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List of Publications by Year in Descending Order

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	Curated variation benchmarks for challenging medically relevant autosomal genes.. *Nature Biotechnology*, **2022**,	44.5	12
92	The Role of the National Institute of Standards in Measurement Assurance for Cell Therapies **2022**, 609-625		
91	Assessing reproducibility of inherited variants detected with short-read whole genome sequencing.. *Genome Biology*, **2022**, 23, 2	18.3	3
90	Chasing perfection: validation and polishing strategies for telomere-to-telomere genome assemblies.. *Nature Methods*, **2022**,	21.6	4
89	Complete genomic and epigenetic maps of human centromeres.. *Science*, **2022**, 376, eabl4178	33.3	19
88	A complete reference genome improves analysis of human genetic variation.. *Science*, **2022**, 376, eabl3533	33.3	12
87	The complete sequence of a human genome.. *Science*, **2022**, 376, 44-53	33.3	107
86	PrecisionFDA Truth Challenge V2: Calling variants from short and long reads in difficult-to-map regions. *Cell Genomics*, **2022**, 2, 100129		4
85	Benchmarking challenging small variants with linked and long reads. *Cell Genomics*, **2022**, 2, 100128		2
84	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	8.1	10
83	Challenges of Accuracy in Germline Clinical Sequencing Data. *JAMA - Journal of the American Medical Association*, **2021**, 326, 268-269	27.4	0
82	Chromosome-scale, haplotype-resolved assembly of human genomes. *Nature Biotechnology*, **2021**, 39, 309-312	44.5	44
81	Performance assessment of DNA sequencing platforms in the ABRF Next-Generation Sequencing Study. *Nature Biotechnology*, **2021**, 39, 1129-1140	44.5	10
80	Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. *Nature Biotechnology*, **2020**, 38, 1044-1053	44.5	143
79	A robust benchmark for detection of germline large deletions and insertions. *Nature Biotechnology*, **2020**, 38, 1347-1355	44.5	98
78	Assembly and annotation of an Ashkenazi human reference genome. *Genome Biology*, **2020**, 21, 129	18.3	20
77	A crowdsourced set of curated structural variants for the human genome. *PLoS Computational Biology*, **2020**, 16, e1007933	5	0

76	A diploid assembly-based benchmark for variants in the major histocompatibility complex. *Nature Communications*, **2020**, 11, 4794	17.4	22
75	A Rigorous Interlaboratory Examination of the Need to Confirm Next-Generation Sequencing-Detected Variants with an Orthogonal Method□n Clinical Genetic Testing. *Journal of Molecular Diagnostics*, **2019**, 21, 318-329	5.1	28
74	High-coverage, long-read sequencing of Han Chinese trio reference samples. *Scientific Data*, **2019**, 6, 91	8.2	4
73	Best practices for benchmarking germline small-variant calls in human genomes. *Nature Biotechnology*, **2019**, 37, 555-560	44.5	125
72	An open resource for accurately benchmarking small variant and reference calls. *Nature Biotechnology*, **2019**, 37, 561-566	44.5	140
71	Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome. *Nature Biotechnology*, **2019**, 37, 1155-1162	44.5	427
70	A strategy for building and using a human reference pangenome. *F1000Research*, **2019**, 8, 1751	3.6	8
69	Unleashing novel STRS via characterization of genome in a bottle reference samples. *Forensic Science International: Genetics Supplement Series*, **2019**, 7, 218-220	0.5	2
68	A strategy for building and using a human reference pangenome. *F1000Research*, **2019**, 8, 1751	3.6	2
67	CrowdVariant: a crowdsourcing approach to classify copy number variants. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2019**, 24, 224-235	1.3	2
66	Determining Performance Metrics for Targeted Next-Generation Sequencing Panels Using Reference Materials. *Journal of Molecular Diagnostics*, **2018**, 20, 583-590	5.1	7
65	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	5.1	13
64	Genome-wide reconstruction of complex structural variants using read clouds. *Nature Methods*, **2017**, 14, 915-920	21.6	65
63	Tools for annotation and comparison of structural variation. *F1000Research*, **2017**, 6, 1795	3.6	11
62	Challenging a bioinformatic tools ability to detect microbial contaminants using whole genome sequencing data. *PeerJ*, **2017**, 5, e3729	3.1	6
61	Extensive sequencing of seven human genomes to characterize benchmark reference materials. *Scientific Data*, **2016**, 3, 160025	8.2	345
60	A research roadmap for next-generation sequencing informatics. *Science Translational Medicine*, **2016**, 8, 335ps10	17.5	29
59	PEPR: pipelines for evaluating prokaryotic references. *Analytical and Bioanalytical Chemistry*, **2016**, 408, 2975-83	4.4	5

