Justin M Zook

List of Publications by Year
in descending order

67 papers	8,875 citations	117625 34 h-index	91884 69 g-index
102 all docs	102 docs citations	102 times ranked	10368 citing authors

#	Article	IF	Citations
1	The Role of the National Institute of Standards in Measurement Assurance for Cell Therapies. , 2022, , 609-625.		0
2	Assessing reproducibility of inherited variants detected with short-read whole genome sequencing. Genome Biology, 2022, 23, 2.	8.8	18
3	Curated variation benchmarks for challenging medically relevant autosomal genes. Nature Biotechnology, 2022, 40, 672-680.	17.5	90
4	Chasing perfection: validation and polishing strategies for telomere-to-telomere genome assemblies. Nature Methods, 2022, 19, 687-695.	19.0	42
5	Complete genomic and epigenetic maps of human centromeres. Science, 2022, 376, eabl4178.	12.6	204
6	A complete reference genome improves analysis of human genetic variation. Science, 2022, 376, eabl3533.	12.6	144
7	The complete sequence of a human genome. Science, 2022, 376, 44-53.	12.6	1,222
8	PrecisionFDA Truth Challenge V2: Calling variants from short and long reads in difficult-to-map regions. Cell Genomics, 2022, 2, 100129.	6.5	72
9	Benchmarking challenging small variants with linked and long reads. Cell Genomics, 2022, 2, 100128.	6.5	77
10	Chromosome-scale, haplotype-resolved assembly of human genomes. Nature Biotechnology, 2021, 39, 309-312.	17.5	109
11	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. Genetics in Medicine, 2021, 23, 1673-1680.	2.4	40
12	Challenges of Accuracy in Germline Clinical Sequencing Data. JAMA - Journal of the American Medical Association, 2021, 326, 268.	7.4	4
13	Performance assessment of DNA sequencing platforms in the ABRF Next-Generation Sequencing Study. Nature Biotechnology, 2021, 39, 1129-1140.	17.5	69
14	A diploid assembly-based benchmark for variants in the major histocompatibility complex. Nature Communications, 2020, 11, 4794.	12.8	56
15	Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. Nature Biotechnology, 2020, 38, 1044-1053.	17.5	344
16	A robust benchmark for detection of germline large deletions and insertions. Nature Biotechnology, 2020, 38, 1347-1355.	17.5	233
17	Assembly and annotation of an Ashkenazi human reference genome. Genome Biology, 2020, 21, 129.	8.8	42
18	A crowdsourced set of curated structural variants for the human genome. PLoS Computational Biology, 2020, 16, e1007933.	3.2	6

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19	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
20	A Rigorous Interlaboratory Examination of the Need to Confirm Next-Generation Sequencingâ€“Detected Variants with an Orthogonal MethodÂin Clinical Genetic Testing. Journal of Molecular Diagnostics, 2019, 21, 318-329.	2.8	49
21	High-coverage, long-read sequencing of Han Chinese trio reference samples. Scientific Data, 2019, 6, 91.	5.3	13
22	Best practices for benchmarking germline small-variant calls in human genomes. Nature Biotechnology, 2019, 37, 555-560.	17.5	273
23	An open resource for accurately benchmarking small variant and reference calls. Nature Biotechnology, 2019, 37, 561-566.	17.5	277
24	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	1.6	5
25	Unleashing novel STRS via characterization of genome in a bottle reference samples. Forensic Science International: Genetics Supplement Series, 2019, 7, 218-220.	0.3	5
26	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	1.6	14
27	CrowdVariant: a crowdsourcing approach to classify copy number variants. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2019, 24, 224-235.	0.7	2
28	Determining Performance Metrics for Targeted Next-Generation Sequencing Panels Using Reference Materials. Journal of Molecular Diagnostics, 2018, 20, 583-590.	2.8	10
29	Principles and Recommendations for Standardizing the Use of the Next-Generation Sequencing Variant File in Clinical Settings. Journal of Molecular Diagnostics, 2017, 19, 417-426.	2.8	19
30	Genome-wide reconstruction of complex structural variants using read clouds. Nature Methods, 2017, 14, 915-920.	19.0	96
31	Tools for annotation and comparison of structural variation. F1000Research, 2017, 6, 1795.	1.6	26
32	Challenging a bioinformatic toolâ€™s ability to detect microbial contaminants usingin silicowhole genome sequencing data. PeerJ, 2017, 5, e3729.	2.0	8
33	Development and Characterization of Reference Materials for Genetic Testing: Focus on Public Partnerships. Annals of Laboratory Medicine, 2016, 36, 513-520.	2.5	21
34	Medical implications of technical accuracy in genome sequencing. Genome Medicine, 2016, 8, 24.	8.2	123
35	Extensive sequencing of seven human genomes to characterize benchmark reference materials. Scientific Data, 2016, 3, 160025.	5.3	575
36	A research roadmap for next-generation sequencing informatics. Science Translational Medicine, 2016, 8, 335ps10.	12.4	37

