

Justin M Zook

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.

93
papers

4,531
citations

29
h-index

66
g-index

102
ext. papers

6,765
ext. citations

15.1
avg, IF

5.12
L-index

#	Paper	IF	Citations
93	Integrating human sequence data sets provides a resource of benchmark SNP and indel genotype calls. <i>Nature Biotechnology</i> , 2014 , 32, 246-51	44.5	571
92	Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome. <i>Nature Biotechnology</i> , 2019 , 37, 1155-1162	44.5	427
91	Assuring the quality of next-generation sequencing in clinical laboratory practice. <i>Nature Biotechnology</i> , 2012 , 30, 1033-6	44.5	372
90	Extensive sequencing of seven human genomes to characterize benchmark reference materials. <i>Scientific Data</i> , 2016 , 3, 160025	8.2	345
89	Stable nanoparticle aggregates/agglomerates of different sizes and the effect of their size on hemolytic cytotoxicity. <i>Nanotoxicology</i> , 2011 , 5, 517-30	5.3	190
88	Measuring silver nanoparticle dissolution in complex biological and environmental matrices using UV-visible absorbance. <i>Analytical and Bioanalytical Chemistry</i> , 2011 , 401, 1993-2002	4.4	170
87	Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. <i>Nature Biotechnology</i> , 2020 , 38, 1044-1053	44.5	143
86	An open resource for accurately benchmarking small variant and reference calls. <i>Nature Biotechnology</i> , 2019 , 37, 561-566	44.5	140
85	Best practices for benchmarking germline small-variant calls in human genomes. <i>Nature Biotechnology</i> , 2019 , 37, 555-560	44.5	125
84	Good laboratory practice for clinical next-generation sequencing informatics pipelines. <i>Nature Biotechnology</i> , 2015 , 33, 689-93	44.5	115
83	Best practices for evaluating single nucleotide variant calling methods for microbial genomics. <i>Frontiers in Genetics</i> , 2015 , 6, 235	4.5	109
82	The complete sequence of a human genome.. <i>Science</i> , 2022 , 376, 44-53	33.3	107
81	A robust benchmark for detection of germline large deletions and insertions. <i>Nature Biotechnology</i> , 2020 , 38, 1347-1355	44.5	98
80	Effects of temperature, acyl chain length, and flow-rate ratio on liposome formation and size in a microfluidic hydrodynamic focusing device. <i>Soft Matter</i> , 2010 , 6, 1352	3.6	97
79	Medical implications of technical accuracy in genome sequencing. <i>Genome Medicine</i> , 2016 , 8, 24	14.4	83
78	Measuring agglomerate size distribution and dependence of localized surface plasmon resonance absorbance on gold nanoparticle agglomerate size using analytical ultracentrifugation. <i>ACS Nano</i> , 2011 , 5, 8070-9	16.7	80
77	An analytical framework for optimizing variant discovery from personal genomes. <i>Nature Communications</i> , 2015 , 6, 6275	17.4	73

76	Comparing Variant Call Files for Performance Benchmarking of Next-Generation Sequencing Variant Calling Pipelines		73
75	svclassify: a method to establish benchmark structural variant calls. <i>BMC Genomics</i> , 2016 , 17, 64	4.5	68
74	Genome-wide reconstruction of complex structural variants using read clouds. <i>Nature Methods</i> , 2017 , 14, 915-920	21.6	65
73	Statistical analysis of fractal-based brain tumor detection algorithms. <i>Magnetic Resonance Imaging</i> , 2005 , 23, 671-8	3.3	60
72	The complete sequence of a human genome		58
71	Synthetic spike-in standards improve run-specific systematic error analysis for DNA and RNA sequencing. <i>PLoS ONE</i> , 2012 , 7, e41356	3.7	44
70	Chromosome-scale, haplotype-resolved assembly of human genomes. <i>Nature Biotechnology</i> , 2021 , 39, 309-312	44.5	44
69	Achieving high-sensitivity for clinical applications using augmented exome sequencing. <i>Genome Medicine</i> , 2015 , 7, 71	14.4	41
68	Electrochemical methods for the determination of the diffusion coefficient of ionophores and ionophore-ion complexes in plasticized PVC membranes. <i>Analyst, The</i> , 2008 , 133, 635-42	5	41
67	Disentangling the effects of polymer coatings on silver nanoparticle agglomeration, dissolution, and toxicity to determine mechanisms of nanotoxicity. <i>Journal of Nanoparticle Research</i> , 2012 , 14, 1	2.3	39
66	Magnetic connectors for microfluidic applications. <i>Lab on A Chip</i> , 2010 , 10, 246-9	7.2	36
65	A robust benchmark for germline structural variant detection		34
64	svviz: a read viewer for validating structural variants. <i>Bioinformatics</i> , 2015 , 31, 3994-6	7.2	29
63	A research roadmap for next-generation sequencing informatics. <i>Science Translational Medicine</i> , 2016 , 8, 335ps10	17.5	29
62	Highly-accurate long-read sequencing improves variant detection and assembly of a human genome		29
61	Efficient de novo assembly of eleven human genomes using PromethION sequencing and a novel nanopore toolkit		29
60	A Rigorous Interlaboratory Examination of the Need to Confirm Next-Generation Sequencing-Detected Variants with an Orthogonal Method in Clinical Genetic Testing. <i>Journal of Molecular Diagnostics</i> , 2019 , 21, 318-329	5.1	28
59	Mathematical model of current-polarized ionophore-based ion-selective membranes. <i>Journal of Physical Chemistry B</i> , 2008 , 112, 2008-15	3.4	26

