George Michalopoulos

List of Publications by Citations

 $\textbf{Source:} \ https://exaly.com/author-pdf/11327495/george-michalopoulos-publications-by-citations.pdf$

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

15 papers 1,695 citations h-index g-index

15 papers 1,843 pext. papers ext. citations 5 avg, IF L-index

#	Paper	IF	Citations
15	Gene expression alterations in prostate cancer predicting tumor aggression and preceding development of malignancy. <i>Journal of Clinical Oncology</i> , 2004 , 22, 2790-9	2.2	587
14	Gene expression profiles of prostate cancer reveal involvement of multiple molecular pathways in the metastatic process. <i>BMC Cancer</i> , 2007 , 7, 64	4.8	357
13	Gene expression analysis of prostate cancers. <i>Molecular Carcinogenesis</i> , 2002 , 33, 25-35	5	196
12	Glutathione peroxidase 3, deleted or methylated in prostate cancer, suppresses prostate cancer growth and metastasis. <i>Cancer Research</i> , 2007 , 67, 8043-50	10.1	175
11	Differences in gene expression in prostate cancer, normal appearing prostate tissue adjacent to cancer and prostate tissue from cancer free organ donors. <i>BMC Cancer</i> , 2005 , 5, 45	4.8	113
10	CSR1 suppresses tumor growth and metastasis of prostate cancer. <i>American Journal of Pathology</i> , 2006 , 168, 597-607	5.8	45
9	Myopodin, a synaptopodin homologue, is frequently deleted in invasive prostate cancers. <i>American Journal of Pathology</i> , 2001 , 159, 1603-12	5.8	42
8	High throughput screening of methylation status of genes in prostate cancer using an oligonucleotide methylation array. <i>Carcinogenesis</i> , 2005 , 26, 471-9	4.6	37
7	Genome-wide methylation analysis of prostate tissues reveals global methylation patterns of prostate cancer. <i>American Journal of Pathology</i> , 2013 , 182, 2028-36	5.8	35
6	Whole-genome methylation sequencing reveals distinct impact of differential methylations on gene transcription in prostate cancer. <i>American Journal of Pathology</i> , 2013 , 183, 1960-1970	5.8	33
5	Genome abnormalities precede prostate cancer and predict clinical relapse. <i>American Journal of Pathology</i> , 2012 , 180, 2240-8	5.8	29
4	Identification of recurrent fusion genes across multiple cancer types. Scientific Reports, 2019, 9, 1074	4.9	24
3	Investigating Multi-cancer Biomarkers and Their Cross-predictability in the Expression Profiles of Multiple Cancer Types. <i>Biomarker Insights</i> , 2009 , 4, 57-79	3.5	16
2	Detection of fusion transcripts in the serum samples of patients with hepatocellular carcinoma. <i>Oncotarget</i> , 2019 , 10, 3352-3360	3.3	5
1	Transcriptome and Exome Analyses of Hepatocellular Carcinoma Reveal Patterns to Predict Cancer Recurrence in Liver Transplant Patients. <i>Hepatology Communications</i> , 2021 ,	6	1