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37	PEPR: pipelines for evaluating prokaryotic references. Analytical and Bioanalytical Chemistry, 2016, 408, 2975-2983.	3.7	5
38	svclassify: a method to establish benchmark structural variant calls. BMC Genomics, 2016, 17, 64.	2.8	98
39	Best practices for evaluating single nucleotide variant calling methods for microbial genomics. Frontiers in Genetics, 2015, 6, 235.	2.3	160
40	An analytical framework for optimizing variant discovery from personal genomes. Nature Communications, 2015, 6, 6275.	12.8	88
41	International interlaboratory study comparing single organism 16S rRNA gene sequencing data: Beyond consensus sequence comparisons. Biomolecular Detection and Quantification, 2015, 3, 17-24.	7.0	3
42	Advancing Benchmarks for Genome Sequencing. Cell Systems, 2015, 1, 176-177.	6.2	6
43	Genomic Reference Materials for Clinical Applications. , 2015, , 393-402.		5
44	Good laboratory practice for clinical next-generation sequencing informatics pipelines. Nature Biotechnology, 2015, 33, 689-693.	17.5	134
45	svviz: a read viewer for validating structural variants. Bioinformatics, 2015, 31, 3994-3996.	4.1	46
46	Achieving high-sensitivity for clinical applications using augmented exome sequencing. Genome Medicine, 2015, 7, 71.	8.2	46
47	Integrating human sequence data sets provides a resource of benchmark SNP and indel genotype calls. Nature Biotechnology, 2014, 32, 246-251.	17.5	722
48	Immobilization of fibrinogen antibody on self-assembled gold monolayers for immunosensor applications. Tissue Engineering and Regenerative Medicine, 2014, 11, 10-15.	3.7	5
49	Disentangling the effects of polymer coatings on silver nanoparticle agglomeration, dissolution, and toxicity to determine mechanisms of nanotoxicity. Journal of Nanoparticle Research, 2012, 14, 1.	1.9	44
50	Assuring the quality of next-generation sequencing in clinical laboratory practice. Nature Biotechnology, 2012, 30, 1033-1036.	17.5	437
51	Synthetic Spike-in Standards Improve Run-Specific Systematic Error Analysis for DNA and RNA Sequencing. PLoS ONE, 2012, 7, e41356.	2.5	52
52	Measuring Agglomerate Size Distribution and Dependence of Localized Surface Plasmon Resonance Absorbance on Gold Nanoparticle Agglomerate Size Using Analytical Ultracentrifugation. ACS Nano, 2011, 5, 8070-8079.	14.6	96
53	Nanomaterial Toxicity: Emerging Standards and Efforts to Support Standards Development. Nanostructure Science and Technology, 2011, , 179-208.	0.1	9
54	Stable nanoparticle aggregates/agglomerates of different sizes and the effect of their size on hemolytic cytotoxicity. Nanotoxicology, 2011, 5, 517-530.	3.0	218

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55	Measuring silver nanoparticle dissolution in complex biological and environmental matrices using UVâ€“visible absorbance. Analytical and Bioanalytical Chemistry, 2011, 401, 1993-2002.	3.7	186
56	Interpretation of chronopotentiometric transients of ion-selective membranes with two transition times. Journal of Electroanalytical Chemistry, 2010, 638, 254-261.	3.8	13
57	Magnetic connectors for microfluidic applications. Lab on A Chip, 2010, 10, 246-249.	6.0	43
58	Effects of temperature, acyl chain length, and flow-rate ratio on liposome formation and size in a microfluidic hydrodynamic focusing device. Soft Matter, 2010, 6, 1352.	2.7	129
59	Assessment of Ionâ€Ionophore Complex Diffusion Coefficients in Solvent Polymeric Membranes. Electroanalysis, 2009, 21, 1923-1930.	2.9	13
60	Chronopotentiometric method for the assessment of ionophore diffusion coefficients in solvent polymeric membranes. Journal of Solid State Electrochemistry, 2009, 13, 171-179.	2.5	24
61	Current-polarized ion-selective membranes: The influence of plasticizer and lipophilic background electrolyte on concentration profiles, resistance, and voltage transients. Sensors and Actuators B: Chemical, 2009, 136, 410-418.	7.8	20
62	Reverse Current Pulse Method To Restore Uniform Concentration Profiles in Ion-Selective Membranes. 2. Comparison of the Efficiency of the Different Protocols. Analytical Chemistry, 2009, 81, 5155-5164.	6.5	9
63	Reverse Current Pulse Method To Restore Uniform Concentration Profiles in Ion-Selective Membranes. 1. Galvanostatic Pulse Methods with Decreased Cycle Time. Analytical Chemistry, 2009, 81, 5146-5154.	6.5	17
64	Mathematical Model of Currentâ€Polarized Ionophoreâ€Based Ionâ€Selective Membranes: Large Current Chronopotentiometry. Electroanalysis, 2008, 20, 259-269.	2.9	30
65	Mathematical Model of Current-Polarized Ionophore-Based Ion-Selective Membranes. Journal of Physical Chemistry B, 2008, 112, 2008-2015.	2.6	28
66	Electrochemical methods for the determination of the diffusion coefficient of ionophores and ionophoreâ€“ion complexes in plasticized PVC membranes. Analyst, The, 2008, 133, 635.	3.5	44
67	Statistical analysis of fractal-based brain tumor detection algorithms. Magnetic Resonance Imaging, 2005, 23, 671-678.	1.8	78