Fritz J Sedlazeck

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

120 papers	6,536 citations	33 h-index	80 g-index
149 ext. papers	11,092 ext. citations	16.6 avg, IF	6.03 L-index

#	Paper	IF	Citations
120	Phased diploid genome assembly with single-molecule real-time sequencing. *Nature Methods*, **2016**, 13, 1050-1054	21.6	1015
119	Accurate detection of complex structural variations using single-molecule sequencing. *Nature Methods*, **2018**, 15, 461-468	21.6	585
118	GenomeScope: fast reference-free genome profiling from short reads. *Bioinformatics*, **2017**, 33, 2202-2204	7.4	540
117	Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome. *Nature Biotechnology*, **2019**, 37, 1155-1162	44.5	427
116	The pineapple genome and the evolution of CAM photosynthesis. *Nature Genetics*, **2015**, 47, 1435-42	36.3	309
115	Updating benchtop sequencing performance comparison. *Nature Biotechnology*, **2013**, 31, 294-6	44.5	255
114	Piercing the dark matter: bioinformatics of long-range sequencing and mapping. *Nature Reviews Genetics*, **2018**, 19, 329-346	30.1	250
113	NextGenMap: fast and accurate read mapping in highly polymorphic genomes. *Bioinformatics*, **2013**, 29, 2790-1	7.2	246
112	Transient structural variations have strong effects on quantitative traits and reproductive isolation in fission yeast. *Nature Communications*, **2017**, 8, 14061	17.4	212
111	RaGOO: fast and accurate reference-guided scaffolding of draft genomes. *Genome Biology*, **2019**, 20, 224	18.3	173
110	Major Impacts of Widespread Structural Variation on Gene Expression and Crop Improvement in Tomato. *Cell*, **2020**, 182, 145-161.e23	56.2	171
109	Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. *Nature Biotechnology*, **2020**, 38, 1044-1053	44.5	143
108	Structural variant calling: the long and the short of it. *Genome Biology*, **2019**, 20, 246	18.3	141
107	Targeted nanopore sequencing with Cas9-guided adapter ligation. *Nature Biotechnology*, **2020**, 38, 433-438	44.5	113
106	The complete sequence of a human genome.. *Science*, **2022**, 376, 44-53	33.3	107
105	A robust benchmark for detection of germline large deletions and insertions. *Nature Biotechnology*, **2020**, 38, 1347-1355	44.5	98
104	Chromosomal-Level Assembly of the Asian Seabass Genome Using Long Sequence Reads and Multi-layered Scaffolding. *PLoS Genetics*, **2016**, 12, e1005954	6	77

103	Complex rearrangements and oncogene amplifications revealed by long-read DNA and RNA sequencing of a breast cancer cell line. *Genome Research*, **2018**, 28, 1126-1135	9.7	74
102	Adenosine deaminases that act on RNA induce reproducible changes in abundance and sequence of embryonic miRNAs. *Genome Research*, **2012**, 22, 1468-76	9.7	71
101	The genomic basis of circadian and circalunar timing adaptations in a midge. *Nature*, **2016**, 540, 69-73	50.4	64
100	A multi-task convolutional deep neural network for variant calling in single molecule sequencing. *Nature Communications*, **2019**, 10, 998	17.4	63
99	Shotgun transcriptome, spatial omics, and isothermal profiling of SARS-CoV-2 infection reveals unique host responses, viral diversification, and drug interactions. *Nature Communications*, **2021**, 12, 1660	17.4	60
98	The complete sequence of a human genome		58
97	Paragraph: a graph-based structural variant genotyper for short-read sequence data. *Genome Biology*, **2019**, 20, 291	18.3	55
96	Shotgun Transcriptome and Isothermal Profiling of SARS-CoV-2 Infection Reveals Unique Host Responses, Viral Diversification, and Drug Interactions **2020**,		51
95	Chromosome-scale, haplotype-resolved assembly of human genomes. *Nature Biotechnology*, **2021**, 39, 309-312	44.5	44
94	Simultaneous profiling of chromatin accessibility and methylation on human cell lines with nanopore sequencing. *Nature Methods*, **2020**, 17, 1191-1199	21.6	40
93	ADAR2 induces reproducible changes in sequence and abundance of mature microRNAs in the mouse brain. *Nucleic Acids Research*, **2014**, 42, 12155-68	20.1	38
92	Duplication of a domestication locus neutralized a cryptic variant that caused a breeding barrier in tomato. *Nature Plants*, **2019**, 5, 471-479	11.5	35
91	Evaluation of the detection of GBA missense mutations and other variants using the Oxford Nanopore MinION. *Molecular Genetics & Genomic Medicine*, **2019**, 7, e564	2.3	35
90	A robust benchmark for germline structural variant detection		34
89	Megabase Length Hypermutation Accompanies Human Structural Variation at 17p11.2. *Cell*, **2019**, 176, 1310-1324.e10	56.2	34
88	The Candida albicans Histone Acetyltransferase Hat1 Regulates Stress Resistance and Virulence via Distinct Chromatin Assembly Pathways. *PLoS Pathogens*, **2015**, 11, e1005218	7.6	33
87	Accurate detection of complex structural variations using single molecule sequencing		33
86	Ancestral Admixture Is the Main Determinant of Global Biodiversity in Fission Yeast. *Molecular Biology and Evolution*, **2019**, 36, 1975-1989	8.3	29

