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List of Publications by Year in descending order

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71
papers

6,038
citations

147801
31
h-index

95266
68
g-index

81
all docs

81
docs citations

81
times ranked

10572
citing authors

#	ARTICLE	IF	CITATIONS
1	Benchmarking challenging small variants with linked and long reads. <i>Cell Genomics</i> , 2022, 2, 100128.	6.5	77
2	LAMP Diagnostics at the Point-of-Care: Emerging Trends and Perspectives for the Developer Community. <i>Expert Review of Molecular Diagnostics</i> , 2021, 21, 43-61.	3.1	105
3	Testing at scale during the COVID-19 pandemic. <i>Nature Reviews Genetics</i> , 2021, 22, 415-426.	16.3	261
4	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.	2.4	40
5	The Environmental Microbiology Minimum Information (EMMI) Guidelines: qPCR and dPCR Quality and Reporting for Environmental Microbiology. <i>Environmental Science & Technology</i> , 2021, 55, 10210-10223.	10.0	117
6	MAQC and the era of genomic medicine. <i>Nature Biotechnology</i> , 2021, 39, 1066-1067.	17.5	8
7	A diploid assembly-based benchmark for variants in the major histocompatibility complex. <i>Nature Communications</i> , 2020, 11, 4794.	12.8	56
8	Cautionary Note on Contamination of Reagents Used for Molecular Detection of SARS-CoV-2. <i>Clinical Chemistry</i> , 2020, 66, 1369-1372.	3.2	46
9	The COVID-19 XPRIZE and the need for scalable, fast, and widespread testing. <i>Nature Biotechnology</i> , 2020, 38, 1021-1024.	17.5	71
10	A robust benchmark for detection of germline large deletions and insertions. <i>Nature Biotechnology</i> , 2020, 38, 1347-1355.	17.5	233
11	Assembly and annotation of an Ashkenazi human reference genome. <i>Genome Biology</i> , 2020, 21, 129.	8.8	42
12	A crowdsourced set of curated structural variants for the human genome. <i>PLoS Computational Biology</i> , 2020, 16, e1007933.	3.2	6
13	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
14	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
15	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
16	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
17	Simultaneous RNA purification and size selection using on-chip isotachopheresis with an ionic spacer. <i>Lab on A Chip</i> , 2019, 19, 2741-2749.	6.0	15
18	A Rigorous Interlaboratory Examination of the Need to Confirm Next-Generation Sequencingâ€”Detected Variants with an Orthogonal MethodÂ”in Clinical Genetic Testing. <i>Journal of Molecular Diagnostics</i> , 2019, 21, 318-329.	2.8	49

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19	High-coverage, long-read sequencing of Han Chinese trio reference samples. <i>Scientific Data</i> , 2019, 6, 91.	5.3	13
20	Best practices for benchmarking germline small-variant calls in human genomes. <i>Nature Biotechnology</i> , 2019, 37, 555-560.	17.5	273
21	An open resource for accurately benchmarking small variant and reference calls. <i>Nature Biotechnology</i> , 2019, 37, 561-566.	17.5	277
22	CrowdVariant: a crowdsourcing approach to classify copy number variants. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2019, 24, 224-235.	0.7	2
23	Cell-based reference samples designed with specific differences in microRNA biomarkers. <i>BMC Biotechnology</i> , 2018, 18, 17.	3.3	2
24	Proffered Papers and Posters Presented at the Seventh International Symposium on Hereditary Breast and Ovarian Cancer—BrCA: From the Personal to the Population. <i>Current Oncology</i> , 2018, 25, 224-262.	2.2	2
25	Unbiased Fitness Estimation of Pooled Barcode or Amplicon Sequencing Studies. <i>Cell Systems</i> , 2018, 7, 521-525.e4.	6.2	27
26	Determining Performance Metrics for Targeted Next-Generation Sequencing Panels Using Reference Materials. <i>Journal of Molecular Diagnostics</i> , 2018, 20, 583-590.	2.8	10
27	Summarizing performance for genome scale measurement of miRNA: reference samples and metrics. <i>BMC Genomics</i> , 2018, 19, 180.	2.8	5
28	Multiplexed precision genome editing with trackable genomic barcodes in yeast. <i>Nature Biotechnology</i> , 2018, 36, 512-520.	17.5	138
29	Measurements of translation initiation from all 64 codons in <i>E. coli</i> . <i>Nucleic Acids Research</i> , 2017, 45, 3615-3626.	14.5	165
30	Genome-wide reconstruction of complex structural variants using read clouds. <i>Nature Methods</i> , 2017, 14, 915-920.	19.0	96
31	External RNA Controls Consortium Beta Version Update. <i>Journal of Genomics</i> , 2016, 4, 19-22.	0.9	28
32	Development and Characterization of Reference Materials for Genetic Testing: Focus on Public Partnerships. <i>Annals of Laboratory Medicine</i> , 2016, 36, 513-520.	2.5	21
33	Medical implications of technical accuracy in genome sequencing. <i>Genome Medicine</i> , 2016, 8, 24.	8.2	123
34	An international comparability study on quantification of mRNA gene expression ratios: CCQM-P103.1. <i>Biomolecular Detection and Quantification</i> , 2016, 8, 15-28.	7.0	15
35	Extensive sequencing of seven human genomes to characterize benchmark reference materials. <i>Scientific Data</i> , 2016, 3, 160025.	5.3	575
36	A research roadmap for next-generation sequencing informatics. <i>Science Translational Medicine</i> , 2016, 8, 335ps10.	12.4	37

