

# Maurizio Callari

## List of Publications by Year in descending order

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Version: 2024-02-01

57  
papers

2,885  
citations

201674

27  
h-index

189892

50  
g-index

61  
all docs

61  
docs citations

61  
times ranked

6505  
citing authors

#	ARTICLE	IF	CITATIONS
1	A Biobank of Breast Cancer Explants with Preserved Intra-tumor Heterogeneity to Screen Anticancer Compounds. <i>Cell</i> , 2016, 167, 260-274.e22.	28.9	376
2	Dynamics of breast-cancer relapse reveal late-recurring ER-positive genomic subgroups. <i>Nature</i> , 2019, 567, 399-404.	27.8	239
3	A transcriptional sketch of a primary human breast cancer by 454 deep sequencing. <i>BMC Genomics</i> , 2009, 10, 163.	2.8	205
4	Challenges in Using Circulating miRNAs as Cancer Biomarkers. <i>BioMed Research International</i> , 2015, 2015, 1-10.	1.9	202
5	miR-21: an oncomir on strike in prostate cancer. <i>Molecular Cancer</i> , 2010, 9, 12.	19.2	189
6	Clonal Decomposition and DNA Replication States Defined by Scaled Single-Cell Genome Sequencing. <i>Cell</i> , 2019, 179, 1207-1221.e22.	28.9	162
7	Bioinformatics tools for secretome analysis. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 2442-2453.	2.3	93
8	Gene expression analysis reveals a different transcriptomic landscape in female and male breast cancer. <i>Breast Cancer Research and Treatment</i> , 2011, 127, 601-610.	2.5	88
9	Complexity in the tumour microenvironment: Cancer associated fibroblast gene expression patterns identify both common and unique features of tumour-stroma crosstalk across cancer types. <i>Seminars in Cancer Biology</i> , 2015, 35, 96-106.	9.6	85
10	Next Generation-Targeted Amplicon Sequencing (NG-TAS): an optimised protocol and computational pipeline for cost-effective profiling of circulating tumour DNA. <i>Genome Medicine</i> , 2019, 11, 1.	8.2	84
11	Impact of biospecimens handling on biomarker research in breast cancer. <i>BMC Cancer</i> , 2009, 9, 409.	2.6	81
12	miR-205 regulates basement membrane deposition in human prostate: implications for cancer development. <i>Cell Death and Differentiation</i> , 2012, 19, 1750-1760.	11.2	77
13	Mesenchymal to amoeboid transition is associated with stem-like features of melanoma cells. <i>Cell Communication and Signaling</i> , 2014, 12, 24.	6.5	77
14	miR-205 Hinders the Malignant Interplay Between Prostate Cancer Cells and Associated Fibroblasts. <i>Antioxidants and Redox Signaling</i> , 2014, 20, 1045-1059.	5.4	63
15	Subtype-Specific Metagene-Based Prediction of Outcome after Neoadjuvant and Adjuvant Treatment in Breast Cancer. <i>Clinical Cancer Research</i> , 2016, 22, 337-345.	7.0	58
16	Computational approach to discriminate human and mouse sequences in patient-derived tumour xenografts. <i>BMC Genomics</i> , 2018, 19, 19.	2.8	55
17	Integrated gene and miRNA expression analysis of prostate cancer associated fibroblasts supports a prominent role for interleukin-6 in fibroblast activation. <i>Oncotarget</i> , 2015, 6, 31441-31460.	1.8	55
18	Comparison of Microarray Platforms for Measuring Differential MicroRNA Expression in Paired Normal/Cancer Colon Tissues. <i>PLoS ONE</i> , 2012, 7, e45105.	2.5	52

#	ARTICLE	IF	CITATIONS
19	Intersect-then-combine approach: improving the performance of somatic variant calling in whole exome sequencing data using multiple aligners and callers. <i>Genome Medicine</i> , 2017, 9, 35.	8.2	48
20	A lipemia-independent NanoDrop <sup>®</sup> -based score to identify hemolysis in plasma and serum samples. <i>Bioanalysis</i> , 2014, 6, 1215-1226.	1.5	47
21	Diagnostic role of circulating extracellular matrix-related proteins in non-small cell lung cancer. <i>BMC Cancer</i> , 2018, 18, 899.	2.6	45
22	Effects of Warm Ischemic Time on Gene Expression Profiling in Colorectal Cancer Tissues and Normal Mucosa. <i>PLoS ONE</i> , 2013, 8, e53406.	2.5	44
23	By promoting cell differentiation, miR-100 sensitizes basal-like breast cancer stem cells to hormonal therapy. <i>Oncotarget</i> , 2015, 6, 2315-2330.	1.8	43
24	miR-30e* is an independent subtype-specific prognostic marker in breast cancer. <i>British Journal of Cancer</i> , 2015, 113, 290-298.	6.4	40
25	Subtype-dependent prognostic relevance of an interferon-induced pathway metagene in node-negative breast cancer. <i>Molecular Oncology</i> , 2014, 8, 1278-1289.	4.6	39
26	Landscapes of cellular phenotypic diversity in breast cancer xenografts and their impact on drug response. <i>Nature Communications</i> , 2021, 12, 1998.	12.8	37
27	Molecular portrait of breast cancer in China reveals comprehensive transcriptomic likeness to Caucasian breast cancer and low prevalence of luminal A subtype. <i>Cancer Medicine</i> , 2015, 4, 1016-1030.	2.8	31
28	Circulating Biomarkers for Prediction of Treatment Response. <i>Journal of the National Cancer Institute Monographs</i> , 2015, 2015, 60-63.	2.1	31
29	Reciprocal regulation of p63 by C/EBP delta in human keratinocytes. <i>BMC Molecular Biology</i> , 2007, 8, 85.	3.0	26
30	Feasibility of circulating miRNA microarray analysis from archival plasma samples. <i>Analytical Biochemistry</i> , 2013, 437, 123-125.	2.4	23
31	Measuring MicroRNA Expression Levels in Oncology: from Samples to Data Analysis. <i>Critical Reviews in Oncogenesis</i> , 2013, 18, 273-287.	0.4	21
32	AF1q: A Novel Mediator of Basal and 4-HPR-Induced Apoptosis in Ovarian Cancer Cells. <i>PLoS ONE</i> , 2012, 7, e39968.	2.5	19
33	Gene Expression Profiling of Circulating Tumor Cells in Breast Cancer. <i>Clinical Chemistry</i> , 2015, 61, 278-289.	3.2	19
34	POSEIDON Trial Phase 1b Results: Safety, Efficacy and Circulating Tumor DNA Response of the Beta Isoform-Sparing PI3K Inhibitor Taselisib (GDC-0032) Combined with Tamoxifen in Hormone Receptor Positive Metastatic Breast Cancer Patients. <i>Clinical Cancer Research</i> , 2019, 25, 6598-6605.	7.0	17
35	Proposal of supervised data analysis strategy of plasma miRNAs from hybridisation array data with an application to assess hemolysis-related deregulation. <i>BMC Bioinformatics</i> , 2015, 16, 388.	2.6	16
36	Use of Formalin-Fixed Paraffin-Embedded Samples for Gene Expression Studies in Breast Cancer Patients. <i>PLoS ONE</i> , 2015, 10, e0123194.	2.5	11

