

# 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	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
2	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
3	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
4	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
5	Molecular heterogeneity in breast carcinoma cells with increased invasive capacities. <i>Radiology and Oncology</i> , 2020, 54, 103-118.	1.7	10
6	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
7	Clonal Decomposition and DNA Replication States Defined by Scaled Single-Cell Genome Sequencing. <i>Cell</i> , 2019, 179, 1207-1221.e22.	28.9	162
8	Dynamics of breast-cancer relapse reveal late-recurring ER-positive genomic subgroups. <i>Nature</i> , 2019, 567, 399-404.	27.8	239
9	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
10	Diagnostic role of circulating extracellular matrix-related proteins in non-small cell lung cancer. <i>BMC Cancer</i> , 2018, 18, 899.	2.6	45
11	Computational approach to discriminate human and mouse sequences in patient-derived tumour xenografts. <i>BMC Genomics</i> , 2018, 19, 19.	2.8	55
12	Predicting and Understanding Cancer Response to Treatment. <i>Disease Markers</i> , 2018, 2018, 1-2.	1.3	2
13	PATRI, a Genomics Data Integration Tool for Biomarker Discovery. <i>BioMed Research International</i> , 2018, 2018, 1-13.	1.9	6
14	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
15	Prognostic and functional role of subtype-specific tumor-stroma interaction in breast cancer. <i>Molecular Oncology</i> , 2017, 11, 1399-1412.	4.6	6
16	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
17	Involvement of AF1q/MLLT11 in the progression of ovarian cancer. <i>Oncotarget</i> , 2017, 8, 23246-23264.	1.8	11
18	Abstract 1747: A microenvironment gene signature predicts poor outcome in patients with luminal breast cancers subjected to local-regional treatment. , 2017, , .		0

#	ARTICLE	IF	CITATIONS
19	Abstract 2991: Integrative analysis of molecular and drug response data from clinical samples and PDTXs to identify pharmacogenomic associations in breast cancer. , 2017, , .		0
20	A Biobank of Breast Cancer Explants with Preserved Intra-tumor Heterogeneity to Screen Anticancer Compounds. Cell, 2016, 167, 260-274.e22.	28.9	376
21	Subtype-Specific Metagene-Based Prediction of Outcome after Neoadjuvant and Adjuvant Treatment in Breast Cancer. Clinical Cancer Research, 2016, 22, 337-345.	7.0	58
22	In-depth characterization of breast cancer tumor-promoting cell transcriptome by RNA sequencing and microarrays. Oncotarget, 2016, 7, 976-994.	1.8	10
23	Abstract 5085: Cancer-associated fibroblasts transcriptional pattern reveals common changes in extracellular matrix-related genes across different cancer types. , 2016, , .		0
24	Molecular portrait of breast cancer in <sc>C</sc>hina reveals comprehensive transcriptomic likeness to <sc>C</sc>aucasian breast cancer and low prevalence of luminal A subtype. Cancer Medicine, 2015, 4, 1016-1030.	2.8	31
25	Proposal of supervised data analysis strategy of plasma miRNAs from hybridisation array data with an application to assess hemolysis-related deregulation. BMC Bioinformatics, 2015, 16, 388.	2.6	16
26	Challenges in Using Circulating miRNAs as Cancer Biomarkers. BioMed Research International, 2015, 2015, 1-10.	1.9	202
27	miR-30e* is an independent subtype-specific prognostic marker in breast cancer. British Journal of Cancer, 2015, 113, 290-298.	6.4	40
28	Circulating Biomarkers for Prediction of Treatment Response. Journal of the National Cancer Institute Monographs, 2015, 2015, 60-63.	2.1	31
29	Complexity in the tumour microenvironment: Cancer associated fibroblast gene expression patterns identify both common and unique features of tumour-stroma crosstalk across cancer types. Seminars in Cancer Biology, 2015, 35, 96-106.	9.6	85
30	Gene Expression Profiling of Circulating Tumor Cells in Breast Cancer. Clinical Chemistry, 2015, 61, 278-289.	3.2	19
31	Use of Formalin-Fixed Paraffin-Embedded Samples for Gene Expression Studies in Breast Cancer Patients. PLoS ONE, 2015, 10, e0123194.	2.5	11
32	By promoting cell differentiation, miR-100 sensitizes basal-like breast cancer stem cells to hormonal therapy. Oncotarget, 2015, 6, 2315-2330.	1.8	43
33	Integrated gene and miRNA expression analysis of prostate cancer associated fibroblasts supports a prominent role for interleukin-6 in fibroblast activation. Oncotarget, 2015, 6, 31441-31460.	1.8	55
34	Abstract P2-03-05: The heterogeneous clinical behavior of luminal breast cancers is associated with different mutational landscapes. , 2015, , .		0
35	Contribution of immune system and tumor-related interferon signaling to epirubicin response in triple-negative (TN) breast cancers.. Journal of Clinical Oncology, 2015, 33, 1081-1081.	1.6	0
36	A lipemia-independent NanoDrop <sup>®</sup> -based score to identify hemolysis in plasma and serum samples. Bioanalysis, 2014, 6, 1215-1226.	1.5	47

