

Marcel Smid

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.

80
papers

4,790
citations

29
h-index

69
g-index

88
ext. papers

6,002
ext. citations

8.6
avg, IF

4.81
L-index

#	Paper	IF	Citations
80	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. <i>Nature</i> , 2016 , 534, 47-54	50.4	1193
79	Subtypes of breast cancer show preferential site of relapse. <i>Cancer Research</i> , 2008 , 68, 3108-14	10.1	563
78	Four miRNAs associated with aggressiveness of lymph node-negative, estrogen receptor-positive human breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 13021-6	11.5	334
77	Selection of bone metastasis seeds by mesenchymal signals in the primary tumor stroma. <i>Cell</i> , 2013 , 154, 1060-1073	56.2	296
76	Genes associated with breast cancer metastatic to bone. <i>Journal of Clinical Oncology</i> , 2006 , 24, 2261-7	2.2	253
75	Ovarian cancer cell line panel (OCCP): clinical importance of in vitro morphological subtypes. <i>PLoS ONE</i> , 2014 , 9, e103988	3.7	228
74	mRNA and microRNA expression profiles in circulating tumor cells and primary tumors of metastatic breast cancer patients. <i>Clinical Cancer Research</i> , 2011 , 17, 3600-18	12.9	192
73	SDHB/SDHA immunohistochemistry in pheochromocytomas and paragangliomas: a multicenter interobserver variation analysis using virtual microscopy: a Multinational Study of the European Network for the Study of Adrenal Tumors (ENS@T). <i>Modern Pathology</i> , 2015 , 28, 807-21	9.8	142
72	miRNA expression profiling of 51 human breast cancer cell lines reveals subtype and driver mutation-specific miRNAs. <i>Breast Cancer Research</i> , 2013 , 15, R33	8.3	140
71	The genomic landscape of metastatic breast cancer highlights changes in mutation and signature frequencies. <i>Nature Genetics</i> , 2019 , 51, 1450-1458	36.3	121
70	Breast cancer genome and transcriptome integration implicates specific mutational signatures with immune cell infiltration. <i>Nature Communications</i> , 2016 , 7, 12910	17.4	74
69	Patterns and incidence of chromosomal instability and their prognostic relevance in breast cancer subtypes. <i>Breast Cancer Research and Treatment</i> , 2011 , 128, 23-30	4.4	67
68	A Systematic Analysis of Oncogenic Gene Fusions in Primary Colon Cancer. <i>Cancer Research</i> , 2017 , 77, 3814-3822	10.1	56
67	The circular RNome of primary breast cancer. <i>Genome Research</i> , 2019 , 29, 356-366	9.7	55
66	A somatic-mutational process recurrently duplicates germline susceptibility loci and tissue-specific super-enhancers in breast cancers. <i>Nature Genetics</i> , 2017 , 49, 341-348	36.3	54
65	Selection of personalized patient therapy through the use of knowledge-based computational models that identify tumor-driving signal transduction pathways. <i>Cancer Research</i> , 2014 , 74, 2936-45	10.1	51
64	Cancer-associated fibroblast-derived Gremlin 1 promotes breast cancer progression. <i>Breast Cancer Research</i> , 2019 , 21, 109	8.3	42

