

Marcel Smid

List of Publications by Year in descending order

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Version: 2024-02-01

84
papers

6,836
citations

117619

34
h-index

66906

78
g-index

88
all docs

88
docs citations

88
times ranked

14420
citing authors

#	ARTICLE	IF	CITATIONS
1	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. <i>Nature</i> , 2016, 534, 47-54.	27.8	1,760
2	Subtypes of Breast Cancer Show Preferential Site of Relapse. <i>Cancer Research</i> , 2008, 68, 3108-3114.	0.9	674
3	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, 13021-13026.	7.1	374
4	Selection of Bone Metastasis Seeds by Mesenchymal Signals in the Primary Tumor Stroma. <i>Cell</i> , 2013, 154, 1060-1073.	28.9	359
5	Ovarian Cancer Cell Line Panel (OCCP): Clinical Importance of In Vitro Morphological Subtypes. <i>PLoS ONE</i> , 2014, 9, e103988.	2.5	319
6	Genes Associated With Breast Cancer Metastatic to Bone. <i>Journal of Clinical Oncology</i> , 2006, 24, 2261-2267.	1.6	278
7	The genomic landscape of metastatic breast cancer highlights changes in mutation and signature frequencies. <i>Nature Genetics</i> , 2019, 51, 1450-1458.	21.4	250
8	mRNA and microRNA Expression Profiles in Circulating Tumor Cells and Primary Tumors of Metastatic Breast Cancer Patients. <i>Clinical Cancer Research</i> , 2011, 17, 3600-3618.	7.0	207
9	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, 807-821.	5.5	176
10	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.	5.0	170
11	Breast cancer genome and transcriptome integration implicates specific mutational signatures with immune cell infiltration. <i>Nature Communications</i> , 2016, 7, 12910.	12.8	119
12	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.	2.6	105
13	Cancer-associated fibroblast-derived Gremlin 1 promotes breast cancer progression. <i>Breast Cancer Research</i> , 2019, 21, 109.	5.0	94
14	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.	12.8	91
15	The circular RNome of primary breast cancer. <i>Genome Research</i> , 2019, 29, 356-366.	5.5	85
16	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.	2.5	83
17	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, 2936-2945.	0.9	82
18	A Systematic Analysis of Oncogenic Gene Fusions in Primary Colon Cancer. <i>Cancer Research</i> , 2017, 77, 3814-3822.	0.9	76

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19	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.	21.4	75
20	Interferon-Stimulated Genes Are Involved in Cross-resistance to Radiotherapy in Tamoxifen-Resistant Breast Cancer. <i>Clinical Cancer Research</i> , 2018, 24, 3397-3408.	7.0	68
21	T lymphocytes facilitate brain metastasis of breast cancer by inducing Guanylate-Binding Protein 1 expression. <i>Acta Neuropathologica</i> , 2018, 135, 581-599.	7.7	63
22	Uncovering the signaling landscape controlling breast cancer cell migration identifies novel metastasis driver genes. <i>Nature Communications</i> , 2019, 10, 2983.	12.8	58
23	MicroRNAs as possible indicators of drug sensitivity in breast cancer cell lines. <i>PLoS ONE</i> , 2019, 14, e0216400.	2.5	54
24	Functional <i>in vivo</i> Assay Reveals Homologous Recombination Deficiency in Breast Cancer Beyond BRCA Gene Defects. <i>Clinical Cancer Research</i> , 2018, 24, 6277-6287.	7.0	53
25	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.	5.0	48
26	DNA damage responsive microRNAs misexpressed in human cancer modulate therapy sensitivity. <i>Molecular Oncology</i> , 2014, 8, 458-468.	4.6	46
27	Partially methylated domains are hypervariable in breast cancer and fuel widespread CpG island hypermethylation. <i>Nature Communications</i> , 2019, 10, 1749.	12.8	46
28	PI3 kinase mutations and mutational load as poor prognostic markers in diffuse glioma patients. <i>Acta Neuropathologica Communications</i> , 2015, 3, 88.	5.2	42
29	Gene expression profiles of circulating tumor cells versus primary tumors in metastatic breast cancer. <i>Cancer Letters</i> , 2015, 362, 36-44.	7.2	41
30	Epithelial-Mesenchymal Transition in Human Prostate Cancer Demonstrates Enhanced Immune Evasion Marked by IDO1 Expression. <i>Cancer Research</i> , 2018, 78, 4671-4679.	0.9	41
31	Whole genome sequencing of metastatic colorectal cancer reveals prior treatment effects and specific metastasis features. <i>Nature Communications</i> , 2021, 12, 574.	12.8	39
32	The advantage of laser capture microdissection over whole tissue analysis in proteomic profiling studies. <i>Proteomics</i> , 2016, 16, 1474-1485.	2.2	38
33	Gene expression profiling assigns CHEK2 1100delC breast cancers to the luminal intrinsic subtypes. <i>Breast Cancer Research and Treatment</i> , 2012, 132, 439-448.	2.5	37
34	mRNA expression profiles in circulating tumor cells of metastatic colorectal cancer patients. <i>Molecular Oncology</i> , 2015, 9, 920-932.	4.6	37
35	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.	1.8	37
36	Molecular characterization of irinotecan (SN-38) resistant human breast cancer cell lines. <i>BMC Cancer</i> , 2016, 16, 34.	2.6	35

