

# Anita Grigoriadis

## List of Publications by Year in descending order

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Version: 2024-02-01

75  
papers

7,159  
citations

117571

34  
h-index

71651

76  
g-index

78  
all docs

78  
docs citations

78  
times ranked

13048  
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>IDH1</i> and <i>IDH2</i> mutations are frequent events in central chondrosarcoma and central and periosteal chondromas but not in other mesenchymal tumours. <i>Journal of Pathology</i> , 2011, 224, 334-343.	2.1	834
2	Carboplatin in BRCA1/2-mutated and triple-negative breast cancer BRCAness subgroups: the TNT Trial. <i>Nature Medicine</i> , 2018, 24, 628-637.	15.2	649
3	BRCA1 Basal-like Breast Cancers Originate from Luminal Epithelial Progenitors and Not from Basal Stem Cells. <i>Cell Stem Cell</i> , 2010, 7, 403-417.	5.2	643
4	<i>FGFR1</i> Amplification Drives Endocrine Therapy Resistance and Is a Therapeutic Target in Breast Cancer. <i>Cancer Research</i> , 2010, 70, 2085-2094.	0.4	629
5	Targeting folate receptor alpha for cancer treatment. <i>Oncotarget</i> , 2016, 7, 52553-52574.	0.8	308
6	Genomic scars as biomarkers of homologous recombination deficiency and drug response in breast and ovarian cancers. <i>Breast Cancer Research</i> , 2014, 16, 211.	2.2	260
7	<i>FGFR1</i> Emerges as a Potential Therapeutic Target for Lobular Breast Carcinomas. <i>Clinical Cancer Research</i> , 2006, 12, 6652-6662.	3.2	256
8	Expression Profiling of Purified Normal Human Luminal and Myoepithelial Breast Cells. <i>Cancer Research</i> , 2004, 64, 3037-3045.	0.4	233
9	<i>PIM1</i> kinase regulates cell death, tumor growth and chemotherapy response in triple-negative breast cancer. <i>Nature Medicine</i> , 2016, 22, 1303-1313.	15.2	188
10	Selectin Ligand Sialyl-Lewis x Antigen Drives Metastasis of Hormone-Dependent Breast Cancers. <i>Cancer Research</i> , 2011, 71, 7683-7693.	0.4	171
11	Tiling Path Genomic Profiling of Grade 3 Invasive Ductal Breast Cancers. <i>Clinical Cancer Research</i> , 2009, 15, 2711-2722.	3.2	152
12	Transcriptome analysis of mammary epithelial subpopulations identifies novel determinants of lineage commitment and cell fate. <i>BMC Genomics</i> , 2008, 9, 591.	1.2	151
13	An integrative genomic and transcriptomic analysis reveals molecular pathways and networks regulated by copy number aberrations in basal-like, HER2 and luminal cancers. <i>Breast Cancer Research and Treatment</i> , 2010, 121, 575-589.	1.1	146
14	Microarray-Based Class Discovery for Molecular Classification of Breast Cancer: Analysis of Interobserver Agreement. <i>Journal of the National Cancer Institute</i> , 2011, 103, 662-673.	3.0	121
15	Establishment of the epithelial-specific transcriptome of normal and malignant human breast cells based on MPSS and array expression data. <i>Breast Cancer Research</i> , 2006, 8, R56.	2.2	118
16	An innate-like $\gamma\delta$ T cell compartment in the human breast is associated with remission in triple-negative breast cancer. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	110
17	Integrated Functional, Gene Expression and Genomic Analysis for the Identification of Cancer Targets. <i>PLoS ONE</i> , 2009, 4, e5120.	1.1	109
18	Molecular and Phenotypic Characterisation of Paediatric Glioma Cell Lines as Models for Preclinical Drug Development. <i>PLoS ONE</i> , 2009, 4, e5209.	1.1	102

