Wendell D Jones

List of Publications by Year
in descending order

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38	4,212	304743	361022
papers	citations	22 h-index	35 g-index

40	40	40	6978
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Ultra-deep sequencing data from a liquid biopsy proficiency study demonstrating analytic validity. Scientific Data, 2022, 9, 170.	5.3	4
2	Ultra-deep multi-oncopanel sequencing of benchmarking samples with a wide range of variant allele frequencies. Scientific Data, 2022, 9, .	5.3	0
3	Deep oncopanel sequencing reveals within block position-dependent quality degradation in FFPE processed samples. Genome Biology, 2022, 23, .	8.8	8
4	Dexrazoxane enhances efficacy of all-trans retinoic acid in acute myeloid leukemia patient blast cells and cell lines. Leukemia and Lymphoma, 2021, 62, 473-477.	1.3	0
5	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. Nature Biotechnology, 2021, 39, 1115-1128.	17.5	126
6	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. Genome Biology, 2021, 22, 109.	8.8	20
7	A verified genomic reference sample for assessing performance of cancer panels detecting small variants of low allele frequency. Genome Biology, 2021, 22, 111.	8.8	29
8	A benchmarking study of SARS-CoV-2 whole-genome sequencing protocols using COVID-19 patient samples. IScience, 2021, 24, 102892.	4.1	39
9	Toward best practice in cancer mutation detection with whole-genome and whole-exome sequencing. Nature Biotechnology, 2021, 39, 1141-1150.	17.5	66
10	Establishing community reference samples, data and call sets for benchmarking cancer mutation detection using whole-genome sequencing. Nature Biotechnology, 2021, 39, 1151-1160.	17.5	39
11	Orchestrating and sharing large multimodal data for transparent and reproducible research. Nature Communications, 2021, 12, 5797.	12.8	10
12	Advancing NGS quality control to enable measurement of actionable mutations in circulating tumor DNA. Cell Reports Methods, 2021, 1, 100106.	2.9	9
13	CNV Radar: an improved method for somatic copy number alteration characterization in oncology. BMC Bioinformatics, 2020, 21, 98.	2.6	8
14	RNA Immune Signatures from Pan-Cancer Analysis Are Prognostic for High-Grade Serous Ovarian Cancer and Other Female Cancers. Cancers, 2020, 12, 620.	3.7	14
15	Genomics and Bioinformatics in Biological Discovery and Pharmaceutical Development. , 2020, , 105-142.		1
16	CBP/p300 Drives the Differentiation of Regulatory T Cells through Transcriptional and Non-Transcriptional Mechanisms. Cancer Research, 2019, 79, 3916-3927.	0.9	26
17	Deleterious effects of formalin-fixation and delays to fixation on RNA and miRNA-Seq profiles. Scientific Reports, 2019, 9, 6980.	3.3	46
18	Increased expression of neurotensin in high grade serous ovarian carcinoma with evidence of serous tubal intraepithelial carcinoma. Journal of Pathology, 2019, 248, 352-362.	4.5	10

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19	Tumor mutational burden is a determinant of immune-mediated survival in breast cancer. OncoImmunology, 2018, 7, e1490854.	4.6	200
20	Applicability of Precision Medicine Approaches to Managing Hypertension in Rural Populations. Journal of Personalized Medicine, 2018, 8, 16.	2.5	5
21	The international MAQC Society launches to enhance reproducibility of high-throughput technologies. Nature Biotechnology, 2017, 35, 1127-1128.	17.5	32
22	Editorâ€™s Highlight: Doseâ€“Response Analysis of RNA-Seq Profiles in Archival Formalin-Fixed Paraffin-Embedded Samples. Toxicological Sciences, 2016, 154, 202-213.	3.1	31
23	Blood-Borne RNA Correlates with Disease Activity and IFN-Stimulated Gene Expression in Systemic Lupus Erythematosus. Journal of Immunology, 2016, 197, 2854-2863.	0.8	18
24	Expression profile of <scp>COL2A1</scp> and the pseudogene <scp>SLC6A10P</scp> predicts tumor recurrence in highâ€grade serous ovarian cancer. International Journal of Cancer, 2016, 138, 679-688.	5.1	32
25	Data-Driven Asthma Endotypes Defined from Blood Biomarker and Gene Expression Data. PLoS ONE, 2015, 10, e0117445.	2.5	30
26	Dysregulation of the epigenome in triple-negative breast cancers: Basal-like and claudin-low breast cancers express aberrant DNA hypermethylation. Experimental and Molecular Pathology, 2013, 95, 276-287.	2.1	59
27	Technical Reproducibility of Genotyping SNP Arrays Used in Genome-Wide Association Studies. PLoS ONE, 2012, 7, e44483.	2.5	59
28	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. Nature Biotechnology, 2010, 28, 827-838.	17.5	795
29	Assessing sources of inconsistencies in genotypes and their effects on genome-wide association studies with HapMap samples. Pharmacogenomics Journal, 2010, 10, 364-374.	2.0	21
30	k-Nearest neighbor models for microarray gene expression analysis and clinical outcome prediction. Pharmacogenomics Journal, 2010, 10, 292-309.	2.0	102
31	Microarray-Based Gene Expression Profiling for Molecular Classification of Breast Cancer and Identification of New Targets for Therapy. Laboratory Medicine, 2010, 41, 364-372.	1.2	30
32	Whole-Genome Gene Expression Profiling of Formalin-Fixed, Paraffin-Embedded Tissue Samples. PLoS ONE, 2009, 4, e8162.	2.5	98
33	Comparison of comparative genomic hybridization technologies across microarray platforms. Journal of Biomolecular Techniques, 2009, 20, 135-51.	1.5	25
34	DNMT3b overexpression contributes to a hypermethylator phenotype in human breast cancer cell lines. Molecular Cancer, 2008, 7, 15.	19.2	192
35	The MicroArray Quality Control (MAQC) project shows inter- and intraplatform reproducibility of gene expression measurements. Nature Biotechnology, 2006, 24, 1151-1161.	17.5	1,927
36	DNA methylation-dependent silencing of CST6 in human breast cancer cell lines. Laboratory Investigation, 2006, 86, 1233-1242.	3.7	48

#	Article	IF	Citations
37	DNA Methylation-Dependent Epigenetic Regulation of Gene Expression in MCF-7 Breast Cancer Cells. Epigenetics, 2006, 1, 33-45.	2.7	44
38	Infinite-failure models for a finite world: a simulation study of fault discovery. IEEE Transactions on Reliability, 1994, 43, 520-526.	4.6	3