Joshua D Campbell

List of Publications by Year
in descending order

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	Inhibition of LSD1 Attenuates Oral Cancer Development and Promotes Therapeutic Efficacy of Immune Checkpoint Blockade and YAP/TAZ Inhibition. Molecular Cancer Research, 2022, 20, 712-721.	3.4	12
2	Multi-modal profiling of human fetal liver hematopoietic stem cells reveals the molecular signature of engraftment. Nature Communications, 2022, 13, 1103.	12.8	16
3	Comprehensive generation, visualization, and reporting of quality control metrics for single-cell RNA sequencing data. Nature Communications, 2022, 13, 1688.	12.8	23
4	Humanized mice reveal a macrophage-enriched gene signature defining human lung tissue protection during SARS-CoV-2 infection. Cell Reports, 2022, 39, 110714.	6.4	14
5	A single-cell lung atlas of complement genes identifies the mesothelium and epithelium as prominent sources of extrahepatic complement proteins. Mucosal Immunology, 2022, 15, 927-939.	6.0	17
6	Inactivation of the Hippo tumor suppressor pathway promotes melanoma. Nature Communications, 2022, 13, .	12.8	10
7	Comparative Genomics Reveals Distinct Immune-oncologic Pathways in African American Men with Prostate Cancer. Clinical Cancer Research, 2021, 27, 320-329.	7.0	46
8	Genetic Ancestry Contributes to Somatic Mutations in Lung Cancers from Admixed Latin American Populations. Cancer Discovery, 2021, 11, 591-598.	9.4	69
9	Whole-genome doubling confers unique genetic vulnerabilities on tumour cells. Nature, 2021, 590, 492-497.	27.8	146
10	Machine learning enables design automation of microfluidic flow-focusing droplet generation. Nature Communications, 2021, 12, 25.	12.8	94
11	Whole-genome characterization of lung adenocarcinomas lacking alterations in the RTK/RAS/RAF pathway. Cell Reports, 2021, 34, 108707.	6.4	16
12	ExperimentSubset: an R package to manage subsets of Bioconductor Experiment objects. Bioinformatics, 2021, 37, 3058-3060.	4.1	6
13	Abstract 171: Cloud-based bulk and single-cell RNAseq pipelines in the Terra platform for the Lung PCA. , 2021, , .		0
14	Elevated T cell repertoire diversity is associated with progression of lung squamous cell premalignant lesions. , 2021, 9, e002647.		1
15	The Mutational Signature Comprehensive Analysis Toolkit (musicatk) for the Discovery, Prediction, and Exploration of Mutational Signatures. Cancer Research, 2021, 81, 5813-5817.	0.9	11
16	Cross organelle stress response disruption promotes gentamicin-induced proteotoxicity. Cell Death and Disease, 2020, 11, 217.	6.3	17
17	Genomic Profiling of Prostate Cancers from Men with African and European Ancestry. Clinical Cancer Research, 2020, 26, 4651-4660.	7.0	68
18	Decontamination of ambient RNA in single-cell RNA-seq with DecontX. Genome Biology, 2020, 21, 57.	8.8	209

