

# 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	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
2	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. <i>Nature Biotechnology</i> , 2021, 39, 1115-1128.	17.5	126
3	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
4	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
5	Abstract 2525: Low frequency TP53 mutations in airway epithelial cells serve as lung cancer risk biomarker. , 2021, , .		0
6	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
7	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
8	Platelet-T cell aggregates in lung cancer patients: Implications for thrombosis. <i>PLoS ONE</i> , 2020, 15, e0236966.	2.5	16
9	Abstract 4609: TP53, PIK3CA, and BRAF somatic mutations in airway epithelial field of injury associated with lung cancer risk. , 2020, , .		0
10	Survival with Parenchymal and Pleural Invasion of Non-“Small Cell Lung Cancers Less than 30 mm. <i>Journal of Thoracic Oncology</i> , 2019, 14, 890-902.	1.1	25
11	Technical advance in targeted NGS analysis enables identification of lung cancer risk-associated low frequency TP53, PIK3CA, and BRAF mutations in airway epithelial cells. <i>BMC Cancer</i> , 2019, 19, 1081.	2.6	12
12	Abstract 3537: Targeted deep sequencing of driver mutations in airway epithelial cells from smokers. , 2019, , .		0
13	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
14	RNAseq analysis of bronchial epithelial cells to identify COPD-associated genes and SNPs. <i>BMC Pulmonary Medicine</i> , 2018, 18, 42.	2.0	20
15	Abstract 1623: Inter-laboratory harmonization of next generation sequencing somatic mutation assays for cancer response prediction. , 2018, , .		0
16	Abstract 2222: Using rare variants to characterize lung cancer risk. , 2018, , .		0
17	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
18	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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19	Haplotype and diplotype analyses of variation in ERCC5 transcription cis-regulation in normal bronchial epithelial cells. <i>Physiological Genomics</i> , 2016, 48, 537-543.	2.3	13
20	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
21	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
22	Abstract 2905: Induction of hTERT and increased proliferative potential in conditionally reprogrammed normal bronchial epithelial cells. , 2016, , .		0
23	Control for stochastic sampling variation and qualitative sequencing error in next generation sequencing. <i>Biomolecular Detection and Quantification</i> , 2015, 5, 30-37.	7.0	17
24	Abstract 4259: Conversion of the Lung Cancer Risk Test (LCRT) to a next generation sequencing (NGS) platform. , 2015, , .		0
25	Abstract 2084: Genetic variation at a cis-acting C/EBPG binding site is associated with allele-specific ERCC5 transcript expression. , 2015, , .		0
26	Abstract 4892: Methods for accurate reporting of confidence intervals in clinical applications of next generation sequencing (NGS). , 2015, , .		0
27	Abstract 3381: Investigation of C/EBPG transcription factor role in regulation of ERCC4 and ERCC5 in human lung cancer cells. , 2014, , .		1
28	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
29	Abstract 3401: Inter-individual variation in MUC5B allele specific expression in normal bronchial epithelial cells and relationship to lung cancer. , 2014, , .		0
30	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
31	Abstract 4251: Identification of expression quantitative trait loci at lung cancer and COPD risk genes in normal bronchial epithelial cells. , 2014, , .		0
32	A new StaRT-PCR approach to detect and quantify fish Viral Hemorrhagic Septicemia virus (VHSV): Enhanced quality control with internal standards. <i>Journal of Virological Methods</i> , 2013, 189, 129-142.	2.1	12
33	Quality Control Methods for Optimal BCR-ABL1 Clinical Testing in Human Whole Blood Samples. <i>Journal of Molecular Diagnostics</i> , 2013, 15, 391-400.	2.8	12
34	CEBPG Exhibits Allele-Specific Expression in Human Bronchial Epithelial Cells. <i>Gene Regulation and Systems Biology</i> , 2013, 7, GRSB.S11879.	2.3	9
35	Accurate Detection and Quantification of the Fish Viral Hemorrhagic Septicemia virus (VHSV) with a Two-Color Fluorometric Real-Time PCR Assay. <i>PLoS ONE</i> , 2013, 8, e71851.	2.5	14
36	Targeted RNA-Sequencing with Competitive Multiplex-PCR Amplicon Libraries. <i>PLoS ONE</i> , 2013, 8, e79120.	2.5	30

