

James C Willey

List of Publications by Year in descending order

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Version: 2024-02-01

74
papers

4,950
citations

361413

20
h-index

206112

48
g-index

76
all docs

76
docs citations

76
times ranked

6757
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	Evaluation of DNA microarray results with quantitative gene expression platforms. <i>Nature Biotechnology</i> , 2006, 24, 1115-1122.	17.5	558
4	The balance of reproducibility, sensitivity, and specificity of lists of differentially expressed genes in microarray studies. <i>BMC Bioinformatics</i> , 2008, 9, S10.	2.6	215
5	Using RNA sample titrations to assess microarray platform performance and normalization techniques. <i>Nature Biotechnology</i> , 2006, 24, 1123-1131.	17.5	168
6	ABCC5, ERCC2, XPA and XRCC1 transcript abundance levels correlate with cisplatin chemoresistance in non-small cell lung cancer cell lines. <i>Molecular Cancer</i> , 2005, 4, 18.	19.2	147
7	Variation in transcriptional regulation of cyclin dependent kinase inhibitor p21waf1/cip1 among human bronchogenic carcinomas. <i>Molecular Cancer</i> , 2005, 4, 23.	19.2	130
8	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. <i>Nature Biotechnology</i> , 2021, 39, 1115-1128.	17.5	126
9	Expression Measurement of Many Genes Simultaneously by Quantitative RT-PCR Using Standardized Mixtures of Competitive Templates. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 1998, 19, 6-17.	2.9	87
10	Stable low-level expression of p21WAF1/CIP1 in A549 human bronchogenic carcinoma cell line-derived clones down-regulates E2F1 mRNA and restores cell proliferation control. <i>Molecular Cancer</i> , 2006, 5, 1.	19.2	70
11	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
12	Pattern of Antioxidant and DNA Repair Gene Expression in Normal Airway Epithelium Associated with Lung Cancer Diagnosis. <i>Cancer Research</i> , 2009, 69, 8629-8635.	0.9	56
13	Developing a Sustainable Process to Provide Quality Control Materials for Genetic Testing. <i>Genetics in Medicine</i> , 2005, 7, 534-549.	2.4	49
14	Transcript profiling of enzymes involved in detoxification of xenobiotics and reactive oxygen in human normal and simian virus 40 T antigen-immortalized oral keratinocytes. <i>International Journal of Cancer</i> , 2002, 99, 776-782.	5.1	37
15	The Gene Expression Index $c-myc \sim E2F-1/p21$ Is Highly Predictive of Malignant Phenotype in Human Bronchial Epithelial Cells. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 1998, 19, 18-24.	2.9	35
16	CEBPG transcription factor correlates with antioxidant and DNA repair genes in normal bronchial epithelial cells but not in individuals with bronchogenic carcinoma. <i>BMC Cancer</i> , 2005, 5, 141.	2.6	33
17	Targeted RNA-Sequencing with Competitive Multiplex-PCR Amplicon Libraries. <i>PLoS ONE</i> , 2013, 8, e79120.	2.5	30
18	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

