

Xavier Sole

List of Publications by Citations

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

40
papers

3,512
citations

19
h-index

47
g-index

47
ext. papers

3,955
ext. citations

11.3
avg, IF

4.53
L-index

#	Paper	IF	Citations
40	SNPStats: a web tool for the analysis of association studies. <i>Bioinformatics</i> , 2006 , 22, 1928-9	7.2	1400
39	Network modeling links breast cancer susceptibility and centrosome dysfunction. <i>Nature Genetics</i> , 2007 , 39, 1338-49	36.3	516
38	SNPassoc: an R package to perform whole genome association studies. <i>Bioinformatics</i> , 2007 , 23, 644-5	7.2	513
37	Differential DNA hypermethylation and hypomethylation signatures in colorectal cancer. <i>Human Molecular Genetics</i> , 2005 , 14, 319-26	5.6	127
36	The TLX1 oncogene drives aneuploidy in T cell transformation. <i>Nature Medicine</i> , 2010 , 16, 1321-7	50.5	123
35	Reverse engineering of TLX oncogenic transcriptional networks identifies RUNX1 as tumor suppressor in T-ALL. <i>Nature Medicine</i> , 2012 , 18, 436-40	50.5	115
34	Aberrant gene expression in mucosa adjacent to tumor reveals a molecular crosstalk in colon cancer. <i>Molecular Cancer</i> , 2014 , 13, 46	42.1	87
33	Comprehensive analysis of copy number aberrations in microsatellite stable colon cancer in view of stromal component. <i>British Journal of Cancer</i> , 2017 , 117, 421-431	8.7	83
32	Clinical value of prognosis gene expression signatures in colorectal cancer: a systematic review. <i>PLoS ONE</i> , 2012 , 7, e48877	3.7	69
31	Discovery and validation of new potential biomarkers for early detection of colon cancer. <i>PLoS ONE</i> , 2014 , 9, e106748	3.7	61
30	Biological reprogramming in acquired resistance to endocrine therapy of breast cancer. <i>Oncogene</i> , 2010 , 29, 6071-83	9.2	53
29	Identification of candidate susceptibility genes for colorectal cancer through eQTL analysis. <i>Carcinogenesis</i> , 2014 , 35, 2039-46	4.6	45
28	Tools for protein-protein interaction network analysis in cancer research. <i>Clinical and Translational Oncology</i> , 2012 , 14, 3-14	3.6	31
27	A mechanism for asymmetric cell division resulting in proliferative asynchronicity. <i>Molecular Cancer Research</i> , 2015 , 13, 223-30	6.6	30
26	JARID1B Enables Transit between Distinct States of the Stem-like Cell Population in Oral Cancers. <i>Cancer Research</i> , 2016 , 76, 5538-49	10.1	28
25	Large differences in global transcriptional regulatory programs of normal and tumor colon cells. <i>BMC Cancer</i> , 2014 , 14, 708	4.8	25
24	Genetic and genomic analysis modeling of germline c-MYC overexpression and cancer susceptibility. <i>BMC Genomics</i> , 2008 , 9, 12	4.5	22

23	Integrative analysis of a cancer somatic mutome. <i>Molecular Cancer</i> , 2007 , 6, 13	42.1	20
22	Biological convergence of cancer signatures. <i>PLoS ONE</i> , 2009 , 4, e4544	3.7	19
21	AKT1 quiescent cancer cells persist after neoadjuvant chemotherapy in triple negative breast cancer. <i>Breast Cancer Research</i> , 2017 , 19, 88	8.3	15
20	AKT Inhibition Promotes Nonautonomous Cancer Cell Survival. <i>Molecular Cancer Therapeutics</i> , 2016 , 15, 142-53	6.1	15
19	Clathrin switches transforming growth factor- β role to pro-tumorigenic in liver cancer. <i>Journal of Hepatology</i> , 2020 , 72, 125-134	13.4	14
18	Gene expression profiling integrated into network modelling reveals heterogeneity in the mechanisms of BRCA1 tumorigenesis. <i>British Journal of Cancer</i> , 2009 , 101, 1469-80	8.7	13
17	Colon-specific eQTL analysis to inform on functional SNPs. <i>British Journal of Cancer</i> , 2018 , 119, 971-977	8.7	13
16	Molecular characterization of a t(9;12)(p21;q13) balanced chromosome translocation in combination with integrative genomics analysis identifies C9orf14 as a candidate tumor-suppressor. <i>Genes Chromosomes and Cancer</i> , 2007 , 46, 155-62	5	10
15	Integrative transcriptome analysis of malignant pleural mesothelioma reveals a clinically relevant immune-based classification 2021 , 9,		9
14	CLEAR-test: combining inference for differential expression and variability in microarray data analysis. <i>Journal of Biomedical Informatics</i> , 2008 , 41, 33-45	10.2	8
13	Integrin α activation induces an anti-melanoma host response. <i>PLoS ONE</i> , 2017 , 12, e0175300	3.7	7
12	AKT1 Quiescent Cancer Cells Promote Solid Tumor Growth. <i>Molecular Cancer Therapeutics</i> , 2018 , 17, 254-263	6.1	7
11	Pre-clinical validation of early molecular markers of sensitivity to aromatase inhibitors in a mouse model of post-menopausal hormone-sensitive breast cancer. <i>Breast Cancer Research and Treatment</i> , 2008 , 109, 463-70	4.4	6
10	DNA methylation events in transcription factors and gene expression changes in colon cancer. <i>Epigenomics</i> , 2020 , 12, 1593-1610	4.4	6
9	The use of caspase inhibitors in pulsed-field gel electrophoresis may improve the estimation of radiation-induced DNA repair and apoptosis. <i>Radiation Oncology</i> , 2011 , 6, 6	4.2	4
8	Validation of RNA arbitrarily primed PCR probes hybridized to glass cDNA microarrays: application to the analysis of limited samples. <i>Clinical Chemistry</i> , 2005 , 51, 93-101	5.5	3
7	Breast cancer dormancy is associated with a 4NG1 state and not senescence. <i>Npj Breast Cancer</i> , 2021 , 7, 140	7.8	3
6	Efficacy of CDK4/6 inhibitors in preclinical models of malignant pleural mesothelioma. <i>British Journal of Cancer</i> , 2021 , 125, 1365-1376	8.7	2

5	Genomic and transcriptomic prognostic factors in R0 Dukes B and C colorectal cancer patients 2007 , 30, 1099		1
4	Gene Expression Profiling as a Potential Tool for Precision Oncology in Non-Small Cell Lung Cancer. <i>Cancers</i> , 2021 , 13,	6.6	1
3	Persistence of AKT1 low quiescent cancer cells after neoadjuvant chemotherapy in triple negative breast cancer patients.. <i>Journal of Clinical Oncology</i> , 2017 , 35, 11579-11579	2.2	
2	Analysis of Population-Based Genetic Association Studies Applied to Cancer Susceptibility and Prognosis 2009 , 149-191		
1	BCL11B Mutations In T-Cell Acute Lymphoblastic Leukemia. <i>Blood</i> , 2010 , 116, 471-471	2.2	