85	Highly-accurate long-read sequencing improves variant detection and assembly of a human genome		29
84	Efficient de novo assembly of eleven human genomes using PromethION sequencing and a novel nanopore toolkit		29
83	Towards population-scale long-read sequencing. *Nature Reviews Genetics*, **2021**, 22, 572-587	30.1	29
82	Discovery and population genomics of structural variation in a songbird genus. *Nature Communications*, **2020**, 11, 3403	17.4	27
81	Combined transcriptome and proteome profiling reveals specific molecular brain signatures for sex, maturation and circalunar clock phase. *ELife*, **2019**, 8,	8.9	26
80	Benchmarking challenging small variants with linked and long reads		26
79	Targeted Nanopore Sequencing with Cas9 for studies of methylation, structural variants, and mutations		26
78	Investigation of product-derived lymphoma following infusion of piggyBac-modified CD19 chimeric antigen receptor T cells. *Blood*, **2021**, 138, 1391-1405	2.2	26
77	precisionFDA Truth Challenge V2: Calling variants from short- and long-reads in difficult-to-map regions		25
76	Comprehensive analysis of structural variants in breast cancer genomes using single-molecule sequencing. *Genome Research*, **2020**, 30, 1258-1273	9.7	25
75	A diploid assembly-based benchmark for variants in the major histocompatibility complex. *Nature Communications*, **2020**, 11, 4794	17.4	22
74	Teaser: Individualized benchmarking and optimization of read mapping results for NGS data. *Genome Biology*, **2015**, 16, 235	18.3	21
73	LRSim: A Linked-Reads Simulator Generating Insights for Better Genome Partitioning. *Computational and Structural Biotechnology Journal*, **2017**, 15, 478-484	6.8	20
72	SARS-CoV-2 genomic diversity and the implications for qRT-PCR diagnostics and transmission. *Genome Research*, **2021**, 31, 635-644	9.7	20
71	Evaluation of computational genotyping of structural variation for clinical diagnoses. *GigaScience*, **2019**, 8,	7.6	18
70	A Genocentric Approach to Discovery of Mendelian Disorders. *American Journal of Human Genetics*, **2019**, 105, 974-986	11	18
69	Accurate chromosome-scale haplotype-resolved assembly of human genomes		18
68	Copy number increases of transposable elements and protein-coding genes in an invasive fish of hybrid origin. *Molecular Ecology*, **2017**, 26, 4712-4724	5.7	17

