Tobias Marschall

List of Publications by Citations

88 papers	3,495 citations	29 h-index	58 g-index
103 ext. papers	6,151 ext. citations	15.6 avg, IF	5.09 L-index

#	Paper	IF	Citations
88	Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome. *Nature Biotechnology*, **2019**, 37, 1155-1162	44.5	427
87	Multi-platform discovery of haplotype-resolved structural variation in human genomes. *Nature Communications*, **2019**, 10, 1784	17.4	346
86	Eleven grand challenges in single-cell data science. *Genome Biology*, **2020**, 21, 31	18.3	274
85	Mapping and phasing of structural variation in patient genomes using nanopore sequencing. *Nature Communications*, **2017**, 8, 1326	17.4	191
84	WhatsHap: Weighted Haplotype Assembly for Future-Generation Sequencing Reads. *Journal of Computational Biology*, **2015**, 22, 498-509	1.7	172
83	Deep sequencing reveals differential expression of microRNAs in favorable versus unfavorable neuroblastoma. *Nucleic Acids Research*, **2010**, 38, 5919-28	20.1	166
82	Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. *Nature Biotechnology*, **2020**, 38, 1044-1053	44.5	143
81	The complete sequence of a human genome.. *Science*, **2022**, 376, 44-53	33.3	107
80	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. *Science* , **2021**, 372,	33.3	100
79	A robust benchmark for detection of germline large deletions and insertions. *Nature Biotechnology*, **2020**, 38, 1347-1355	44.5	98
78	WhatsHap: fast and accurate read-based phasing		85
77	Characteristics of de novo structural changes in the human genome. *Genome Research*, **2015**, 25, 792-801	9.7	83
76	CLEVER: clique-enumerating variant finder. *Bioinformatics*, **2012**, 28, 2875-82	7.2	79
75	A high-quality human reference panel reveals the complexity and distribution of genomic structural variants. *Nature Communications*, **2016**, 7, 12989	17.4	70
74	Viral quasispecies assembly via maximal clique enumeration. *PLoS Computational Biology*, **2014**, 10, e1003515	3	70
73	Dense and accurate whole-chromosome haplotyping of individual genomes. *Nature Communications*, **2017**, 8, 1293	17.4	60
72	The complete sequence of a human genome		58

71	Negative selection in humans and fruit flies involves synergistic epistasis. *Science*, **2017**, 356, 539-542	33.3	53
70	Discovering motifs that induce sequencing errors. *BMC Bioinformatics*, **2013**, 14 Suppl 5, S1	3.6	44
69	Chromosome-scale, haplotype-resolved assembly of human genomes. *Nature Biotechnology*, **2021**, 39, 309-312	44.5	44
68	Fully phased human genome assembly without parental data using single-cell strand sequencing and long reads. *Nature Biotechnology*, **2021**, 39, 302-308	44.5	42
67	Efficient exact motif discovery. *Bioinformatics*, **2009**, 25, i356-64	7.2	38
66	Pangenome Graphs. *Annual Review of Genomics and Human Genetics*, **2020**, 21, 139-162	9.7	37
65	A graph-based approach to diploid genome assembly. *Bioinformatics*, **2018**, 34, i105-i114	7.2	36
64	MATE-CLEVER: Mendelian-inheritance-aware discovery and genotyping of midsize and long indels. *Bioinformatics*, **2013**, 29, 3143-50	7.2	35
63	A robust benchmark for germline structural variant detection		34
62	Bit-parallel sequence-to-graph alignment. *Bioinformatics*, **2019**, 35, 3599-3607	7.2	32
61	Highly-accurate long-read sequencing improves variant detection and assembly of a human genome		29
60	Efficient de novo assembly of eleven human genomes using PromethION sequencing and a novel nanopore toolkit		29
59	Haplotype-aware diplotyping from noisy long reads. *Genome Biology*, **2019**, 20, 116	18.3	28
58	Multi-platform discovery of haplotype-resolved structural variation in human genomes		26
57	Benchmarking challenging small variants with linked and long reads		26
56	GraphAligner: rapid and versatile sequence-to-graph alignment. *Genome Biology*, **2020**, 21, 253	18.3	25
55	Read-based phasing of related individuals. *Bioinformatics*, **2016**, 32, i234-i242	7.2	25
54	A diploid assembly-based benchmark for variants in the major histocompatibility complex. *Nature Communications*, **2020**, 11, 4794	17.4	22