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37	Gradient Elution Moving Boundary Electrophoresis Enables Rapid Analysis of Acids in Complex Biomass-Derived Streams. ACS Sustainable Chemistry and Engineering, 2016, 4, 7175-7185.	6.7	8
38	Evaluation of the External RNA Controls Consortium (ERCC) reference material using a modified Latin square design. BMC Biotechnology, 2016, 16, 54.	3.3	41
39	In Vivo Site-Specific Protein Tagging with Diverse Amines Using an Engineered Sortase Variant. Journal of the American Chemical Society, 2016, 138, 7496-7499.	13.7	77
40	PEPR: pipelines for evaluating prokaryotic references. Analytical and Bioanalytical Chemistry, 2016, 408, 2975-2983.	3.7	5
41	When Wavelengths Collide: Bias in Cell Abundance Measurements Due to Expressed Fluorescent Proteins. ACS Synthetic Biology, 2016, 5, 1024-1027.	3.8	32
42	Best practices for evaluating single nucleotide variant calling methods for microbial genomics. Frontiers in Genetics, 2015, 6, 235.	2.3	160
43	Unmet needs: Research helps regulators do their jobs. Science Translational Medicine, 2015, 7, 315ps22.	12.4	15
44	Advancing Benchmarks for Genome Sequencing. Cell Systems, 2015, 1, 176-177.	6.2	6
45	Good laboratory practice for clinical next-generation sequencing informatics pipelines. Nature Biotechnology, 2015, 33, 689-693.	17.5	134
46	Minimum information for reporting next generation sequence genotyping (MIRING): Guidelines for reporting HLA and KIR genotyping via next generation sequencing. Human Immunology, 2015, 76, 954-962.	2.4	28
47	svviz: a read viewer for validating structural variants. Bioinformatics, 2015, 31, 3994-3996.	4.1	46
48	Achieving high-sensitivity for clinical applications using augmented exome sequencing. Genome Medicine, 2015, 7, 71.	8.2	46
49	Use of Cause-and-Effect Analysis to Design a High-Quality Nanocytotoxicology Assay. Chemical Research in Toxicology, 2015, 28, 21-30.	3.3	65
50	Integrating human sequence data sets provides a resource of benchmark SNP and indel genotype calls. Nature Biotechnology, 2014, 32, 246-251.	17.5	722
51	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. Nature Communications, 2014, 5, 5125.	12.8	122
52	Ontology analysis of global gene expression differences of human bone marrow stromal cells cultured on 3D scaffolds or 2D films. Biomaterials, 2014, 35, 6716-6726.	11.4	32
53	Characterization of in vitro transcription amplification linearity and variability in the low copy number regime using External RNA Control Consortium (ERCC) spike-ins. Analytical and Bioanalytical Chemistry, 2013, 405, 315-320.	3.7	10
54	Wave numbers and pressure-induced shifts of Ar I atomic lines measured by Fourier transform spectroscopy. Journal of Physics B: Atomic, Molecular and Optical Physics, 2012, 45, 115001.	1.5	3

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55	Synthetic spike-in standards for RNA-seq experiments. <i>Genome Research</i> , 2011, 21, 1543-1551.	5.5	588
56	The determination of stem cell fate by 3D scaffold structures through the control of cell shape. <i>Biomaterials</i> , 2011, 32, 9188-9196.	11.4	264
57	Image-based feedback control for real-time sorting of microspheres in a microfluidic device. <i>Lab on a Chip</i> , 2010, 10, 2402.	6.0	14
58	Use of Standard Reference Material 2242 (Relative Intensity Correction Standard for Raman) Tj ETQq0 0 0 rgBT /Overclock 10 Tf 50 622	1.8	1
59	[5] Standards in Gene Expression Microarray Experiments. <i>Methods in Enzymology</i> , 2006, 411, 63-78.	1.0	17
60	The External RNA Controls Consortium: a progress report. <i>Nature Methods</i> , 2005, 2, 731-734.	19.0	328
61	Wave numbers and Ar pressure-induced shifts of 198Hg atomic lines measured by Fourier transform spectroscopy. <i>Journal of Physics B: Atomic, Molecular and Optical Physics</i> , 2005, 38, 3739-3753.	1.5	11
62	Traceability of Single-Element Calibration Solutions. <i>Analytical Chemistry</i> , 2005, 77, 136 A-141 A.	6.5	20
63	Single-Element Solution Comparisons with a High-Performance Inductively Coupled Plasma Optical Emission Spectrometric Method. <i>Analytical Chemistry</i> , 2001, 73, 4821-4829.	6.5	55
64	Using inductively coupled plasma-mass spectrometry for calibration transfer between environmental CRMs. <i>Fresenius' Journal of Analytical Chemistry</i> , 2001, 370, 259-263.	1.5	12
65	An ICP-OES Method with 0.2 Expanded Uncertainties for the Characterization of LiAlO ₂ . <i>Analytical Chemistry</i> , 2000, 72, 3504-3511.	6.5	31
66	A Drift Correction Procedure. <i>Analytical Chemistry</i> , 1998, 70, 3184-3190.	6.5	68
67	System-ready behaviors for integration. <i>Laboratory Robotics and Automation</i> , 1997, 9, 113-118.	0.2	0
68	Design and initial characterization of a glow discharge atomic emission instrument for macro-scale elemental composition mapping of solid surfaces. <i>Spectrochimica Acta, Part B: Atomic Spectroscopy</i> , 1995, 50, 1045-1058.	2.9	11
69	Integrating Automated Systems With Modular Architecture. <i>Analytical Chemistry</i> , 1994, 66, 361A-367A.	6.5	7
70	Fourier transform atomic emission studies using a glow discharge as the emission source. <i>Spectrochimica Acta, Part B: Atomic Spectroscopy</i> , 1993, 48, 1325-1337.	2.9	7
71	Preparation and certification of a rhodium standard reference material solution. <i>Analytical Chemistry</i> , 1993, 65, 2899-2902.	6.5	9