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37	Phosphoserine aminotransferase 1 is associated to poor outcome on tamoxifen therapy in recurrent breast cancer. <i>Scientific Reports</i> , 2017, 7, 2099.	3.3	33
38	Confirmation of a metastasis-specific microRNA signature in primary colon cancer. <i>Scientific Reports</i> , 2018, 8, 5242.	3.3	33
39	Mitochondrial DNA content in breast cancer: Impact on <i>in vitro</i> and <i>in vivo</i> phenotype and patient prognosis. <i>Oncotarget</i> , 2016, 7, 29166-29176.	1.8	33
40	4â€protein signature predicting tamoxifen treatment outcome in recurrent breast cancer. <i>Molecular Oncology</i> , 2016, 10, 24-39.	4.6	31
41	Comprehensive evaluation of methods to assess overall and cell-specific immune infiltrates in breast cancer. <i>Breast Cancer Research</i> , 2019, 21, 151.	5.0	30
42	Differential quantities of immune checkpoint-expressing CD8 T cells in soft tissue sarcoma subtypes. , 2020, 8, e000271.		29
43	Androgen receptor expression in circulating tumor cells of patients with metastatic breast cancer. <i>International Journal of Cancer</i> , 2019, 145, 1083-1089.	5.1	27
44	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.	7.0	26
45	Annexin-A1 and caldesmon are associated with resistance to tamoxifen in estrogen receptor positive recurrent breast cancer. <i>Oncotarget</i> , 2016, 7, 3098-3110.	1.8	26
46	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.	2.6	25
47	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, 104-109.	7.2	22
48	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.	2.8	22
49	Co-regulated gene expression of splicing factors as drivers of cancer progression. <i>Scientific Reports</i> , 2019, 9, 5484.	3.3	22
50	Circulating Tumor Cell Enumeration and Characterization in Metastatic Castration-Resistant Prostate Cancer Patients Treated with Cabazitaxel. <i>Cancers</i> , 2019, 11, 1212.	3.7	21
51	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, 802.	3.7	20
52	Differential reprogramming of breast cancer subtypes in 3D cultures and implications for sensitivity to targeted therapy. <i>Scientific Reports</i> , 2021, 11, 7259.	3.3	20
53	Prognostic significance of nuclear expression of UMP-CMP kinase in triple negative breast cancer patients. <i>Scientific Reports</i> , 2016, 6, 32027.	3.3	19
54	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.	5.9	19