63	Interferon-Stimulated Genes Are Involved in Cross-resistance to Radiotherapy in Tamoxifen-Resistant Breast Cancer. <i>Clinical Cancer Research</i> , 2018 , 24, 3397-3408	12.9	41
62	T lymphocytes facilitate brain metastasis of breast cancer by inducing Guanylate-Binding Protein 1 expression. <i>Acta Neuropathologica</i> , 2018 , 135, 581-599	14.3	38
61	DNA damage responsive microRNAs misexpressed in human cancer modulate therapy sensitivity. <i>Molecular Oncology</i> , 2014 , 8, 458-68	7.9	37
60	mRNA expression profiles in circulating tumor cells of metastatic colorectal cancer patients. <i>Molecular Oncology</i> , 2015 , 9, 920-32	7.9	34
59	MicroRNAs as possible indicators of drug sensitivity in breast cancer cell lines. <i>PLoS ONE</i> , 2019 , 14, e0216400	14.00	33
58	Gene expression profiling assigns CHEK2 1100delC breast cancers to the luminal intrinsic subtypes. <i>Breast Cancer Research and Treatment</i> , 2012 , 132, 439-48	4.4	33
57	Gene length corrected trimmed mean of M-values (GeTMM) processing of RNA-seq data performs similarly in intersample analyses while improving intrasample comparisons. <i>BMC Bioinformatics</i> , 2018 , 19, 236	3.6	32
56	A kinase inhibitor screen identifies a dual cdc7/CDK9 inhibitor to sensitise triple-negative breast cancer to EGFR-targeted therapy. <i>Breast Cancer Research</i> , 2019 , 21, 77	8.3	32
55	Gene expression profiles of circulating tumor cells versus primary tumors in metastatic breast cancer. <i>Cancer Letters</i> , 2015 , 362, 36-44	9.9	31
54	Functional Assay Reveals Homologous Recombination Deficiency in Breast Cancer Beyond BRCA Gene Defects. <i>Clinical Cancer Research</i> , 2018 , 24, 6277-6287	12.9	31
53	Molecular characteristics of circulating tumor cells resemble the liver metastasis more closely than the primary tumor in metastatic colorectal cancer. <i>Oncotarget</i> , 2016 , 7, 59058-59069	3.3	31
52	Uncovering the signaling landscape controlling breast cancer cell migration identifies novel metastasis driver genes. <i>Nature Communications</i> , 2019 , 10, 2983	17.4	29
51	Molecular characterization of irinotecan (SN-38) resistant human breast cancer cell lines. <i>BMC Cancer</i> , 2016 , 16, 34	4.8	28
50	4-protein signature predicting tamoxifen treatment outcome in recurrent breast cancer. <i>Molecular Oncology</i> , 2016 , 10, 24-39	7.9	27
49	PI3 kinase mutations and mutational load as poor prognostic markers in diffuse glioma patients. <i>Acta Neuropathologica Communications</i> , 2015 , 3, 88	7.3	27
48	Mitochondrial DNA content in breast cancer: Impact on in vitro and in vivo phenotype and patient prognosis. <i>Oncotarget</i> , 2016 , 7, 29166-76	3.3	27
47	The advantage of laser-capture microdissection over whole tissue analysis in proteomic profiling studies. <i>Proteomics</i> , 2016 , 16, 1474-85	4.8	26
46	Epithelial-Mesenchymal Transition in Human Prostate Cancer Demonstrates Enhanced Immune Evasion Marked by IDO1 Expression. <i>Cancer Research</i> , 2018 , 78, 4671-4679	10.1	25