58	Mathematical Model of Current-Polarized Ionophore-Based Ion-Selective Membranes: Large Current Chronopotentiometry. <i>Electroanalysis</i> , 2008 , 20, 259-269	3	26
57	Benchmarking challenging small variants with linked and long reads		26
56	Reproducible integration of multiple sequencing datasets to form high-confidence SNP, indel, and reference calls for five human genome reference materials		26
55	precisionFDA Truth Challenge V2: Calling variants from short- and long-reads in difficult-to-map regions		25
54	Chronopotentiometric method for the assessment of ionophore diffusion coefficients in solvent polymeric membranes. <i>Journal of Solid State Electrochemistry</i> , 2009 , 13, 171-179	2.6	24
53	A diploid assembly-based benchmark for variants in the major histocompatibility complex. <i>Nature Communications</i> , 2020 , 11, 4794	17.4	22
52	Assembly and annotation of an Ashkenazi human reference genome. <i>Genome Biology</i> , 2020 , 21, 129	18.3	20
51	Complete genomic and epigenetic maps of human centromeres.. <i>Science</i> , 2022 , 376, eabl4178	33.3	19
50	Accurate chromosome-scale haplotype-resolved assembly of human genomes		18
49	Current-polarized ion-selective membranes: The influence of plasticizer and lipophilic background electrolyte on concentration profiles, resistance, and voltage transients. <i>Sensors and Actuators B: Chemical</i> , 2009 , 136, 410-418	8.5	15
48	Reverse current pulse method to restore uniform concentration profiles in ion-selective membranes. 1. Galvanostatic pulse methods with decreased cycle time. <i>Analytical Chemistry</i> , 2009 , 81, 5146-54	7.8	15
47	Principles and Recommendations for Standardizing the Use of the Next-Generation Sequencing Variant File in Clinical Settings. <i>Journal of Molecular Diagnostics</i> , 2017 , 19, 417-426	5.1	13
46	Best Practices for Benchmarking Germline Small Variant Calls in Human Genomes		13
45	Assessment of Ion-Ionophore Complex Diffusion Coefficients in Solvent Polymeric Membranes. <i>Electroanalysis</i> , 2009 , 21, 1923-1930	3	12
44	Curated variation benchmarks for challenging medically relevant autosomal genes.. <i>Nature Biotechnology</i> , 2022 ,	44.5	12
43	Development and Characterization of Reference Materials for Genetic Testing: Focus on Public Partnerships. <i>Annals of Laboratory Medicine</i> , 2016 , 36, 513-20	3.1	12
42	Chasing perfection: validation and polishing strategies for telomere-to-telomere genome assemblies		12
41	A complete reference genome improves analysis of human genetic variation.. <i>Science</i> , 2022 , 376, eabl35333	33.3	12