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19	Genomic Complexity Profiling Reveals That <i>HORMAD1</i> Overexpression Contributes to Homologous Recombination Deficiency in Triple-Negative Breast Cancers. <i>Cancer Discovery</i> , 2015, 5, 488-505.	7.7	97
20	<i>ROR1</i> <sup>3+</sup> Innate Lymphoid Cells Promote Lymph Node Metastasis of Breast Cancers. <i>Cancer Research</i> , 2017, 77, 1083-1096.	0.4	93
21	CT-X antigen expression in human breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 13493-13498.	3.3	92
22	Comparison of basal-like triple-negative breast cancer defined by morphology, immunohistochemistry and transcriptional profiles. <i>Modern Pathology</i> , 2013, 26, 955-966.	2.9	79
23	Integrated genomic analysis of triple-negative breast cancers reveals novel microRNAs associated with clinical and molecular phenotypes and sheds light on the pathways they control. <i>BMC Genomics</i> , 2013, 14, 643.	1.2	76
24	Molecular characterisation of cell line models for triple-negative breast cancers. <i>BMC Genomics</i> , 2012, 13, 619.	1.2	69
25	Functional and prognostic significance of the genomic amplification of <i>frizzled 6</i> ( <i>FZD6</i> ) in breast cancer. <i>Journal of Pathology</i> , 2017, 241, 350-361.	2.1	66
26	Anti-Folate Receptor Alpha-Targeted Antibody Therapies Restrict the Growth of Triple-negative Breast Cancer. <i>Clinical Cancer Research</i> , 2018, 24, 5098-5111.	3.2	65
27	<i>GD3</i> Synthase Expression Enhances Proliferation and Tumor Growth of MDA-MB-231 Breast Cancer Cells through c-Met Activation. <i>Molecular Cancer Research</i> , 2010, 8, 1526-1535.	1.5	64
28	A high-resolution integrated analysis of genetic and expression profiles of breast cancer cell lines. <i>Breast Cancer Research and Treatment</i> , 2009, 118, 481-498.	1.1	58
29	A whole-genome massively parallel sequencing analysis of <i>BRCA1</i> mutant oestrogen receptor-negative and -positive breast cancers. <i>Journal of Pathology</i> , 2012, 227, 29-41.	2.1	58
30	Evaluation of CDK12 Protein Expression as a Potential Novel Biomarker for DNA Damage Response-Targeted Therapies in Breast Cancer. <i>Molecular Cancer Therapeutics</i> , 2018, 17, 306-315.	1.9	52
31	Immunological Visibility: Posttranscriptional Regulation of Human NKG2D Ligands by the EGF Receptor Pathway. <i>Science Translational Medicine</i> , 2014, 6, 231ra49.	5.8	49
32	Big Data: the challenge for small research groups in the era of cancer genomics. <i>British Journal of Cancer</i> , 2015, 113, 1405-1412.	2.9	44
33	Repurposing Tin Mesoporphyrin as an Immune Checkpoint Inhibitor Shows Therapeutic Efficacy in Preclinical Models of Cancer. <i>Clinical Cancer Research</i> , 2018, 24, 1617-1628.	3.2	44
34	Dual Mechanisms of LYN Kinase Dysregulation Drive Aggressive Behavior in Breast Cancer Cells. <i>Cell Reports</i> , 2018, 25, 3674-3692.e10.	2.9	43
35	Pan-cancer transcriptomic analysis dissects immune and proliferative functions of APOBEC3 cytidine deaminases. <i>Nucleic Acids Research</i> , 2019, 47, 1178-1194.	6.5	41
36	Tumor-Infiltrating B Lymphocyte Profiling Identifies IgG-Biased, Clonally Expanded Prognostic Phenotypes in Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2021, 81, 4290-4304.	0.4	40

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37	IL15RA Drives Antagonistic Mechanisms of Cancer Development and Immune Control in Lymphocyte-Enriched Triple-Negative Breast Cancers. <i>Cancer Research</i> , 2014, 74, 4908-4921.	0.4	39
38	Identification of a gene regulatory network associated with prion replication. <i>EMBO Journal</i> , 2014, 33, 1527-1547.	3.5	39
39	Integrated genomics and functional validation identifies malignant cell specific dependencies in triple negative breast cancer. <i>Nature Communications</i> , 2018, 9, 1044.	5.8	39
40	Integrin-Mediated Macrophage Adhesion Promotes Lymphovascular Dissemination in Breast Cancer. <i>Cell Reports</i> , 2019, 27, 1967-1978.e4.	2.9	39
41	Genome-wide transcriptomic profiling of microdissected human breast tissue reveals differential expression of KIT (c-Kit, CD117) and oestrogen receptor $\pm$ (ER $\pm$ ) in response to therapeutic radiation. <i>Journal of Pathology</i> , 2009, 219, 131-140.	2.1	36
42	Mouse mammary stem cells express prognostic markers for triple-negative breast cancer. <i>Breast Cancer Research</i> , 2015, 17, 31.	2.2	35
43	Lipogenic signalling modulates prostate cancer cell adhesion and migration via modification of Rho GTPases. <i>Oncogene</i> , 2020, 39, 3666-3679.	2.6	35
44	Genomic analysis defines clonal relationships of ductal carcinoma in situ and recurrent invasive breast cancer. <i>Nature Genetics</i> , 2022, 54, 850-860.	9.4	34
45	Transcriptomic analysis of tubular carcinomas of the breast reveals similarities and differences with molecular subtype-matched ductal and lobular carcinomas. <i>Journal of Pathology</i> , 2010, 222, 64-75.	2.1	33
46	Mutation Processes in 293-Based Clones Overexpressing the DNA Cytosine Deaminase APOBEC3B. <i>PLoS ONE</i> , 2016, 11, e0155391.	1.1	33
47	Digital imaging in the immunohistochemical evaluation of the proliferation markers Ki67, MCM2 and Geminin, in early breast cancer, and their putative prognostic value. <i>BMC Cancer</i> , 2015, 15, 546.	1.1	32
48	Perilobar Nephrogenic Rests Are Nonobligate Molecular Genetic Precursor Lesions of Insulin-Like Growth Factor-II-Associated Wilms Tumors. <i>Clinical Cancer Research</i> , 2008, 14, 7635-7644.	3.2	30
49	Conditional deletion of the <i>Lkb1</i> gene in the mouse mammary gland induces tumour formation. <i>Journal of Pathology</i> , 2009, 219, 306-316.	2.1	30
50	Robust BRCA1-like classification of copy number profiles of samples repeated across different datasets and platforms. <i>Molecular Oncology</i> , 2015, 9, 1274-1286.	2.1	29
51	Identification of differentially expressed sense and antisense transcript pairs in breast epithelial tissues. <i>BMC Genomics</i> , 2009, 10, 324.	1.2	28
52	DART: Denoising Algorithm based on Relevance network Topology improves molecular pathway activity inference. <i>BMC Bioinformatics</i> , 2011, 12, 403.	1.2	26
53	Histological scoring of immune and stromal features in breast and axillary lymph nodes is prognostic for distant metastasis in lymph node-positive breast cancers. <i>Journal of Pathology: Clinical Research</i> , 2018, 4, 39-54.	1.3	26
54	An RNAi screen of Rho signalling networks identifies RhoH as a regulator of Rac1 in prostate cancer cell migration. <i>BMC Biology</i> , 2018, 16, 29.	1.7	26