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37	Involvement of AF1q/MLLT11 in the progression of ovarian cancer. <i>Oncotarget</i> , 2017, 8, 23246-23264.	1.8	11
38	Molecular heterogeneity in breast carcinoma cells with increased invasive capacities. <i>Radiology and Oncology</i> , 2020, 54, 103-118.	1.7	10
39	Accurate Data Processing Improves the Reliability of Affymetrix Gene Expression Profiles from FFPE Samples. <i>PLoS ONE</i> , 2014, 9, e86511.	2.5	10
40	In-depth characterization of breast cancer tumor-promoting cell transcriptome by RNA sequencing and microarrays. <i>Oncotarget</i> , 2016, 7, 976-994.	1.8	10
41	Epithelioid Pleural Mesothelioma Is Characterized by Tertiary Lymphoid Structures in Long Survivors: Results from the MATCH Study. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5786.	4.1	9
42	MicroRNA Detection in Plasma Samples. <i>Journal of Molecular Diagnostics</i> , 2013, 15, 138-139.	2.8	6
43	Prognostic and functional role of subtype-specific tumor-stroma interaction in breast cancer. <i>Molecular Oncology</i> , 2017, 11, 1399-1412.	4.6	6
44	PATRI, a Genomics Data Integration Tool for Biomarker Discovery. <i>BioMed Research International</i> , 2018, 2018, 1-13.	1.9	6
45	Clonal populations of a human TNBC model display significant functional heterogeneity and divergent growth dynamics in distinct contexts. <i>Oncogene</i> , 2022, 41, 112-124.	5.9	6
46	Predicting and Understanding Cancer Response to Treatment. <i>Disease Markers</i> , 2018, 2018, 1-2.	1.3	2
47	Mechanisms of responsiveness to and resistance against trabectedin in murine models of human myxoid liposarcoma. <i>Genomics</i> , 2021, 113, 3439-3448.	2.9	2
48	Proliferation-, estrogen-, and T-cell-related metagenes to predict outcome after adjuvant/neoadjuvant chemotherapy for operable breast cancer in the ECTO trial. <i>Journal of Clinical Oncology</i> , 2013, 31, 1014-1014.	1.6	2
49	Abstract B18: MiR-205 puts the brakes on the malignant interplay between prostate cancer cells and associated fibroblasts. , 2013, , .		1
50	Dissecting Time- from Tumor-Related Gene Expression Variability in Bilateral Breast Cancer. <i>International Journal of Molecular Sciences</i> , 2018, 19, 196.	4.1	0
51	An immune-related signature for prediction of risk of late recurrences beyond proliferation and ER-related genes in ER-positive breast cancer. <i>Journal of Clinical Oncology</i> , 2014, 32, 530-530.	1.6	0
52	Abstract P2-03-05: The heterogeneous clinical behavior of luminal breast cancers is associated with different mutational landscapes. , 2015, , .		0
53	Contribution of immune system and tumor-related interferon signaling to epirubicin response in triple-negative (TN) breast cancers. <i>Journal of Clinical Oncology</i> , 2015, 33, 1081-1081.	1.6	0
54	Abstract 5085: Cancer-associated fibroblasts transcriptional pattern reveals common changes in extracellular matrix-related genes across different cancer types. , 2016, , .		0

#	ARTICLE	IF	CITATIONS
55	Abstract 1747: A microenvironment gene signature predicts poor outcome in patients with luminal breast cancers subjected to local-regional treatment. , 2017, , .		0
56	Abstract 2991: Integrative analysis of molecular and drug response data from clinical samples and PDTXs to identify pharmacogenomic associations in breast cancer. , 2017, , .		0
57	Title is missing!. , 2014, 9, e86511.		0