Jason R Walker

List of Publications by Year
in descending order

24 papers	8,099 citations	430874 18 h-index	580821 25 g-index
27 all docs	27 docs citations	27 times ranked	15231 citing authors

#	Article	IF	Citations
1	Failure to Detect Mutations in U2AF1 due to Changes in the GRCh38 Reference Sequence. Journal of Molecular Diagnostics, 2022, 24, 219-223.	2.8	13
2	Stem cell architecture drives myelodysplastic syndrome progression and predicts response to venetoclax-based therapy. Nature Medicine, 2022, 28, 557-567.	30.7	26
3	Genomic and transcriptomic somatic alterations of hepatocellular carcinoma in non-cirrhotic livers. Cancer Genetics, 2022, 264-265, 90-99.	0.4	3
4	A community approach to the cancer-variant-interpretation bottleneck. Nature Cancer, 2022, 3, 522-525.	13.2	3
5	The clonal evolution of metastatic colorectal cancer. Science Advances, 2020, 6, eaay9691.	10.3	41
6	CIViCpy: A Python Software Development and Analysis Toolkit for the CIViC Knowledgebase. JCO Clinical Cancer Informatics, 2020, 4, 245-253.	2.1	10
7	pVACtools: A Computational Toolkit to Identify and Visualize Cancer Neoantigens. Cancer Immunology Research, 2020, 8, 409-420.	3.4	132
8	Targeted Sequencing of 7 Genes Can Help Reduce Pathologic Misclassification of MDS. Blood, 2020, 136, 32-33.	1.4	2
9	Comprehensive gene expression meta-analysis identifies signature genes that distinguish microglia from peripheral monocytes/macrophages in health and glioma. Acta Neuropathologica Communications, 2019, 7, 20.	5.2	124
10	Clonal Cytopenias of Undetermined Significance Are Common in Cytopenic Adults Evaluated for MDS in the National MDS Study. Blood, 2019, 134, 4271-4271.	1.4	0
11	CIViC is a community knowledgebase for expert crowdsourcing the clinical interpretation of variants in cancer. Nature Genetics, 2017, 49, 170-174.	21.4	460
12	DGIdb 2.0: mining clinically relevant drug–gene interactions. Nucleic Acids Research, 2016, 44, D1036-D1044.	14.5	359
13	Optimizing Cancer Genome Sequencing and Analysis. Cell Systems, 2015, 1, 210-223.	6.2	174
14	Genome Modeling System: A Knowledge Management Platform for Genomics. PLoS Computational Biology, 2015, 11, e1004274.	3.2	83
15	Informatics for RNA Sequencing: A Web Resource for Analysis on the Cloud. PLoS Computational Biology, 2015, 11, e1004393.	3.2	74
16	RNA–sequencing reveals oligodendrocyte and neuronal transcripts in microglia relevant to central nervous system disease. Glia, 2015, 63, 531-548.	4.9	44
17	RNA Sequencing of Tumor-Associated Microglia Reveals Ccl5 as a Stromal Chemokine Critical for Neurofibromatosis-1 Glioma Growth. Neoplasia, 2015, 17, 776-788.	5.3	75
18	cDNA Hybrid Capture Improves Transcriptome Analysis on Low-Input and Archived Samples. Journal of Molecular Diagnostics, 2014, 16, 440-451.	2.8	40

#	Article	IF	Citations
19	Genomic impact of transient low-dose decitabine treatment on primary AML cells. Blood, 2013, 121, 1633-1643.	1.4	137
20	F11R Is a Novel Monocyte Prognostic Biomarker for Malignant Glioma. PLoS ONE, 2013, 8, e77571.	2.5	40
21	Genomic Landscape of Non-Small Cell Lung Cancer in Smokers and Never-Smokers. Cell, 2012, 150, 1121-1134.	28.9	1,038
22	The Origin and Evolution of Mutations in Acute Myeloid Leukemia. Cell, 2012, 150, 264-278.	28.9	1,365
23	<i>DNMT3A</i>Mutations in Acute Myeloid Leukemia. New England Journal of Medicine, 2010, 363, 2424-2433.	27.0	1,777
24	Recurring Mutations Found by Sequencing an Acute Myeloid Leukemia Genome. New England Journal of Medicine, 2009, 361, 1058-1066.	27.0	2,009