58	svclassify: a method to establish benchmark structural variant calls. *BMC Genomics*, **2016**, 17, 64	4.5	68
57	Development and Characterization of Reference Materials for Genetic Testing: Focus on Public Partnerships. *Annals of Laboratory Medicine*, **2016**, 36, 513-20	3.1	12
56	Medical implications of technical accuracy in genome sequencing. *Genome Medicine*, **2016**, 8, 24	14.4	83
55	Good laboratory practice for clinical next-generation sequencing informatics pipelines. *Nature Biotechnology*, **2015**, 33, 689-93	44.5	115
54	svviz: a read viewer for validating structural variants. *Bioinformatics*, **2015**, 31, 3994-6	7.2	29
53	Achieving high-sensitivity for clinical applications using augmented exome sequencing. *Genome Medicine*, **2015**, 7, 71	14.4	41
52	Best practices for evaluating single nucleotide variant calling methods for microbial genomics. *Frontiers in Genetics*, **2015**, 6, 235	4.5	109
51	An analytical framework for optimizing variant discovery from personal genomes. *Nature Communications*, **2015**, 6, 6275	17.4	73
50	International interlaboratory study comparing single organism 16S rRNA gene sequencing data: Beyond consensus sequence comparisons. *Biomolecular Detection and Quantification*, **2015**, 3, 17-24	12	3
49	Advancing Benchmarks for Genome Sequencing. *Cell Systems*, **2015**, 1, 176-7	10.6	4
48	Genomic Reference Materials for Clinical Applications **2015**, 393-402		3
47	Integrating human sequence data sets provides a resource of benchmark SNP and indel genotype calls. *Nature Biotechnology*, **2014**, 32, 246-51	44.5	571
46	Immobilization of fibrinogen antibody on self-assembled gold monolayers for immunosensor applications. *Tissue Engineering and Regenerative Medicine*, **2014**, 11, 10-15	4.5	4
45	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	2.3	39
44	Assuring the quality of next-generation sequencing in clinical laboratory practice. *Nature Biotechnology*, **2012**, 30, 1033-6	44.5	372
43	Synthetic spike-in standards improve run-specific systematic error analysis for DNA and RNA sequencing. *PLoS ONE*, **2012**, 7, e41356	3.7	44
42	Nanomaterial Toxicity: Emerging Standards and Efforts to Support Standards Development. *Nanostructure Science and Technology*, **2011**, 179-208	0.9	9
41	Stable nanoparticle aggregates/agglomerates of different sizes and the effect of their size on hemolytic cytotoxicity. *Nanotoxicology*, **2011**, 5, 517-30	5.3	190

40	Measuring silver nanoparticle dissolution in complex biological and environmental matrices using UV-visible absorbance. *Analytical and Bioanalytical Chemistry*, **2011**, 401, 1993-2002	4.4	170
39	Measuring agglomerate size distribution and dependence of localized surface plasmon resonance absorbance on gold nanoparticle agglomerate size using analytical ultracentrifugation. *ACS Nano*, **2011**, 5, 8070-9	16.7	80
38	Magnetic connectors for microfluidic applications. *Lab on A Chip*, **2010**, 10, 246-9	7.2	36
37	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	3.6	97
36	Interpretation of chronopotentiometric transients of ion-selective membranes with two transition times. *Journal of Electroanalytical Chemistry*, **2010**, 638, 254-261	4.1	11
35	Assessment of Ion-Ionophore Complex Diffusion Coefficients in Solvent Polymeric Membranes. *Electroanalysis*, **2009**, 21, 1923-1930	3	12
34	Chronopotentiometric method for the assessment of ionophore diffusion coefficients in solvent polymeric membranes. *Journal of Solid State Electrochemistry*, **2009**, 13, 171-179	2.6	24
33	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	8.5	15
32	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, 5155-64	7.8	9
31	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, 5146-54	7.8	15
30	Mathematical model of current-polarized ionophore-based ion-selective membranes. *Journal of Physical Chemistry B*, **2008**, 112, 2008-15	3.4	26
29	Electrochemical methods for the determination of the diffusion coefficient of ionophores and ionophore-ion complexes in plasticized PVC membranes. *Analyst, The*, **2008**, 133, 635-42	5	41
28	Mathematical Model of Current-Polarized Ionophore-Based Ion-Selective Membranes: Large Current Chronopotentiometry. *Electroanalysis*, **2008**, 20, 259-269	3	26
27	Statistical analysis of fractal-based brain tumor detection algorithms. *Magnetic Resonance Imaging*, **2005**, 23, 671-8	3.3	60
26	svviz: a read viewer for validating structural variants		4
25	Comparing Variant Call Files for Performance Benchmarking of Next-Generation Sequencing Variant Calling Pipelines		73
24	Genome-wide reconstruction of complex structural variants using read clouds		8
23	Assembly and Annotation of an Ashkenazi Human Reference Genome		2

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21	Multi-Platform Assessment of DNA Sequencing Performance using Human and Bacterial Reference Genomes in the ABRF Next-Generation Sequencing Study	1
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15	genomeview - an extensible python-based genomics visualization engine	1
14	Highly-accurate long-read sequencing improves variant detection and assembly of a human genome	29
13	High-coverage, long-read sequencing of Han Chinese trio reference samples	1
12	SVCurator: A Crowdsourcing app to visualize evidence of structural variants for the human genome	4
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10	Efficient de novo assembly of eleven human genomes using PromethION sequencing and a novel nanopore toolkit	29
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