Fritz J Sedlazeck

List of Publications by Year
in descending order

87	14,707	87401 40	53065 89
papers	citations	h-index	g-index

149	149	149	19128
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Accurate profiling of forensic autosomal STRs using the Oxford Nanopore Technologies MinION device. Forensic Science International: Genetics, 2022, 56, 102629.	1.6	12
2	Assessing reproducibility of inherited variants detected with short-read whole genome sequencing. Genome Biology, 2022, 23, 2.	3.8	18
3	Ultrarapid Nanopore Genome Sequencing in a Critical Care Setting. New England Journal of Medicine, 2022, 386, 700-702.	13.9	116
4	Centers for Mendelian Genomics: A decade of facilitating gene discovery. Genetics in Medicine, 2022, 24, 784-797.	1.1	44
5	Curated variation benchmarks for challenging medically relevant autosomal genes. Nature Biotechnology, 2022, 40, 672-680.	9.4	90
6	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
7	Fully resolved assembly of Cryptosporidium parvum. GigaScience, 2022, 11, .	3.3	8
8	Rescuing low frequency variants within intra-host viral populations directly from Oxford Nanopore sequencing data. Nature Communications, 2022, 13, 1321.	5.8	11
9	Accelerated identification of disease-causing variants with ultra-rapid nanopore genome sequencing. Nature Biotechnology, 2022, 40, 1035-1041.	9.4	45
10	Towards accurate and reliable resolution of structural variants for clinical diagnosis. Genome Biology, 2022, 23, 68.	3.8	34
11	A complete reference genome improves analysis of human genetic variation. Science, 2022, 376, eabl3533.	6.0	144
12	The complete sequence of a human genome. Science, 2022, 376, 44-53.	6.0	1,222
13	Searching thousands of genomes to classify somatic and novel structural variants using STIX. Nature Methods, 2022, 19, 445-448.	9.0	8
14	PrecisionFDA Truth Challenge V2: Calling variants from short and long reads in difficult-to-map regions. Cell Genomics, 2022, 2, 100129.	3.0	72
15	TOP-LD: A tool to explore linkage disequilibrium with TOPMed whole-genome sequence data. American Journal of Human Genetics, 2022, 109, 1175-1181.	2.6	25
16	Benchmarking challenging small variants with linked and long reads. Cell Genomics, 2022, 2, 100128.	3.0	77
17	Chromosome-scale, haplotype-resolved assembly of human genomes. Nature Biotechnology, 2021, 39, 309-312.	9.4	109
18	SARS-CoV-2 genomic diversity and the implications for qRT-PCR diagnostics and transmission. Genome Research, 2021, 31, 635-644.	2.4	39

#	Article	IF	Citations
19	AnÂinternationalÂvirtualÂhackathon toÂbuildÂtools for theÂanalysis ofÂstructuralÂvariants withinÂspeciesÂranging fromÂcoronaviruses toÂvertebrates. F1000Research, 2021, 10, 246.	0.8	3
20	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.	5.8	132
21	muCNV: genotyping structural variants for population-level sequencing. Bioinformatics, 2021, 37, 2055-2057.	1.8	7
22	Optimized sample selection for cost-efficient long-read population sequencing. Genome Research, 2021, 31, 910-918.	2.4	4
23	Long-read sequencing for diagnosis in the Undiagnosed Diseases Network. Molecular Genetics and Metabolism, 2021, 132, S253-S254.	0.5	1
24	Intronic Haplotypes in the <scp>GBA</scp> Gene Do Not Predict Age at Diagnosis of Parkinson's Disease. Movement Disorders, 2021, 36, 1456-1460.	2.2	5
25	Investigation of product-derived lymphoma following infusion of piggyBac-modified CD19 chimeric antigen receptor T cells. Blood, 2021, 138, 1391-1405.	0.6	87
26	Towards population-scale long-read sequencing. Nature Reviews Genetics, 2021, 22, 572-587.	7.7	163
27	Oligonucleotide capture sequencing of the SARS-CoV-2 genome and subgenomic fragments from COVID-19 individuals. PLoS ONE, 2021, 16, e0244468.	1.1	20
28	Vulcan: Improved long-read mapping and structural variant calling via dual-mode alignment. GigaScience, 2021, 10, .	3.3	14
29	High resolution copy number inference in cancer using short-molecule nanopore sequencing. Nucleic Acids Research, 2021, 49, e124-e124.	6.5	14
30	Performance assessment of DNA sequencing platforms in the ABRF Next-Generation Sequencing Study. Nature Biotechnology, 2021, 39, 1129-1140.	9.4	69
31	PRINCESS: comprehensive detection of haplotype resolved SNVs, SVs, and methylation. Genome Biology, 2021, 22, 268.	3.8	28
32	AnÂinternationalÂvirtualÂhackathon toÂbuildÂtools for theÂanalysis ofÂstructuralÂvariants withinÂspeciesÂranging fromÂcoronaviruses toÂvertebrates. F1000Research, 2021, 10, 246.	0.8	2
33	Hidden biases in germline structural variant detection. Genome Biology, 2021, 22, 347.	3.8	19
34	Simultaneous profiling of chromatin accessibility and methylation on human cell lines with nanopore sequencing. Nature Methods, 2020, 17, 1191-1199.	9.0	133
35	Complex mosaic structural variations in human fetal brains. Genome Research, 2020, 30, 1695-1704.	2.4	21
36	Comprehensive analysis of structural variants in breast cancer genomes using single-molecule sequencing. Genome Research, 2020, 30, 1258-1273.	2.4	72