45	Confirmation of a metastasis-specific microRNA signature in primary colon cancer. <i>Scientific Reports</i> , 2018 , 8, 5242	4.9	24
44	An 8-gene mRNA expression profile in circulating tumor cells predicts response to aromatase inhibitors in metastatic breast cancer patients. <i>BMC Cancer</i> , 2016 , 16, 123	4.8	20
43	Phosphoserine aminotransferase 1 is associated to poor outcome on tamoxifen therapy in recurrent breast cancer. <i>Scientific Reports</i> , 2017 , 7, 2099	4.9	19
42	Partially methylated domains are hypervariable in breast cancer and fuel widespread CpG island hypermethylation. <i>Nature Communications</i> , 2019 , 10, 1749	17.4	19
41	Identification of microRNA biomarkers for response of advanced soft tissue sarcomas to eribulin: Translational results of the EORTC 62052 trial. <i>European Journal of Cancer</i> , 2017 , 75, 33-40	7.5	18
40	GATA3 mRNA expression, but not mutation, associates with longer progression-free survival in ER-positive breast cancer patients treated with first-line tamoxifen for recurrent disease. <i>Cancer Letters</i> , 2016 , 376, 104-9	9.9	18
39	Annexin-A1 and caldesmon are associated with resistance to tamoxifen in estrogen receptor positive recurrent breast cancer. <i>Oncotarget</i> , 2016 , 7, 3098-110	3.3	16
38	Androgen receptor expression in circulating tumor cells of patients with metastatic breast cancer. <i>International Journal of Cancer</i> , 2019 , 145, 1083-1089	7.5	15
37	Proper genomic profiling of (BRCA1-mutated) basal-like breast carcinomas requires prior removal of tumor infiltrating lymphocytes. <i>Molecular Oncology</i> , 2015 , 9, 877-88	7.9	14
36	Predicting paclitaxel-induced neutropenia using the DMET platform. <i>Pharmacogenomics</i> , 2015 , 16, 1231-1241	4.6	14
35	Comprehensive evaluation of methods to assess overall and cell-specific immune infiltrates in breast cancer. <i>Breast Cancer Research</i> , 2019 , 21, 151	8.3	14
34	Clonality, Antigen Recognition, and Suppression of CD8 T Cells Differentially Affect Prognosis of Breast Cancer Subtypes. <i>Clinical Cancer Research</i> , 2020 , 26, 505-517	12.9	13
33	Circulating Tumor Cell Enumeration and Characterization in Metastatic Castration-Resistant Prostate Cancer Patients Treated with Cabazitaxel. <i>Cancers</i> , 2019 , 11,	6.6	10
32	Co-regulated gene expression of splicing factors as drivers of cancer progression. <i>Scientific Reports</i> , 2019 , 9, 5484	4.9	10
31	ER and PI3K Pathway Activity in Primary ER Positive Breast Cancer Is Associated with Progression-Free Survival of Metastatic Patients under First-Line Tamoxifen. <i>Cancers</i> , 2020 , 12,	6.6	10
30	Vascular pattern analysis for the prediction of clinical behaviour in pheochromocytomas and paragangliomas. <i>PLoS ONE</i> , 2015 , 10, e0121361	3.7	10
29	An increased cell cycle gene network determines MEK and Akt inhibitor double resistance in triple-negative breast cancer. <i>Scientific Reports</i> , 2019 , 9, 13308	4.9	9
28	Understanding drugs in breast cancer through drug sensitivity screening. <i>SpringerPlus</i> , 2015 , 4, 611		9