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19	Standardized RT-PCR and the Standardized Expression Measurement Center. , 2004, 258, 13-42.		27
20	Survival with Parenchymal and Pleural Invasion of Non-“Small Cell Lung Cancers Less than 30 mm. Journal of Thoracic Oncology, 2019, 14, 890-902.	1.1	25
21	Reproducible Gene Expression Measurement Among Multiple Laboratories Obtained in a Blinded Study Using Standardized RT (StaRT)-PCR. Molecular Diagnosis and Therapy, 2001, 6, 217-225.	1.1	23
22	Cis-acting genetic variation at an E2F1/YY1 response site and putative p53 site is associated with altered allele-specific expression of ERCC5 (XPG) transcript in normal human bronchial epithelium. Carcinogenesis, 2010, 31, 1242-1250.	2.8	20
23	RNAseq analysis of bronchial epithelial cells to identify COPD-associated genes and SNPs. BMC Pulmonary Medicine, 2018, 18, 42.	2.0	20
24	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. Genome Biology, 2021, 22, 109.	8.8	20
25	Control for stochastic sampling variation and qualitative sequencing error in next generation sequencing. Biomolecular Detection and Quantification, 2015, 5, 30-37.	7.0	17
26	Multiplex standardized RT-PCR for expression analysis of many genes in small samples. Biochemical and Biophysical Research Communications, 2002, 293, 509-516.	2.1	16
27	Fetal-“juvenile origins of point mutations in the adult human tracheal-“bronchial epithelium: Absence of detectable effects of age, gender or smoking status. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2008, 646, 25-40.	1.0	16
28	Platelet-T cell aggregates in lung cancer patients: Implications for thrombosis. PLoS ONE, 2020, 15, e0236966.	2.5	16
29	Radon-induced neoplastic transformation of human bronchial epithelial cells. Radiation Oncology Investigations, 1995, 3, 398-403.	0.9	15
30	Accurate Detection and Quantification of the Fish Viral Hemorrhagic Septicemia virus (VHSV) with a Two-Color Fluorometric Real-Time PCR Assay. PLoS ONE, 2013, 8, e71851.	2.5	14
31	Haplotype and diplotype analyses of variation in <i>ERCC5</i> transcription <i>cis</i> -regulation in normal bronchial epithelial cells. Physiological Genomics, 2016, 48, 537-543.	2.3	13
32	The c-myc x E2F-1/p21 Interactive Gene Expression Index Augments Cytomorphologic Diagnosis of Lung Cancer in Fine-Needle Aspirate Specimens. Journal of Molecular Diagnostics, 2003, 5, 176-183.	2.8	12
33	Distributions of five common point mutants in the human tracheal-bronchial epithelium. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2006, 596, 113-127.	1.0	12
34	A new StaRT-PCR approach to detect and quantify fish Viral Hemorrhagic Septicemia virus (VHSV): Enhanced quality control with internal standards. Journal of Virological Methods, 2013, 189, 129-142.	2.1	12
35	Quality Control Methods for Optimal BCR-ABL1 Clinical Testing in Human Whole Blood Samples. Journal of Molecular Diagnostics, 2013, 15, 391-400.	2.8	12
36	Technical advance in targeted NGS analysis enables identification of lung cancer risk-associated low frequency TP53, PIK3CA, and BRAF mutations in airway epithelial cells. BMC Cancer, 2019, 19, 1081.	2.6	12

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37	Alterations of p53 in tumorigenic human bronchial epithelial cells correlate with metastatic potential. <i>Carcinogenesis</i> , 1999, 20, 1529-1534.	2.8	9
38	CEBPG Exhibits Allele-Specific Expression in Human Bronchial Epithelial Cells. <i>Gene Regulation and Systems Biology</i> , 2013, 7, GRSB.S11879.	2.3	9
39	Lung cancer risk test trial: study design, participant baseline characteristics, bronchoscopy safety, and establishment of a biospecimen repository. <i>BMC Pulmonary Medicine</i> , 2016, 16, 16.	2.0	9
40	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
41	Abstract 2890: ERCC5 variant rs2296147 T-allele creates a predicted TP53 binding site and up-regulates transcript abundance in normal bronchial epithelial cells, while rs17655 C-allele is linked to miRNA binding site variant and down regulates. <i>Cancer Research</i> , 2016, 76, 2890-2890.	0.9	8
42	A Multiplex Two-Color Real-Time PCR Method for Quality-Controlled Molecular Diagnostic Testing of FFPE Samples. <i>PLoS ONE</i> , 2014, 9, e89395.	2.5	8
43	Use of Standardized Reverse Transcription-Polymerase Chain Reaction and the Standardized Expression Measurement Center in Multi-institutional Trials To Develop Meaningful Lung Cancer Classification Based on Molecular Genetic Criteria. <i>Chest</i> , 2004, 125, 155S-156S.	0.8	7
44	Quality-Controlled Measurement Methods for Quantification of Variations in Transcript Abundance in Whole Blood Samples from Healthy Volunteers. <i>Clinical Chemistry</i> , 2007, 53, 1030-1037.	3.2	6
45	A lung cancer risk classifier comprising genome maintenance genes measured in normal bronchial epithelial cells. <i>BMC Cancer</i> , 2017, 17, 301.	2.6	4
46	Genome-wide interaction analysis identified low-frequency variants with sex disparity in lung cancer risk. <i>Human Molecular Genetics</i> , 2022, 31, 2831-2843.	2.9	4
47	Patterns of Gene Expression in Human Airway Epithelial Cells. <i>Chest</i> , 1997, 111, 83S.	0.8	3
48	Abstract 4156: Inter-individual variation in allele specific expression of catalase (CAT) in normal bronchial epithelial cells and association of putative cis-regulatory CAT SNP rs12807961 with lung cancer risk. , 2014, , .		2
49	The interactive transcript abundance index [c-myc*p73 \pm]/[p21*Bcl-2] correlates with baseline level of apoptosis and response to CPT-11 in human bronchogenic carcinoma cell lines. <i>International Journal of Oncology</i> , 2007, 30, 1553-60.	3.3	1
50	Abstract 3381: Investigation of C/EBPG transcription factor role in regulation of ERCC4 and ERCC5 in human lung cancer cells. , 2014, , .		1
51	Abstract 4150: Quantitative sequencing following PCR-driven library preparation with internal standard mixtures has improved analytical performance and lower cost.. , 2013, , .		1
52	Multi-Institutional Trial Of A Lung Cancer Risk Test. , 2010, , .		0
53	Magic Of Magician's Doves. , 2010, , .		0
54	Control for stochastic sampling variation and qualitative sequencing error in next generation sequencing analysis of KRAS actionable mutations. <i>Journal of Thoracic Oncology</i> , 2016, 11, S53-S54.	1.1	0