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55	Regulator of G-protein signalling 2 mRNA is differentially expressed in mammary epithelial subpopulations and over-expressed in the majority of breast cancers. <i>Breast Cancer Research</i> , 2007, 9, R85.	2.2	24
56	Synergistic T cell signaling by 41BB and CD28 is optimally achieved by membrane proximal positioning within parallel chimeric antigen receptors. <i>Cell Reports Medicine</i> , 2021, 2, 100457.	3.3	24
57	Random Forest Modelling of High-Dimensional Mixed-Type Data for Breast Cancer Classification. <i>Cancers</i> , 2021, 13, 991.	1.7	21
58	Delineation of a 1Mb breakpoint region at 1p13 in Wilms tumors by fine-tiling oligonucleotide array CGH. <i>Genes Chromosomes and Cancer</i> , 2007, 46, 607-615.	1.5	19
59	Comparative Membranome Expression Analysis in Primary Tumors and Derived Cell Lines. <i>PLoS ONE</i> , 2010, 5, e11742.	1.1	18
60	Selection and evolution in the genomic landscape of copy number alterations in ductal carcinoma in situ (DCIS) and its progression to invasive carcinoma of ductal/no special type: a meta-analysis. <i>Breast Cancer Research and Treatment</i> , 2015, 153, 101-121.	1.1	17
61	A Four-gene Decision Tree Signature Classification of Triple-negative Breast Cancer: Implications for Targeted Therapeutics. <i>Molecular Cancer Therapeutics</i> , 2019, 18, 204-212.	1.9	17
62	Molecular patterns of cancer colonisation in lymph nodes of breast cancer patients. <i>Breast Cancer Research</i> , 2018, 20, 143.	2.2	16
63	PIK3CA mutations are common in lobular carcinoma in situ, but are not a biomarker of progression. <i>Breast Cancer Research</i> , 2017, 19, 7.	2.2	14
64	Splicing imbalances in basal-like breast cancer underpin perturbation of cell surface and oncogenic pathways and are associated with patients' survival. <i>Scientific Reports</i> , 2017, 7, 40177.	1.6	12
65	Immune Crosstalk Between Lymph Nodes and Breast Carcinomas, With a Focus on B Cells. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 673051.	1.6	10
66	Genomic distance entrained clustering and regression modelling highlights interacting genomic regions contributing to proliferation in breast cancer. <i>BMC Systems Biology</i> , 2010, 4, 127.	3.0	9
67	Systemic immune reaction in axillary lymph nodes adds to tumor-infiltrating lymphocytes in triple-negative breast cancer prognostication. <i>Npj Breast Cancer</i> , 2021, 7, 86.	2.3	9
68	Tandem duplications contribute to not one but two distinct phenotypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5257-8.	3.3	8
69	Systematic identification of functionally relevant risk alleles to stratify aggressive versus indolent prostate cancer. <i>Oncotarget</i> , 2018, 9, 12812-12824.	0.8	8
70	Profiling the Immune Stromal Interface in Breast Cancer and Its Potential for Clinical Impact. <i>Breast Care</i> , 2012, 7, 273-280.	0.8	7
71	Functional screening reveals HORMAD1-driven gene dependencies associated with translesion synthesis and replication stress tolerance. <i>Oncogene</i> , 2022, 41, 3969-3977.	2.6	6
72	CDK Inhibition Primes for Anti-PD-L1 Treatment in Triple-Negative Breast Cancer Models. <i>Cancers</i> , 2022, 14, 3361.	1.7	6

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73	Gene expression modules in primary breast cancers as risk factors for organotropic patterns of first metastatic spread: a case control study. <i>Breast Cancer Research</i> , 2017, 19, 113.	2.2	5
74	Prognostic signatures in breast cancer: correlation does not imply causation. <i>Breast Cancer Research</i> , 2012, 14, 313.	2.2	4
75	The ForeSee (4C) Approach for Integrative Analysis in Gene Discovery. <i>Methods in Molecular Biology</i> , 2011, 760, 53-71.	0.4	0