27	Differential quantities of immune checkpoint-expressing CD8 T cells in soft tissue sarcoma subtypes 2020 , 8,		9
26	Prognostic significance of nuclear expression of UMP-CMP kinase in triple negative breast cancer patients. <i>Scientific Reports</i> , 2016 , 6, 32027	4.9	8
25	The Prevalence of CD146 Expression in Breast Cancer Subtypes and Its Relation to Outcome. <i>Cancers</i> , 2018 , 10,	6.6	8
24	MicroRNA expression in pre-treatment plasma of patients with benign breast diseases and breast cancer. <i>Oncotarget</i> , 2018 , 9, 24335-24346	3.3	8
23	Integrative analysis of genomic amplification-dependent expression and loss-of-function screen identifies ASAP1 as a driver gene in triple-negative breast cancer progression. <i>Oncogene</i> , 2020 , 39, 4118-4131	9.2	7
22	Spatial immunophenotypes predict response to anti-PD1 treatment and capture distinct paths of T cell evasion in triple negative breast cancer. <i>Nature Communications</i> , 2021 , 12, 5668	17.4	7
21	Proteomic characterization of microdissected breast tissue environment provides a protein-level overview of malignant transformation. <i>Proteomics</i> , 2017 , 17, 1600213	4.8	6
20	High mRNA expression of splice variant SYK short correlates with hepatic disease progression in chemo-naïve lymph node negative colon cancer patients. <i>PLoS ONE</i> , 2017 , 12, e0185607	3.7	6
19	A Method to Correlate mRNA Expression Datasets Obtained from Fresh Frozen and Formalin-Fixed, Paraffin-Embedded Tissue Samples: A Matter of Thresholds. <i>PLoS ONE</i> , 2015 , 10, e0144097	3.7	6
18	Molecular Comparison of Imatinib-Naïve and Resistant Gastrointestinal Stromal Tumors: Differentially Expressed microRNAs and mRNAs. <i>Cancers</i> , 2019 , 11,	6.6	5
17	Differential reprogramming of breast cancer subtypes in 3D cultures and implications for sensitivity to targeted therapy. <i>Scientific Reports</i> , 2021 , 11, 7259	4.9	5
16	Mitochondrial RNA Expression and Single Nucleotide Variants in Association with Clinical Parameters in Primary Breast Cancers. <i>Cancers</i> , 2018 , 10,	6.6	5
15	Whole genome sequencing of metastatic colorectal cancer reveals prior treatment effects and specific metastasis features. <i>Nature Communications</i> , 2021 , 12, 574	17.4	5
14	Intratumoral heterogeneity of second-harmonic generation scattering from tumor collagen and its effects on metastatic risk prediction. <i>BMC Cancer</i> , 2020 , 20, 1217	4.8	4
13	Apolipoprotein B mRNA-Editing Catalytic Polypeptide-Like-Induced Protein Changes in Estrogen Receptor-Positive, Human Epidermal Growth Factor Receptor 2-Negative Breast Cancer Throughout Disease Progression.. <i>JCO Precision Oncology</i> , 2022 , 6, e2100190	3.6	2
12	Fusion transcripts and their genomic breakpoints in polyadenylated and ribosomal RNA-minus RNA sequencing data. <i>GigaScience</i> , 2021 , 10,	7.6	2
11	Downregulation of matrix Gla protein is a biomarker for tamoxifen-resistant and radioresistant breast cancer. <i>Biomarkers in Medicine</i> , 2019 , 13, 841-850	2.3	1
10	Global proteomic characterization of microdissected estrogen receptor positive breast tumors. <i>Data in Brief</i> , 2015 , 5, 399-402	1.2	1

9	Identification of potential molecular biomarkers for response of soft tissue sarcoma to eribulin: Translational results of EORTC trial 62052.. <i>Journal of Clinical Oncology</i> , 2013 , 31, 10573-10573	2.2	1
8	Metabotropic glutamate receptor 1 is associated with unfavorable prognosis in ER-negative and triple-negative breast cancer. <i>Scientific Reports</i> , 2020 , 10, 22292	4.9	1
7	Wnt targets genes are not differentially expressed in desmoid tumors bearing different activating Eatenin mutations. <i>European Journal of Surgical Oncology</i> , 2019 , 45, 691-698	3.6	1
6	A panel of DNA methylation markers for the classification of consensus molecular subtypes 2 and 3 in patients with colorectal cancer. <i>Molecular Oncology</i> , 2021 , 15, 3348-3362	7.9	0
5	Response. <i>Journal of the National Cancer Institute</i> , 2014 , 106,	9.7	
4	Gene expression profiles of primary tumors versus circulating tumor cells in metastatic breast cancer.. <i>Journal of Clinical Oncology</i> , 2014 , 32, 11017-11017	2.2	
3	A pharmacogenetic model predicting low paclitaxel clearance based on the DMET platform.. <i>Journal of Clinical Oncology</i> , 2013 , 31, 2597-2597	2.2	
2	A panel of DNA methylation markers for the classification of consensus molecular subtypes 2 and 3 in patients with colorectal cancer.. <i>Journal of Clinical Oncology</i> , 2021 , 39, 3545-3545	2.2	
1	A tale on rabbit ears and pan-handles, the rings that rule all. <i>EBioMedicine</i> , 2019 , 49, 17-18	8.8	