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55	Abstract 2525: Low frequency TP53 mutations in airway epithelial cells serve as lung cancer risk biomarker. , 2021, , .		0
56	Abstract 825: Development of RNA quality-control methods to improve tissue archiving and molecular diagnostic testing. , 2010, , .		0
57	Abstract 4988:Cis-acting genetic variation is associated with altered allele-specific expression of CEBPG transcript in normal human bronchial epithelium. , 2010, , .		0
58	Abstract 2232: Effectiveness evaluation of an in vitro nucleic acid amplification test for quantification of BCR-ABL fusion transcript variants in human whole blood. , 2011, , .		0
59	Abstract 3168: An antioxidant and DNA repair gene expression pattern associated with lung cancer risk is also associated with COPD risk. , 2011, , .		0
60	Abstract 5538: Development of RNA quality control methods to improve BCR-ABL measurement in whole blood samples. , 2012, , .		0
61	Abstract 5549: Normal bronchial epithelial cells (NBEC) sample RNA quality characteristics that will yield reliable measurement of lung cancer risk test. , 2012, , .		0
62	Abstract 5541: Molecular diagnostic tests to augment cytomorphologic diagnosis of lung cancer. , 2012, , .		0
63	Abstract 61: Use of two-color fluorometric real-time PCR to develop molecular diagnostic tests with intrinsic quality control that augment cytomorphologic diagnosis of lung cancer.. , 2013, , .		0
64	Abstract 3401: Inter-individual variation in MUC5B allele specific expression in normal bronchial epithelial cells and relationship to lung cancer. , 2014, , .		0
65	Abstract 4251: Identification of expression quantitative trait loci at lung cancer and COPD risk genes in normal bronchial epithelial cells. , 2014, , .		0
66	Abstract 4259: Conversion of the Lung Cancer Risk Test (LCRT) to a next generation sequencing (NGS) platform. , 2015, , .		0
67	Abstract 2084: Genetic variation at a cis-acting C/EBPG binding site is associated with allele-specific ERCC5 transcript expression. , 2015, , .		0
68	Abstract 4892: Methods for accurate reporting of confidence intervals in clinical applications of next generation sequencing (NGS). , 2015, , .		0
69	Abstract 2905: Induction of hTERT and increased proliferative potential in conditionally reprogrammed normal bronchial epithelial cells. , 2016, , .		0
70	Abstract 1623: Inter-laboratory harmonization of next generation sequencing somatic mutation assays for cancer response prediction. , 2018, , .		0
71	Abstract 2222: Using rare variants to characterize lung cancer risk. , 2018, , .		0
72	Abstract 4609: TP53, PIK3CA, and BRAF somatic mutations in airway epithelial field of injury associated with lung cancer risk. , 2020, , .		0

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73	Abstract 3537: Targeted deep sequencing of driver mutations in airway epithelial cells from smokers. , 2019, , .		0
74	Abstract 432: Novel method for NGS analysis of actionable mutations in circulating tumor DNA specimens: improved quality control and 20-fold lower sequencing required. , 2019, , .		0