: enumerating bubbles and superbubbles in genome graphs. Bioinformatics, 2022, 38, 4217-4219.	4.1	1
10	Chromosome-scale, haplotype-resolved assembly of human genomes. Nature Biotechnology, 2021, 39, 309-312.	17.5	109
11	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
12	ASHLEYS: automated quality control for single-cell Strand-seq data. Bioinformatics, 2021, 37, 3356-3357.	4.1	9
13	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	12.6	358
14	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
15	MBG: Minimizer-based sparse de Bruijn Graph construction. Bioinformatics, 2021, 37, 2476-2478.	4.1	49
16	Single-cell analysis of structural variations and complex rearrangements with tri-channel processing. Nature Biotechnology, 2020, 38, 343-354.	17.5	59
17	Haplotype threading: accurate polyploid phasing from long reads. Genome Biology, 2020, 21, 252.	8.8	50
18	A diploid assembly-based benchmark for variants in the major histocompatibility complex. Nature Communications, 2020, 11, 4794.	12.8	56

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19	GraphAligner: rapid and versatile sequence-to-graph alignment. Genome Biology, 2020, 21, 253.	8.8	90
20	Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. Nature Biotechnology, 2020, 38, 1044-1053.	17.5	344
21	Pangenome Graphs. Annual Review of Genomics and Human Genetics, 2020, 21, 139-162.	6.2	148
22	A robust benchmark for detection of germline large deletions and insertions. Nature Biotechnology, 2020, 38, 1347-1355.	17.5	233
23	Recurrent inversion toggling and great ape genome evolution. Nature Genetics, 2020, 52, 849-858.	21.4	40
24	Chromatyping: Reconstructing Nucleosome Profiles from NOMe Sequencing Data. Journal of Computational Biology, 2020, 27, 330-341.	1.6	0
25	Eleven grand challenges in single-cell data science. Genome Biology, 2020, 21, 31.	8.8	742
26	Varlociraptor: enhancing sensitivity and controlling false discovery rate in somatic indel discovery. Genome Biology, 2020, 21, 98.	8.8	12
27	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
28	Fully-sensitive seed finding in sequence graphs using a hybrid index. Bioinformatics, 2019, 35, i81-i89.	4.1	12
29	Haplotype-aware diplotyping from noisy long reads. Genome Biology, 2019, 20, 116.	8.8	43
30	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
31	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
32	Bit-parallel sequence-to-graph alignment. Bioinformatics, 2019, 35, 3599-3607.	4.1	50
33	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	1.6	5
34	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	1.6	14
35	A graph-based approach to diploid genome assembly. Bioinformatics, 2018, 34, i105-i114.	4.1	59
36	Strand-seq enables reliable separation of long reads by chromosome via expectation maximization. Bioinformatics, 2018, 34, i115-i123.	4.1	24

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37	Chromatyping: Reconstructing Nucleosome Profiles from NOMe Sequencing Data. Lecture Notes in Computer Science, 2018, , 21-36.	1.3	0
38	Negative selection in humans and fruit flies involves synergistic epistasis. Science, 2017, 356, 539-542.	12.6	103
39	A Guided Tour to Computational Haplotyping. Lecture Notes in Computer Science, 2017, , 50-63.	1.3	3
40	Genotyping inversions and tandem duplications. Bioinformatics, 2017, 33, 4015-4023.	4.1	12
41	Dense and accurate whole-chromosome haplotyping of individual genomes. Nature Communications, 2017, 8, 1293.	12.8	83
42	Mapping and phasing of structural variation in patient genomes using nanopore sequencing. Nature Communications, 2017, 8, 1326.	12.8	315
43	Read-based phasing of related individuals. Bioinformatics, 2016, 32, i234-i242.	4.1	40
44	A high-quality human reference panel reveals the complexity and distribution of genomic structural variants. Nature Communications, 2016, 7, 12989.	12.8	99
45	Detecting horizontal gene transfer by mapping sequencing reads across species boundaries. Bioinformatics, 2016, 32, i595-i604.	4.1	23
46	PWHATSHAP: efficient haplotyping for future generation sequencing. BMC Bioinformatics, 2016, 17, 342.	2.6	11
47	Genome sequence analysis with MonetDB. Datenbank-Spektrum, 2015, 15, 185-191.	1.3	7
48	Repeat- and error-aware comparison of deletions. Bioinformatics, 2015, 31, 2947-2954.	4.1	16
49	Characteristics of de novo structural changes in the human genome. Genome Research, 2015, 25, 792-801.	5.5	115
50	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
51	SV-AUTOPILOT: optimized, automated construction of structural variation discovery and benchmarking pipelines. BMC Genomics, 2015, 16, 238.	2.8	5
52	Viral Quasispecies Assembly via Maximal Clique Enumeration. PLoS Computational Biology, 2014, 10, e1003515.	3.2	93
53	Discovering motifs that induce sequencing errors. BMC Bioinformatics, 2013, 14, S1.	2.6	47
54	MATE-CLEVER: Mendelian-inheritance-aware discovery and genotyping of midsize and long indels. Bioinformatics, 2013, 29, 3143-3150.	4.1	44

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55	Identifying transcriptional miRNA biomarkers by integrating high-throughput sequencing and real-time PCR data. Methods, 2013, 59, 154-163.	3.8	10
56	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
57	CLEVER: clique-enumerating variant finder. Bioinformatics, 2012, 28, 2875-2882.	4.1	101
58	Probabilistic Arithmetic Automata and Their Applications. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1737-1750.	3.0	11
59	An Algorithm to Compute the Character Access Count Distribution for Pattern Matching Algorithms. Algorithms, 2011, 4, 285-306.	2.1	3
60	Deep sequencing reveals differential expression of microRNAs in favorable versus unfavorable neuroblastoma. Nucleic Acids Research, 2010, 38, 5919-5928.	14.5	183
61	Efficient exact motif discovery. Bioinformatics, 2009, 25, i356-i364.	4.1	48