67	Advanced methylome analysis after bisulfite deep sequencing: an example in Arabidopsis. *PLoS ONE*, **2012**, 7, e41528	3.7	17
66	Parliament2: Accurate structural variant calling at scale. *GigaScience*, **2020**, 9,	7.6	17
65	Phased Diploid Genome Assembly with Single Molecule Real-Time Sequencing		16
64	xAtlas: Scalable small variant calling across heterogeneous next-generation sequencing experiments		15
63	Simultaneous profiling of chromatin accessibility and methylation on human cell lines with nanopore sequencing		15
62	Fast and accurate reference-guided scaffolding of draft genomes		15
61	Atlas-CNV: a validated approach to call single-exon CNVs in the eMERGESeq gene panel. *Genetics in Medicine*, **2019**, 21, 2135-2144	8.1	13
60	Hidden genomic diversity of SARS-CoV-2: implications for qRT-PCR diagnostics and transmission **2020**,		13
59	Curated variation benchmarks for challenging medically relevant autosomal genes.. *Nature Biotechnology*, **2022**,	44.5	12
58	Parliament2: Fast Structural Variant Calling Using Optimized Combinations of Callers		12
57	A complete reference genome improves analysis of human genetic variation.. *Science*, **2022**, 376, eabl3533	33.3	12
56	Tools for annotation and comparison of structural variation. *F1000Research*, **2017**, 6, 1795	3.6	11
55	Clairvoyante: a multi-task convolutional deep neural network for variant calling in Single Molecule Sequencing		11
54	Genome-wide patterns of transposon proliferation in an evolutionary young hybrid fish. *Molecular Ecology*, **2019**, 28, 1491-1505	5.7	11
53	Ultrarapid Nanopore Genome Sequencing in a Critical Care Setting.. *New England Journal of Medicine*, **2022**,	59.2	10
52	Performance assessment of DNA sequencing platforms in the ABRF Next-Generation Sequencing Study. *Nature Biotechnology*, **2021**, 39, 1129-1140	44.5	10
51	Complex mosaic structural variations in human fetal brains. *Genome Research*, **2020**, 30, 1695-1704	9.7	9
50	A complete reference genome improves analysis of human genetic variation		9

49	A strategy for building and using a human reference pangenome. *F1000Research*, **2019**, 8, 1751	3.6	8
48	SplitThreader: Exploration and analysis of rearrangements in cancer genomes		8
47	Oligonucleotide capture sequencing of the SARS-CoV-2 genome and subgenomic fragments from COVID-19 individuals **2020**,		8
46	Paragraph: A graph-based structural variant genotyper for short-read sequence data		8
45	Towards a Comprehensive Variation Benchmark for Challenging Medically-Relevant Autosomal Genes		8
44	Oligonucleotide capture sequencing of the SARS-CoV-2 genome and subgenomic fragments from COVID-19 individuals. *PLoS ONE*, **2021**, 16, e0244468	3.7	8
43	Oligonucleotide Capture Sequencing of the SARS-CoV-2 Genome and Subgenomic Fragments from COVID-19 Individuals **2020**,		7
42	DangerTrack: A scoring system to detect difficult-to-assess regions. *F1000Research*, **2017**, 6, 443	3.6	6
41	Complex rearrangements and oncogene amplifications revealed by long-read DNA and RNA sequencing of a breast cancer cell line		6
40	Ectodysplasin signalling genes and phenotypic evolution in sculpins (Cottus). *Proceedings of the Royal Society B: Biological Sciences*, **2015**, 282,	4.4	5
39	Centers for Mendelian Genomics: A decade of facilitating gene discovery.. *Genetics in Medicine*, **2022**,	8.1	5
38	GenomeScope: Fast reference-free genome profiling from short reads		5
37	PhaseME: Automatic rapid assessment of phasing quality and phasing improvement. *GigaScience*, **2020**, 9,	7.6	5
36	SVCollector: Optimized sample selection for validating and long-read resequencing of structural variants		4
35	Approaches to Whole Mitochondrial Genome Sequencing on the Oxford Nanopore MinION. *Current Protocols in Human Genetics*, **2019**, 104, e94	3.2	4
34	Accelerated identification of disease-causing variants with ultra-rapid nanopore genome sequencing.. *Nature Biotechnology*, **2022**,	44.5	4
33	PrecisionFDA Truth Challenge V2: Calling variants from short and long reads in difficult-to-map regions. *Cell Genomics*, **2022**, 2, 100129		4
32	Decreased expression of endogenous feline leukemia virus in cat lymphomas: a case control study. *BMC Veterinary Research*, **2015**, 11, 90	2.7	3