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19	Generation of Genetically Engineered Mouse Lung Organoid Models for Squamous Cell Lung Cancers Allows for the Study of Combinatorial Immunotherapy. Clinical Cancer Research, 2020, 26, 3431-3442.	7.0	41
20	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. Cell, 2020, 181, 236-249.	28.9	334
21	Genetics of Lung Cancer. Respiratory Medicine, 2020, , 87-103.	0.1	0
22	Transcriptional, Protein-Level and Functional Profiling of Human Fetal Liver (FL)-Derived Hematopoietic Stem Cells (HSCs) at Single Cell Resolution. Blood, 2020, 136, 33-33.	1.4	0
23	Molecular subtyping reveals immune alterations associated with progression of bronchial premalignant lesions. Nature Communications, 2019, 10, 1856.	12.8	70
24	scruff: an R/Bioconductor package for preprocessing single-cell RNA-sequencing data. BMC Bioinformatics, 2019, 20, 222.	2.6	19
25	Assessment of a Highly Multiplexed RNA Sequencing Platform and Comparison to Existing High-Throughput Gene Expression Profiling Techniques. Frontiers in Genetics, 2019, 10, 150.	2.3	4
26	Genomic and immune profiling of pre-invasive lung adenocarcinoma. Nature Communications, 2019, 10, 5472.	12.8	127
27	Characterizing smoking-induced transcriptional heterogeneity in the human bronchial epithelium at single-cell resolution. Science Advances, 2019, 5, eaaw3413.	10.3	64
28	Characterizing the T cell repertoire in lung squamous cell premalignancy and its association with lesion outcome.. Journal of Clinical Oncology, 2019, 37, 102-102.	1.6	0
29	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. Cell Reports, 2018, 23, 194-212.e6.	6.4	245
30	Somatic Superenhancer Duplications and Hotspot Mutations Lead to Oncogenic Activation of the KLF5 Transcription Factor. Cancer Discovery, 2018, 8, 108-125.	9.4	99
31	NetSig: network-based discovery from cancer genomes. Nature Methods, 2018, 15, 61-66.	19.0	95
32	Comparison of Prevalence and Types of Mutations in Lung Cancers Among Black and White Populations. JAMA Oncology, 2017, 3, 801.	7.1	78
33	Alterations in Bronchial Airway miRNA Expression for Lung Cancer Detection. Cancer Prevention Research, 2017, 10, 651-659.	1.5	31
34	The cellular and molecular determinants of emphysematous destruction in COPD. Scientific Reports, 2017, 7, 9562.	3.3	53
35	Genomic approaches to accelerate cancer interception. Lancet Oncology, The, 2017, 18, e494-e502.	10.7	43
36	Identification of transforming growth factor-beta-regulated microRNAs and the microRNA-targetomes in primary lung fibroblasts. PLoS ONE, 2017, 12, e0183815.	2.5	34

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37	Institutional implementation of clinical tumor profiling on an unselected cancer population. JCI Insight, 2016, 1, e87062.	5.0	340
38	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. Nature Genetics, 2016, 48, 607-616.	21.4	933
39	The Case for a Pre-Cancer Genome Atlas (PCGA). Cancer Prevention Research, 2016, 9, 119-124.	1.5	85
40	SubmiRine: assessing variants in microRNA targets using clinical genomic data sets. Nucleic Acids Research, 2015, 43, 3886-3898.	14.5	16
41	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. Respiratory Research, 2015, 16, 22.	3.6	15
42	Integrative Analysis of DNA Methylation and Gene Expression Data Identifies EPAS1 as a Key Regulator of COPD. PLoS Genetics, 2015, 11, e1004898.	3.5	82
43	Assessment of microRNA differential expression and detection in multiplexed small RNA sequencing data. Rna, 2015, 21, 164-171.	3.5	31
44	MODMatcher: Multi-Omics Data Matcher for Integrative Genomic Analysis. PLoS Computational Biology, 2014, 10, e1003790.	3.2	35
45	A Dynamic Bronchial Airway Gene Expression Signature of Chronic Obstructive Pulmonary Disease and Lung Function Impairment. American Journal of Respiratory and Critical Care Medicine, 2013, 187, 933-942.	5.6	142
46	miR-638 regulates gene expression networks associated with emphysematous lung destruction. Genome Medicine, 2013, 5, 114.	8.2	62
47	MicroRNA 4423 is a primate-specific regulator of airway epithelial cell differentiation and lung carcinogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 18946-18951.	7.1	57
48	A single-sample microarray normalization method to facilitate personalized-medicine workflows. Genomics, 2012, 100, 337-344.	2.9	212
49	A gene expression signature of emphysema-related lung destruction and its reversal by the tripeptide GHK. Genome Medicine, 2012, 4, 67.	8.2	94
50	Applying gene expression microarrays to pulmonary disease. Respirology, 2011, 16, 407-418.	2.3	9