

Wendell D Jones

List of Publications by Year in descending order

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Version: 2024-02-01

38
papers

4,212
citations

304743

22
h-index

361022

35
g-index

40
all docs

40
docs citations

40
times ranked

6978
citing authors

#	ARTICLE	IF	CITATIONS
1	The MicroArray Quality Control (MAQC) project shows inter- and intraplatform reproducibility of gene expression measurements. <i>Nature Biotechnology</i> , 2006, 24, 1151-1161.	17.5	1,927
2	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. <i>Nature Biotechnology</i> , 2010, 28, 827-838.	17.5	795
3	Tumor mutational burden is a determinant of immune-mediated survival in breast cancer. <i>OncoImmunology</i> , 2018, 7, e1490854.	4.6	200
4	DNMT3b overexpression contributes to a hypermethylator phenotype in human breast cancer cell lines. <i>Molecular Cancer</i> , 2008, 7, 15.	19.2	192
5	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. <i>Nature Biotechnology</i> , 2021, 39, 1115-1128.	17.5	126
6	k-Nearest neighbor models for microarray gene expression analysis and clinical outcome prediction. <i>Pharmacogenomics Journal</i> , 2010, 10, 292-309.	2.0	102
7	Whole-Genome Gene Expression Profiling of Formalin-Fixed, Paraffin-Embedded Tissue Samples. <i>PLoS ONE</i> , 2009, 4, e8162.	2.5	98
8	Toward best practice in cancer mutation detection with whole-genome and whole-exome sequencing. <i>Nature Biotechnology</i> , 2021, 39, 1141-1150.	17.5	66
9	Dysregulation of the epigenome in triple-negative breast cancers: Basal-like and claudin-low breast cancers express aberrant DNA hypermethylation. <i>Experimental and Molecular Pathology</i> , 2013, 95, 276-287.	2.1	59
10	Technical Reproducibility of Genotyping SNP Arrays Used in Genome-Wide Association Studies. <i>PLoS ONE</i> , 2012, 7, e44483.	2.5	59
11	DNA methylation-dependent silencing of CST6 in human breast cancer cell lines. <i>Laboratory Investigation</i> , 2006, 86, 1233-1242.	3.7	48
12	Deleterious effects of formalin-fixation and delays to fixation on RNA and miRNA-Seq profiles. <i>Scientific Reports</i> , 2019, 9, 6980.	3.3	46
13	DNA Methylation-Dependent Epigenetic Regulation of Gene Expression in MCF-7 Breast Cancer Cells. <i>Epigenetics</i> , 2006, 1, 33-45.	2.7	44
14	A benchmarking study of SARS-CoV-2 whole-genome sequencing protocols using COVID-19 patient samples. <i>IScience</i> , 2021, 24, 102892.	4.1	39
15	Establishing community reference samples, data and call sets for benchmarking cancer mutation detection using whole-genome sequencing. <i>Nature Biotechnology</i> , 2021, 39, 1151-1160.	17.5	39
16	Expression profile of <i>COL2A1</i> and the pseudogene <i>SLC6A10P</i> predicts tumor recurrence in high-grade serous ovarian cancer. <i>International Journal of Cancer</i> , 2016, 138, 679-688.	5.1	32
17	The international MAQC Society launches to enhance reproducibility of high-throughput technologies. <i>Nature Biotechnology</i> , 2017, 35, 1127-1128.	17.5	32
18	Editor's Highlight: Dose-Response Analysis of RNA-Seq Profiles in Archival Formalin-Fixed Paraffin-Embedded Samples. <i>Toxicological Sciences</i> , 2016, 154, 202-213.	3.1	31

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19	Microarray-Based Gene Expression Profiling for Molecular Classification of Breast Cancer and Identification of New Targets for Therapy. <i>Laboratory Medicine</i> , 2010, 41, 364-372.	1.2	30
20	Data-Driven Asthma Endotypes Defined from Blood Biomarker and Gene Expression Data. <i>PLoS ONE</i> , 2015, 10, e0117445.	2.5	30
21	A verified genomic reference sample for assessing performance of cancer panels detecting small variants of low allele frequency. <i>Genome Biology</i> , 2021, 22, 111.	8.8	29
22	CBP/p300 Drives the Differentiation of Regulatory T Cells through Transcriptional and Non-Transcriptional Mechanisms. <i>Cancer Research</i> , 2019, 79, 3916-3927.	0.9	26
23	Comparison of comparative genomic hybridization technologies across microarray platforms. <i>Journal of Biomolecular Techniques</i> , 2009, 20, 135-51.	1.5	25
24	Assessing sources of inconsistencies in genotypes and their effects on genome-wide association studies with HapMap samples. <i>Pharmacogenomics Journal</i> , 2010, 10, 364-374.	2.0	21
25	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. <i>Genome Biology</i> , 2021, 22, 109.	8.8	20
26	Blood-Borne RNA Correlates with Disease Activity and IFN-Stimulated Gene Expression in Systemic Lupus Erythematosus. <i>Journal of Immunology</i> , 2016, 197, 2854-2863.	0.8	18
27	RNA Immune Signatures from Pan-Cancer Analysis Are Prognostic for High-Grade Serous Ovarian Cancer and Other Female Cancers. <i>Cancers</i> , 2020, 12, 620.	3.7	14
28	Increased expression of neurotensin in high grade serous ovarian carcinoma with evidence of serous tubal intraepithelial carcinoma. <i>Journal of Pathology</i> , 2019, 248, 352-362.	4.5	10
29	Orchestrating and sharing large multimodal data for transparent and reproducible research. <i>Nature Communications</i> , 2021, 12, 5797.	12.8	10
30	Advancing NGS quality control to enable measurement of actionable mutations in circulating tumor DNA. <i>Cell Reports Methods</i> , 2021, 1, 100106.	2.9	9
31	CNV Radar: an improved method for somatic copy number alteration characterization in oncology. <i>BMC Bioinformatics</i> , 2020, 21, 98.	2.6	8
32	Deep oncopanel sequencing reveals within block position-dependent quality degradation in FFPE processed samples. <i>Genome Biology</i> , 2022, 23, .	8.8	8
33	Applicability of Precision Medicine Approaches to Managing Hypertension in Rural Populations. <i>Journal of Personalized Medicine</i> , 2018, 8, 16.	2.5	5
34	Ultra-deep sequencing data from a liquid biopsy proficiency study demonstrating analytic validity. <i>Scientific Data</i> , 2022, 9, 170.	5.3	4
35	Infinite-failure models for a finite world: a simulation study of fault discovery. <i>IEEE Transactions on Reliability</i> , 1994, 43, 520-526.	4.6	3
36	Genomics and Bioinformatics in Biological Discovery and Pharmaceutical Development. , 2020, , 105-142.		1

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37	Dexrazoxane enhances efficacy of all- <i>trans</i> retinoic acid in acute myeloid leukemia patient blast cells and cell lines. <i>Leukemia and Lymphoma</i> , 2021, 62, 473-477.	1.3	0
38	Ultra-deep multi-oncopanel sequencing of benchmarking samples with a wide range of variant allele frequencies. <i>Scientific Data</i> , 2022, 9, .	5.3	0