

# Joshua D Campbell

## List of Publications by Year in descending order

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Version: 2024-02-01

50  
papers

4,250  
citations

186265

28  
h-index

223800

46  
g-index

63  
all docs

63  
docs citations

63  
times ranked

9827  
citing authors

#	ARTICLE	IF	CITATIONS
1	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. <i>Nature Genetics</i> , 2016, 48, 607-616.	21.4	933
2	Institutional implementation of clinical tumor profiling on an unselected cancer population. <i>JCI Insight</i> , 2016, 1, e87062.	5.0	340
3	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. <i>Cell</i> , 2020, 181, 236-249.	28.9	334
4	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , 2018, 23, 194-212.e6.	6.4	245
5	A single-sample microarray normalization method to facilitate personalized-medicine workflows. <i>Genomics</i> , 2012, 100, 337-344.	2.9	212
6	Decontamination of ambient RNA in single-cell RNA-seq with DecontX. <i>Genome Biology</i> , 2020, 21, 57.	8.8	209
7	Whole-genome doubling confers unique genetic vulnerabilities on tumour cells. <i>Nature</i> , 2021, 590, 492-497.	27.8	146
8	A Dynamic Bronchial Airway Gene Expression Signature of Chronic Obstructive Pulmonary Disease and Lung Function Impairment. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2013, 187, 933-942.	5.6	142
9	Genomic and immune profiling of pre-invasive lung adenocarcinoma. <i>Nature Communications</i> , 2019, 10, 5472.	12.8	127
10	Somatic Superenhancer Duplications and Hotspot Mutations Lead to Oncogenic Activation of the KLF5 Transcription Factor. <i>Cancer Discovery</i> , 2018, 8, 108-125.	9.4	99
11	NetSig: network-based discovery from cancer genomes. <i>Nature Methods</i> , 2018, 15, 61-66.	19.0	95
12	A gene expression signature of emphysema-related lung destruction and its reversal by the tripeptide GHK. <i>Genome Medicine</i> , 2012, 4, 67.	8.2	94
13	Machine learning enables design automation of microfluidic flow-focusing droplet generation. <i>Nature Communications</i> , 2021, 12, 25.	12.8	94
14	The Case for a Pre-Cancer Genome Atlas (PCGA). <i>Cancer Prevention Research</i> , 2016, 9, 119-124.	1.5	85
15	Integrative Analysis of DNA Methylation and Gene Expression Data Identifies EPAS1 as a Key Regulator of COPD. <i>PLoS Genetics</i> , 2015, 11, e1004898.	3.5	82
16	Comparison of Prevalence and Types of Mutations in Lung Cancers Among Black and White Populations. <i>JAMA Oncology</i> , 2017, 3, 801.	7.1	78
17	Molecular subtyping reveals immune alterations associated with progression of bronchial premalignant lesions. <i>Nature Communications</i> , 2019, 10, 1856.	12.8	70
18	Genetic Ancestry Contributes to Somatic Mutations in Lung Cancers from Admixed Latin American Populations. <i>Cancer Discovery</i> , 2021, 11, 591-598.	9.4	69