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37	miR-205 Hinders the Malignant Interplay Between Prostate Cancer Cells and Associated Fibroblasts. Antioxidants and Redox Signaling, 2014, 20, 1045-1059.	5.4	63
38	Mesenchymal to amoeboid transition is associated with stem-like features of melanoma cells. Cell Communication and Signaling, 2014, 12, 24.	6.5	77
39	Subtype-dependent prognostic relevance of an interferon-induced pathway metagene in node-negative breast cancer. Molecular Oncology, 2014, 8, 1278-1289.	4.6	39
40	Accurate Data Processing Improves the Reliability of Affymetrix Gene Expression Profiles from FFPE Samples. PLoS ONE, 2014, 9, e86511.	2.5	10
41	An immune-related signature for prediction of risk of late recurrences beyond proliferation and ER-related genes in ER-positive breast cancer.. Journal of Clinical Oncology, 2014, 32, 530-530.	1.6	0
42	Title is missing!. , 2014, 9, e86511.		0
43	Feasibility of circulating miRNA microarray analysis from archival plasma samples. Analytical Biochemistry, 2013, 437, 123-125.	2.4	23
44	MicroRNA Detection in Plasma Samples. Journal of Molecular Diagnostics, 2013, 15, 138-139.	2.8	6
45	Bioinformatics tools for secretome analysis. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 2442-2453.	2.3	93
46	Effects of Warm Ischemic Time on Gene Expression Profiling in Colorectal Cancer Tissues and Normal Mucosa. PLoS ONE, 2013, 8, e53406.	2.5	44
47	Abstract B18: MiR-205 puts the brakes on the malignant interplay between prostate cancer cells and associated fibroblasts. , 2013, , .		1
48	Measuring MicroRNA Expression Levels in Oncology: from Samples to Data Analysis. Critical Reviews in Oncogenesis, 2013, 18, 273-287.	0.4	21
49	Proliferation-, estrogen-, and T-cell-related metagenes to predict outcome after adjuvant/neoadjuvant chemotherapy for operable breast cancer in the ECTO trial.. Journal of Clinical Oncology, 2013, 31, 1014-1014.	1.6	2
50	miR-205 regulates basement membrane deposition in human prostate: implications for cancer development. Cell Death and Differentiation, 2012, 19, 1750-1760.	11.2	77
51	AF1q: A Novel Mediator of Basal and 4-HPR-Induced Apoptosis in Ovarian Cancer Cells. PLoS ONE, 2012, 7, e39968.	2.5	19
52	Comparison of Microarray Platforms for Measuring Differential MicroRNA Expression in Paired Normal/Cancer Colon Tissues. PLoS ONE, 2012, 7, e45105.	2.5	52
53	Gene expression analysis reveals a different transcriptomic landscape in female and male breast cancer. Breast Cancer Research and Treatment, 2011, 127, 601-610.	2.5	88
54	miR-21: an oncomir on strike in prostate cancer. Molecular Cancer, 2010, 9, 12.	19.2	189

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55	A transcriptional sketch of a primary human breast cancer by 454 deep sequencing. BMC Genomics, 2009, 10, 163.	2.8	205
56	Impact of biospecimens handling on biomarker research in breast cancer. BMC Cancer, 2009, 9, 409.	2.6	81
57	Reciprocal regulation of p63 by C/EBP delta in human keratinocytes. BMC Molecular Biology, 2007, 8, 85.	3.0	26