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37	A diploid assembly-based benchmark for variants in the major histocompatibility complex. Nature Communications, 2020, 11, 4794.	5.8	56
38	PhaseME: Automatic rapid assessment of phasing quality and phasing improvement. GigaScience, 2020, 9, .	3.3	8
39	Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. Nature Biotechnology, 2020, 38, 1044-1053.	9.4	344
40	A robust benchmark for detection of germline large deletions and insertions. Nature Biotechnology, 2020, 38, 1347-1355.	9.4	233
41	Major Impacts of Widespread Structural Variation on Gene Expression and Crop Improvement in Tomato. Cell, 2020, 182, 145-161.e23.	13.5	464
42	Discovery and population genomics of structural variation in a songbird genus. Nature Communications, 2020, 11, 3403.	5.8	83
43	Targeted nanopore sequencing with Cas9-guided adapter ligation. Nature Biotechnology, 2020, 38, 433-438.	9.4	286
44	Parliament2: Accurate structural variant calling at scale. GigaScience, 2020, 9, .	3.3	51
45	Potential applications of nanopore sequencing for forensic analysis. Forensic Science Review, 2020, 32, 23-54.	0.6	5
46	Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome. Nature Biotechnology, 2019, 37, 1155-1162.	9.4	1,010
47	A Genocentric Approach to Discovery of Mendelian Disorders. American Journal of Human Genetics, 2019, 105, 974-986.	2.6	30
48	RaGOO: fast and accurate reference-guided scaffolding of draft genomes. Genome Biology, 2019, 20, 224.	3.8	469
49	Evaluation of computational genotyping of structural variation for clinical diagnoses. GigaScience, 2019, 8, .	3.3	36
50	Ancestral Admixture Is the Main Determinant of Global Biodiversity in Fission Yeast. Molecular Biology and Evolution, 2019, 36, 1975-1989.	3.5	50
51	Duplication of a domestication locus neutralized a cryptic variant that caused a breeding barrier in tomato. Nature Plants, 2019, 5, 471-479.	4.7	66
52	Atlas-CNV: a validated approach to call single-exon CNVs in the eMERGESeq gene panel. Genetics in Medicine, 2019, 21, 2135-2144.	1.1	19
53	Megabase Length Hypermutation Accompanies Human Structural Variation at 17p11.2. Cell, 2019, 176, 1310-1324.e10.	13.5	73
54	A multi-task convolutional deep neural network for variant calling in single molecule sequencing. Nature Communications, 2019, 10, 998.	5.8	102