#	ARTICLE	IF	CITATIONS
19	Genomic Profiling of Prostate Cancers from Men with African and European Ancestry. <i>Clinical Cancer Research</i> , 2020, 26, 4651-4660.	7.0	68
20	Characterizing smoking-induced transcriptional heterogeneity in the human bronchial epithelium at single-cell resolution. <i>Science Advances</i> , 2019, 5, eaaw3413.	10.3	64
21	miR-638 regulates gene expression networks associated with emphysematous lung destruction. <i>Genome Medicine</i> , 2013, 5, 114.	8.2	62
22	MicroRNA 4423 is a primate-specific regulator of airway epithelial cell differentiation and lung carcinogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 18946-18951.	7.1	57
23	The cellular and molecular determinants of emphysematous destruction in COPD. <i>Scientific Reports</i> , 2017, 7, 9562.	3.3	53
24	Comparative Genomics Reveals Distinct Immune-oncologic Pathways in African American Men with Prostate Cancer. <i>Clinical Cancer Research</i> , 2021, 27, 320-329.	7.0	46
25	Genomic approaches to accelerate cancer interception. <i>Lancet Oncology</i> , The, 2017, 18, e494-e502.	10.7	43
26	Generation of Genetically Engineered Mouse Lung Organoid Models for Squamous Cell Lung Cancers Allows for the Study of Combinatorial Immunotherapy. <i>Clinical Cancer Research</i> , 2020, 26, 3431-3442.	7.0	41
27	MODMatcher: Multi-Omics Data Matcher for Integrative Genomic Analysis. <i>PLoS Computational Biology</i> , 2014, 10, e1003790.	3.2	35
28	Identification of transforming growth factor-beta-regulated microRNAs and the microRNA-targetomes in primary lung fibroblasts. <i>PLoS ONE</i> , 2017, 12, e0183815.	2.5	34
29	Assessment of microRNA differential expression and detection in multiplexed small RNA sequencing data. <i>Rna</i> , 2015, 21, 164-171.	3.5	31
30	Alterations in Bronchial Airway miRNA Expression for Lung Cancer Detection. <i>Cancer Prevention Research</i> , 2017, 10, 651-659.	1.5	31
31	Comprehensive generation, visualization, and reporting of quality control metrics for single-cell RNA sequencing data. <i>Nature Communications</i> , 2022, 13, 1688.	12.8	23
32	scruff: an R/Bioconductor package for preprocessing single-cell RNA-sequencing data. <i>BMC Bioinformatics</i> , 2019, 20, 222.	2.6	19
33	Cross organelle stress response disruption promotes gentamicin-induced proteotoxicity. <i>Cell Death and Disease</i> , 2020, 11, 217.	6.3	17
34	A single-cell lung atlas of complement genes identifies the mesothelium and epithelium as prominent sources of extrahepatic complement proteins. <i>Mucosal Immunology</i> , 2022, 15, 927-939.	6.0	17
35	SubmiRine: assessing variants in microRNA targets using clinical genomic data sets. <i>Nucleic Acids Research</i> , 2015, 43, 3886-3898.	14.5	16
36	Whole-genome characterization of lung adenocarcinomas lacking alterations in the RTK/RAS/RAF pathway. <i>Cell Reports</i> , 2021, 34, 108707.	6.4	16

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37	Multi-modal profiling of human fetal liver hematopoietic stem cells reveals the molecular signature of engraftment. <i>Nature Communications</i> , 2022, 13, 1103.	12.8	16
38	Transcription factor and microRNA interactions in lung cells: an inhibitory link between NK2 homeobox 1, miR-200c and the developmental and oncogenic factors Nfib and Myb. <i>Respiratory Research</i> , 2015, 16, 22.	3.6	15
39	Humanized mice reveal a macrophage-enriched gene signature defining human lung tissue protection during SARS-CoV-2 infection. <i>Cell Reports</i> , 2022, 39, 110714.	6.4	14
40	Inhibition of LSD1 Attenuates Oral Cancer Development and Promotes Therapeutic Efficacy of Immune Checkpoint Blockade and YAP/TAZ Inhibition. <i>Molecular Cancer Research</i> , 2022, 20, 712-721.	3.4	12
41	The Mutational Signature Comprehensive Analysis Toolkit (musicatk) for the Discovery, Prediction, and Exploration of Mutational Signatures. <i>Cancer Research</i> , 2021, 81, 5813-5817.	0.9	11
42	Inactivation of the Hippo tumor suppressor pathway promotes melanoma. <i>Nature Communications</i> , 2022, 13, .	12.8	10
43	Applying gene expression microarrays to pulmonary disease. <i>Respirology</i> , 2011, 16, 407-418.	2.3	9
44	ExperimentSubset: an R package to manage subsets of Bioconductor Experiment objects. <i>Bioinformatics</i> , 2021, 37, 3058-3060.	4.1	6
45	Assessment of a Highly Multiplexed RNA Sequencing Platform and Comparison to Existing High-Throughput Gene Expression Profiling Techniques. <i>Frontiers in Genetics</i> , 2019, 10, 150.	2.3	4
46	Elevated T cell repertoire diversity is associated with progression of lung squamous cell premalignant lesions. , 2021, 9, e002647.		1
47	Abstract 171: Cloud-based bulk and single-cell RNAseq pipelines in the Terra platform for the Lung PCA. , 2021, , .		0
48	Characterizing the T cell repertoire in lung squamous cell premalignancy and its association with lesion outcome.. <i>Journal of Clinical Oncology</i> , 2019, 37, 102-102.	1.6	0
49	Genetics of Lung Cancer. <i>Respiratory Medicine</i> , 2020, , 87-103.	0.1	0
50	Transcriptional, Protein-Level and Functional Profiling of Human Fetal Liver (FL)-Derived Hematopoietic Stem Cells (HSCs) at Single Cell Resolution. <i>Blood</i> , 2020, 136, 33-33.	1.4	0