31	Assessing reproducibility of inherited variants detected with short-read whole genome sequencing.. *Genome Biology*, **2022**, 23, 2	18.3	3
30	Comprehensive analysis of structural variants in breast cancer genomes using single molecule sequencing		3
29	Rescuing Low Frequency Variants within Intra-Host Viral Populations directly from Oxford Nanopore sequencing data **2021**,		3
28	Rescuing low frequency variants within intra-host viral populations directly from Oxford Nanopore sequencing data.. *Nature Communications*, **2022**, 13, 1321	17.4	3
27	Hidden biases in germline structural variant detection.. *Genome Biology*, **2021**, 22, 347	18.3	3
26	The population genomics of structural variation in a songbird genus		2
25	SVCollector: Optimized sample selection for cost-efficient long-read population sequencing		2
24	Detection of GBA missense mutations and other variants using the Oxford Nanopore MinION		2
23	An international virtual hackathon to build tools for the analysis of structural variants within species ranging from coronaviruses to vertebrates. *F1000Research*, **2021**, 10, 246	3.6	2
22	Optimized sample selection for cost-efficient long-read population sequencing. *Genome Research*, **2021**, 31, 910-918	9.7	2
21	Intronic Haplotypes in the GBA Gene Do Not Predict Age at Diagnosis of Parkinson's Disease. *Movement Disorders*, **2021**, 36, 1456-1460	7	2
20	A strategy for building and using a human reference pangenome. *F1000Research*, **2019**, 8, 1751	3.6	2
19	Benchmarking challenging small variants with linked and long reads. *Cell Genomics*, **2022**, 2, 100128		2
18	Ultra-Rapid Nanopore Whole Genome Genetic Diagnosis of Dilated Cardiomyopathy in an Adolescent With Cardiogenic Shock.. *Circulation Genomic and Precision Medicine*, **2022**, CIRCGEN121003591	5.2	1
17	Transient structural variations have strong effects on quantitative traits and reproductive isolation in fission yeast		1
16	LRSim: a Linked Reads Simulator generating insights for better genome partitioning		1
15	Multi-Platform Assessment of DNA Sequencing Performance using Human and Bacterial Reference Genomes in the ABRF Next-Generation Sequencing Study		1
14	muCNV: Genotyping Structural Variants for Population-level Sequencing. *Bioinformatics*, **2021**,	7.2	1

13	Construction of a new chromosome-scale, long-read reference genome assembly of the Syrian hamster, Mesocricetus auratus		1
12	Vulcan: Improved long-read mapping and structural variant calling via dual-mode alignment. *GigaScience*, **2021**, 10,	7.6	1
11	High resolution copy number inference in cancer using short-molecule nanopore sequencing. *Nucleic Acids Research*, **2021**, 49, e124	20.1	1
10	An international virtual hackathon to build tools for the analysis of structural variants within species ranging from coronaviruses to vertebrates. *F1000Research*, **2021**, 10, 246	3.6	1
9	Truvari: Refined Structural Variant Comparison Preserves Allelic Diversity		1
8	Towards accurate and reliable resolution of structural variants for clinical diagnosis.. *Genome Biology*, **2022**, 23, 68	18.3	1
7	Whole genome sequencing identifies common and rare structural variants contributing to hematologic traits in the NHLBI TOPMed program		1
6	Accurate profiling of forensic autosomal STRs using the Oxford Nanopore Technologies MinION device. *Forensic Science International: Genetics*, **2022**, 56, 102629	4.3	0
5	PRINCESS: comprehensive detection of haplotype resolved SNVs, SVs, and methylation. *Genome Biology*, **2021**, 22, 268	18.3	0
4	Potential applications of nanopore sequencing for forensic analysis. *Forensic Science Review*, **2020**, 32, 23-54	1.5	0
3	Benefit-of-doubt (BOD) scoring: a sequencing-based method for SNP candidate assessment from high to medium read number data sets. *Genomics*, **2013**, 101, 204-9	4.3	
2	Methods developed during the first National Center for Biotechnology Information Structural Variation Codeathon at Baylor College of Medicine. *F1000Research*,9, 1141	3.6	
1	The third international hackathon for applying insights into large-scale genomic composition to use cases in a wide range of organisms. *F1000Research*,11, 530	3.6	