40	Interpretation of chronopotentiometric transients of ion-selective membranes with two transition times. <i>Journal of Electroanalytical Chemistry</i> , 2010 , 638, 254-261	4.1	11
39	Tools for annotation and comparison of structural variation. <i>F1000Research</i> , 2017 , 6, 1795	3.6	11
38	One in seven pathogenic variants can be challenging to detect by NGS: an analysis of 450,000 patients with implications for clinical sensitivity and genetic test implementation. <i>Genetics in Medicine</i> , 2021 , 23, 1673-1680	8.1	10
37	Performance assessment of DNA sequencing platforms in the ABRF Next-Generation Sequencing Study. <i>Nature Biotechnology</i> , 2021 , 39, 1129-1140	44.5	10
36	Nanomaterial Toxicity: Emerging Standards and Efforts to Support Standards Development. <i>Nanostructure Science and Technology</i> , 2011 , 179-208	0.9	9
35	Reverse current pulse method to restore uniform concentration profiles in ion-selective membranes. 2. Comparison of the efficiency of the different protocols. <i>Analytical Chemistry</i> , 2009 , 81, 5155-64	7.8	9
34	A complete reference genome improves analysis of human genetic variation		9
33	A strategy for building and using a human reference pangenome. <i>F1000Research</i> , 2019 , 8, 1751	3.6	8
32	Genome-wide reconstruction of complex structural variants using read clouds		8
31	Towards a Comprehensive Variation Benchmark for Challenging Medically-Relevant Autosomal Genes		8
30	Complete genomic and epigenetic maps of human centromeres		8
29	Determining Performance Metrics for Targeted Next-Generation Sequencing Panels Using Reference Materials. <i>Journal of Molecular Diagnostics</i> , 2018 , 20, 583-590	5.1	7
28	Challenging a bioinformatic tools ability to detect microbial contaminants using whole genome sequencing data. <i>PeerJ</i> , 2017 , 5, e3729	3.1	6
27	PEPR: pipelines for evaluating prokaryotic references. <i>Analytical and Bioanalytical Chemistry</i> , 2016 , 408, 2975-83	4.4	5
26	High-coverage, long-read sequencing of Han Chinese trio reference samples. <i>Scientific Data</i> , 2019 , 6, 91	8.2	4
25	Immobilization of fibrinogen antibody on self-assembled gold monolayers for immunosensor applications. <i>Tissue Engineering and Regenerative Medicine</i> , 2014 , 11, 10-15	4.5	4
24	Advancing Benchmarks for Genome Sequencing. <i>Cell Systems</i> , 2015 , 1, 176-7	10.6	4
23	svviz: a read viewer for validating structural variants		4

22	An interlaboratory study of complex variant detection		4
21	SVCurator: A Crowdsourcing app to visualize evidence of structural variants for the human genome		4
20	A Diploid Assembly-based Benchmark for Variants in the Major Histocompatibility Complex		4
19	Chasing perfection: validation and polishing strategies for telomere-to-telomere genome assemblies.. <i>Nature Methods</i> , 2022 ,	21.6	4
18	PrecisionFDA Truth Challenge V2: Calling variants from short and long reads in difficult-to-map regions. <i>Cell Genomics</i> , 2022 , 2, 100129		4
17	International interlaboratory study comparing single organism 16S rRNA gene sequencing data: Beyond consensus sequence comparisons. <i>Biomolecular Detection and Quantification</i> , 2015 , 3, 17-24	12	3
16	Genomic Reference Materials for Clinical Applications 2015 , 393-402		3
15	Assessing reproducibility of inherited variants detected with short-read whole genome sequencing.. <i>Genome Biology</i> , 2022 , 23, 2	18.3	3
14	One in seven pathogenic variants can be challenging to detect by NGS: An analysis of 450,000 patients with implications for clinical sensitivity and genetic test implementation		3
13	Automated assembly of high-quality diploid human reference genomes		3
12	Unleashing novel STRS via characterization of genome in a bottle reference samples. <i>Forensic Science International: Genetics Supplement Series</i> , 2019 , 7, 218-220	0.5	2
11	Assembly and Annotation of an Ashkenazi Human Reference Genome		2
10	A strategy for building and using a human reference pangenome. <i>F1000Research</i> , 2019 , 8, 1751	3.6	2
9	CrowdVariant: a crowdsourcing approach to classify copy number variants. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2019 , 24, 224-235	1.3	2
8	Benchmarking challenging small variants with linked and long reads. <i>Cell Genomics</i> , 2022 , 2, 100128		2
7	Multi-Platform Assessment of DNA Sequencing Performance using Human and Bacterial Reference Genomes in the ABRF Next-Generation Sequencing Study		1
6	genomeview - an extensible python-based genomics visualization engine		1
5	High-coverage, long-read sequencing of Han Chinese trio reference samples		1

- 4 CrowdVariant: a crowdsourcing approach to classify copy number variants 1
- 3 A crowdsourced set of curated structural variants for the human genome. *PLoS Computational Biology*, **2020**, 16, e1007933 5 0
- 2 Challenges of Accuracy in Germline Clinical Sequencing Data. *JAMA - Journal of the American Medical Association*, **2021**, 326, 268-269 27.4 0
- 1 The Role of the National Institute of Standards in Measurement Assurance for Cell Therapies **2022**, 609-625