53	Next-generation RNA sequencing reveals differential expression of MYCN target genes and suggests the mTOR pathway as a promising therapy target in MYCN-amplified neuroblastoma. *International Journal of Cancer*, **2013**, 132, E106-15	7.5	21
52	Haplotype threading: accurate polyploid phasing from long reads. *Genome Biology*, **2020**, 21, 252	18.3	21
51	A fully phased accurate assembly of an individual human genome		20
50	Accurate chromosome-scale haplotype-resolved assembly of human genomes		18
49	Strand-seq enables reliable separation of long reads by chromosome via expectation maximization. *Bioinformatics*, **2018**, 34, i115-i123	7.2	17
48	Single-cell analysis of structural variations and complex rearrangements with tri-channel processing. *Nature Biotechnology*, **2020**, 38, 343-354	44.5	17
47	Detecting horizontal gene transfer by mapping sequencing reads across species boundaries. *Bioinformatics*, **2016**, 32, i595-i604	7.2	14
46	Recurrent inversion toggling and great ape genome evolution. *Nature Genetics*, **2020**, 52, 849-858	36.3	13
45	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	11	13
44	Repeat- and error-aware comparison of deletions. *Bioinformatics*, **2015**, 31, 2947-54	7.2	12
43	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	3.7	11
42	Pangenome-based genome inference		11
41	Genotyping inversions and tandem duplications. *Bioinformatics*, **2017**, 33, 4015-4023	7.2	10
40	GraphAligner: Rapid and Versatile Sequence-to-Graph Alignment		10
39	PWHATSHAP: efficient haplotyping for future generation sequencing. *BMC Bioinformatics*, **2016**, 17, 342	3.6	9
38	Identifying transcriptional miRNA biomarkers by integrating high-throughput sequencing and real-time PCR data. *Methods*, **2013**, 59, 154-63	4.6	9
37	Probabilistic arithmetic automata and their applications. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2012**, 9, 1737-50	3	9
36	Fully-sensitive seed finding in sequence graphs using a hybrid index. *Bioinformatics*, **2019**, 35, i81-i89	7.2	8

35	A strategy for building and using a human reference pangenome. *F1000Research*, **2019**, 8, 1751	3.6	8
34	AERON: Transcript quantification and gene-fusion detection using long reads		7
33	The Human Pangenome Project: a global resource to map genomic diversity.. *Nature*, **2022**, 604, 437-446	50.4	7
32	Computational Pan-Genomics: Status, Promises and Challenges		6
31	Mapping and phasing of structural variation in patient genomes using nanopore sequencing		6
30	Haplotype Threading: Accurate Polyploid Phasing from Long Reads		6
29	Genome sequence analysis with MonetDB. *Datenbank-Spektrum*, **2015**, 15, 185-191	0.6	5
28	A multi-platform reference for somatic structural variation detection		5
27	Selecting Reads for Haplotype Assembly		4
26	Haplotype-aware genotyping from noisy long reads		4
25	A Diploid Assembly-based Benchmark for Variants in the Major Histocompatibility Complex		4
24	MBG: Minimizer-based Sparse de Bruijn Graph Construction. *Bioinformatics*, **2021**,	7.2	4
23	SV-AUTOPILOT: optimized, automated construction of structural variation discovery and benchmarking pipelines. *BMC Genomics*, **2015**, 16, 238	4.5	3
22	Varlociraptor: enhancing sensitivity and controlling false discovery rate in somatic indel discovery. *Genome Biology*, **2020**, 21, 98	18.3	3
21	An Algorithm to Compute the Character Access Count Distribution for Pattern Matching Algorithms. *Algorithms*, **2011**, 4, 285-306	1.8	3
20	K18.1 translates T cell receptor signals into thymic regulatory T cell development. *Cell Research*, **2021**,	24.7	3
19	A high-quality reference panel reveals the complexity and distribution of structural genome changes in a human population		3
18	Expectations and blind spots for structural variation detection from short-read alignment and long-read assembly		3

17	De novo assembly of 64 haplotype-resolved human genomes of diverse ancestry and integrated analysis of structural variation		3
16	Automated assembly of high-quality diploid human reference genomes		3
15	A Guided Tour to Computational Haplotyping. *Lecture Notes in Computer Science*, **2017**, 50-63	0.9	2
14	12 Grand Challenges in Single-Cell Data Science		2
13	Dense and accurate whole-chromosome haplotyping of individual genomes		2
12	MBG: Minimizer-based Sparse de Bruijn Graph Construction		2
11	Fully-sensitive Seed Finding in Sequence Graphs Using a Hybrid Index		2
10	ASHLEYS: automated quality control for single-cell Strand-seq data. *Bioinformatics*, **2021**,	7.2	2
9	A strategy for building and using a human reference pangenome. *F1000Research*, **2019**, 8, 1751	3.6	2
8	Haplotype-resolved inversion landscape reveals hotspots of mutational recurrence associated with genomic disorders		2
7	Recurrent inversion polymorphisms in humans associate with genetic instability and genomic disorders.. *Cell*, **2022**,	56.2	2
6	Benchmarking challenging small variants with linked and long reads. *Cell Genomics*, **2022**, 2, 100128		2
5	Enhancing sensitivity and controlling false discovery rate in somatic indel discovery		1
4	Pangenome-based genome inference allows efficient and accurate genotyping across a wide spectrum of variant classes.. *Nature Genetics*, **2022**,	36.3	1
3	Chromatyping: Reconstructing Nucleosome Profiles from NOMe Sequencing Data. *Journal of Computational Biology*, **2020**, 27, 330-341	1.7	
2	Chromatyping: Reconstructing Nucleosome Profiles from NOMe Sequencing Data. *Lecture Notes in Computer Science*, **2018**, 21-36	0.9	
1	Discovering and Genotyping Twilight Zone Deletions **2016**, 149-173		