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55	The Prevalence of CD146 Expression in Breast Cancer Subtypes and Its Relation to Outcome. <i>Cancers</i> , 2018, 10, 134.	3.7	18
56	Proper genomic profiling of (<i>BRCA1</i> -mutated) basal-like breast carcinomas requires prior removal of tumor infiltrating lymphocytes. <i>Molecular Oncology</i> , 2015, 9, 877-888.	4.6	16
57	Predicting paclitaxel-induced neutropenia using the DMET platform. <i>Pharmacogenomics</i> , 2015, 16, 1231-1241.	1.3	15
58	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.	3.3	15
59	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.	2.5	14
60	Vascular Pattern Analysis for the Prediction of Clinical Behaviour in Pheochromocytomas and Paragangliomas. <i>PLoS ONE</i> , 2015, 10, e0121361.	2.5	14
61	Understanding drugs in breast cancer through drug sensitivity screening. <i>SpringerPlus</i> , 2015, 4, 611.	1.2	11
62	Metabotropic glutamate receptor 1 is associated with unfavorable prognosis in ER-negative and triple-negative breast cancer. <i>Scientific Reports</i> , 2020, 10, 22292.	3.3	11
63	MicroRNA expression in pre-treatment plasma of patients with benign breast diseases and breast cancer. <i>Oncotarget</i> , 2018, 9, 24335-24346.	1.8	11
64	Intratumoral heterogeneity of second-harmonic generation scattering from tumor collagen and its effects on metastatic risk prediction. <i>BMC Cancer</i> , 2020, 20, 1217.	2.6	10
65	Fusion transcripts and their genomic breakpoints in polyadenylated and ribosomal RNA ⁻ minus RNA sequencing data. <i>GigaScience</i> , 2021, 10, .	6.4	10
66	Molecular Comparison of Imatinib-Naïve and Resistant Gastrointestinal Stromal Tumors: Differentially Expressed microRNAs and mRNAs. <i>Cancers</i> , 2019, 11, 882.	3.7	9
67	Proteomic characterization of microdissected breast tissue environment provides a protein-level overview of malignant transformation. <i>Proteomics</i> , 2017, 17, 1600213.	2.2	7
68	Mitochondrial RNA Expression and Single Nucleotide Variants in Association with Clinical Parameters in Primary Breast Cancers. <i>Cancers</i> , 2018, 10, 500.	3.7	7
69	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.	2.5	6
70	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.	3.0	5
71	Wnt targets genes are not differentially expressed in desmoid tumors bearing different activating β -catenin mutations. <i>European Journal of Surgical Oncology</i> , 2019, 45, 691-698.	1.0	4
72	Downregulation of matrix Gla protein is a biomarker for tamoxifen-resistant and radioresistant breast cancer. <i>Biomarkers in Medicine</i> , 2019, 13, 841-850.	1.4	3

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73	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.	4.6	3
74	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.	1.6	2
75	Lost by Transcription: Fork Failures, Elevated Expression, and Clinical Consequences Related to Deletions in Metastatic Colorectal Cancer. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5080.	4.1	2
76	Global proteomic characterization of microdissected estrogen receptor positive breast tumors. <i>Data in Brief</i> , 2015, 5, 399-402.	1.0	1
77	Circular RNA in Chemonaive Lymph Node Negative Colon Cancer Patients. <i>Cancers</i> , 2021, 13, 1903.	3.7	1
78	Transcriptomic Properties of HER2+ Ductal Carcinoma In Situ of the Breast Associate with Absence of Immune Cells. <i>Biology</i> , 2021, 10, 768.	2.8	1
79	Identifying Transcripts with Tandem Duplications from RNA-Sequencing Data to Predict BRCA1-Type Primary Breast Cancer. <i>Cancers</i> , 2022, 14, 753.	3.7	1
80	Response. <i>Journal of the National Cancer Institute</i> , 2014, 106, dju254-dju254.	6.3	0
81	A tale on rabbit ears and pan-handles, the rings that rule all. <i>EBioMedicine</i> , 2019, 49, 17-18.	6.1	0
82	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.	1.6	0
83	A pharmacogenetic model predicting low paclitaxel clearance based on the DMET platform.. <i>Journal of Clinical Oncology</i> , 2013, 31, 2597-2597.	1.6	0
84	Gene expression profiles of primary tumors versus circulating tumor cells in metastatic breast cancer.. <i>Journal of Clinical Oncology</i> , 2014, 32, 11017-11017.	1.6	0