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37	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
38	Abstract 4150: Quantitative sequencing following PCR-driven library preparation with internal standard mixtures has improved analytical performance and lower cost.. , 2013, , .		1
39	Abstract 5538: Development of RNA quality control methods to improve BCR-ABL measurement in whole blood samples. , 2012, , .		0
40	Abstract 5549: Normal bronchial epithelial cells (NBEC) sample RNA quality characteristics that will yield reliable measurement of lung cancer risk test. , 2012, , .		0
41	Abstract 5541: Molecular diagnostic tests to augment cytomorphologic diagnosis of lung cancer. , 2012, , .		0
42	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
43	Abstract 3168: An antioxidant and DNA repair gene expression pattern associated with lung cancer risk is also associated with COPD risk. , 2011, , .		0
44	Multi-Institutional Trial Of A Lung Cancer Risk Test. , 2010, , .		0
45	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
46	Magic Of Magician's Doves. , 2010, , .		0
47	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. <i>Carcinogenesis</i> , 2010, 31, 1242-1250.	2.8	20
48	Abstract 825: Development of RNA quality-control methods to improve tissue archiving and molecular diagnostic testing. , 2010, , .		0
49	Abstract 4988:Cis-acting genetic variation is associated with altered allele-specific expression of CEBPB transcript in normal human bronchial epithelium. , 2010, , .		0
50	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
51	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
52	Fetalâ€œjuvenile origins of point mutations in the adult human trachealâ€œbronchial epithelium: Absence of detectable effects of age, gender or smoking status. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2008, 646, 25-40.	1.0	16
53	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
54	The interactive transcript abundance index [c-myc*p73Î±]/[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

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55	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
56	Evaluation of DNA microarray results with quantitative gene expression platforms. <i>Nature Biotechnology</i> , 2006, 24, 1115-1122.	17.5	558
57	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
58	Using RNA sample titrations to assess microarray platform performance and normalization techniques. <i>Nature Biotechnology</i> , 2006, 24, 1123-1131.	17.5	168
59	Distributions of five common point mutants in the human tracheal-bronchial epithelium. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2006, 596, 113-127.	1.0	12
60	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
61	Developing a Sustainable Process to Provide Quality Control Materials for Genetic Testing. <i>Genetics in Medicine</i> , 2005, 7, 534-549.	2.4	49
62	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
63	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
64	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
65	Standardized RT-PCR and the Standardized Expression Measurement Center. , 2004, 258, 13-42.		27
66	The c-myc x E2F-1/p21 Interactive Gene Expression Index Augments Cytomorphologic Diagnosis of Lung Cancer in Fine-Needle Aspirate Specimens. <i>Journal of Molecular Diagnostics</i> , 2003, 5, 176-183.	2.8	12
67	Multiplex standardized RT-PCR for expression analysis of many genes in small samples. <i>Biochemical and Biophysical Research Communications</i> , 2002, 293, 509-516.	2.1	16
68	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
69	Reproducible Gene Expression Measurement Among Multiple Laboratories Obtained in a Blinded Study Using Standardized RT (StaRT)-PCR. <i>Molecular Diagnosis and Therapy</i> , 2001, 6, 217-225.	1.1	23
70	Alterations of p53 in tumorigenic human bronchial epithelial cells correlate with metastatic potential. <i>Carcinogenesis</i> , 1999, 20, 1529-1534.	2.8	9
71	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
72	The Gene Expression Index c-myc $\times$ 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

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73	Patterns of Gene Expression in Human Airway Epithelial Cells. Chest, 1997, 111, 83S.	0.8	3
74	Radon-induced neoplastic transformation of human bronchial epithelial cells. Radiation Oncology Investigations, 1995, 3, 398-403.	0.9	15