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55	Paragraph: a graph-based structural variant genotyper for short-read sequence data. Genome Biology, 2019, 20, 291.	3.8	104
56	Approaches to Whole Mitochondrial Genome Sequencing on the Oxford Nanopore MinION. Current Protocols in Human Genetics, 2019, 104, e94.	3.5	13
57	Structural variant calling: the long and the short of it. Genome Biology, 2019, 20, 246.	3.8	409
58	Evaluation of the detection of GBA missense mutations and other variants using the Oxford Nanopore MinION. Molecular Genetics & Genomic Medicine, 2019, 7, e564.	0.6	65
59	Genomeâ€wide patterns of transposon proliferation in an evolutionary young hybrid fish. Molecular Ecology, 2019, 28, 1491-1505.	2.0	18
60	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	0.8	5
61	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	0.8	14
62	Combined transcriptome and proteome profiling reveals specific molecular brain signatures for sex, maturation and circalunar clock phase. ELife, 2019, 8, .	2.8	51
63	Accurate detection of complex structural variations using single-molecule sequencing. Nature Methods, 2018, 15, 461-468.	9.0	1,175
64	Piercing the dark matter: bioinformatics of long-range sequencing and mapping. Nature Reviews Genetics, 2018, 19, 329-346.	7.7	395
65	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.	2.4	142
66	Transient structural variations have strong effects on quantitative traits and reproductive isolation in fission yeast. Nature Communications, 2017, 8, 14061.	5.8	472
67	GenomeScope: fast reference-free genome profiling from short reads. Bioinformatics, 2017, 33, 2202-2204.	1.8	1,183
68	Copy number increases of transposable elements and proteinâ€coding genes in an invasive fish of hybrid origin. Molecular Ecology, 2017, 26, 4712-4724.	2.0	28
69	LRSim: A Linked-Reads Simulator Generating Insights for Better Genome Partitioning. Computational and Structural Biotechnology Journal, 2017, 15, 478-484.	1.9	42
70	DangerTrack: A scoring system to detect difficult-to-assess regions. F1000Research, 2017, 6, 443.	0.8	10
71	Tools for annotation and comparison of structural variation. F1000Research, 2017, 6, 1795.	0.8	26
72	Chromosomal-Level Assembly of the Asian Seabass Genome Using Long Sequence Reads and Multi-layered Scaffolding. PLoS Genetics, 2016, 12, e1005954.	1.5	105

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73	The genomic basis of circadian and circalunar timing adaptations in a midge. Nature, 2016, 540, 69-73.	13.7	96
74	Phased diploid genome assembly with single-molecule real-time sequencing. Nature Methods, 2016, 13, 1050-1054.	9.0	1,658
75	Ectodysplasin signalling genes and phenotypic evolution in sculpins (Cottus). Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20150746.	1.2	9
76	The Candida albicans Histone Acetyltransferase Hat1 Regulates Stress Resistance and Virulence via Distinct Chromatin Assembly Pathways. PLoS Pathogens, 2015, 11, e1005218.	2.1	48
77	Decreased expression of endogenous feline leukemia virus in cat lymphomas: a case control study. BMC Veterinary Research, 2015, 11, 90.	0.7	8
78	Teaser: Individualized benchmarking and optimization of read mapping results for NGS data. Genome Biology, 2015, 16, 235.	3.8	25
79	The pineapple genome and the evolution of CAM photosynthesis. Nature Genetics, 2015, 47, 1435-1442.	9.4	472
80	ADAR2 induces reproducible changes in sequence and abundance of mature microRNAs in the mouse brain. Nucleic Acids Research, 2014, 42, 12155-12168.	6.5	42
81	NextGenMap: fast and accurate read mapping in highly polymorphic genomes. Bioinformatics, 2013, 29, 2790-2791.	1.8	408
82	Benefit-of-doubt (BOD) scoring: A sequencing-based method for SNP candidate assessment from high to medium read number data sets. Genomics, 2013, 101, 204-209.	1.3	0
83	Updating benchtop sequencing performance comparison. Nature Biotechnology, 2013, 31, 294-296.	9.4	423
84	Adenosine deaminases that act on RNA induce reproducible changes in abundance and sequence of embryonic miRNAs. Genome Research, 2012, 22, 1468-1476.	2.4	80
85	Advanced Methylome Analysis after Bisulfite Deep Sequencing: An Example in Arabidopsis. PLoS ONE, 2012, 7, e41528.	1.1	19
86	Methods developed during the first National Center for Biotechnology Information Structural Variation Codeathon at Baylor College of Medicine. F1000Research, 0, 9, 1141.	0.8	0
87	The third international hackathon for applying insights into large-scale genomic composition to use cases in a wide range of organisms. F1000Research, 0, 11, 530.	0.8	1