

Anita Grigoriadis

List of Publications by Year in Descending Order

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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.

72
papers

5,510
citations

33
h-index

74
g-index

78
ext. papers

6,436
ext. citations

9.8
avg. IF

4.92
L-index

#	Paper	IF	Citations
72	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	18	8
71	Immune Crosstalk Between Lymph Nodes and Breast Carcinomas, With a Focus on B Cells. <i>Frontiers in Molecular Biosciences</i> , 2021 , 8, 673051	5.6	3
70	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	10.1	10
69	Random Forest Modelling of High-Dimensional Mixed-Type Data for Breast Cancer Classification. <i>Cancers</i> , 2021 , 13,	6.6	3
68	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	7.8	1
67	Lipogenic signalling modulates prostate cancer cell adhesion and migration via modification of Rho GTPases. <i>Oncogene</i> , 2020 , 39, 3666-3679	9.2	17
66	Integrin-Mediated Macrophage Adhesion Promotes Lymphovascular Dissemination in Breast Cancer. <i>Cell Reports</i> , 2019 , 27, 1967-1978.e4	10.6	33
65	An innate-like V α 11 T cell compartment in the human breast is associated with remission in triple-negative breast cancer. <i>Science Translational Medicine</i> , 2019 , 11,	17.5	56
64	Pan-cancer transcriptomic analysis dissects immune and proliferative functions of APOBEC3 cytidine deaminases. <i>Nucleic Acids Research</i> , 2019 , 47, 1178-1194	20.1	29
63	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	6.1	14
62	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	12.9	24
61	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	5.3	14
60	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	7.3	18
59	Carboplatin in BRCA1/2-mutated and triple-negative breast cancer BRCAness subgroups: the TNT Trial. <i>Nature Medicine</i> , 2018 , 24, 628-637	50.5	410
58	Integrated genomics and functional validation identifies malignant cell specific dependencies in triple negative breast cancer. <i>Nature Communications</i> , 2018 , 9, 1044	17.4	29
57	Anti-Folate Receptor Alpha-Directed Antibody Therapies Restrict the Growth of Triple-negative Breast Cancer. <i>Clinical Cancer Research</i> , 2018 , 24, 5098-5111	12.9	41
56	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	6.1	37

55	Molecular patterns of cancer colonisation in lymph nodes of breast cancer patients. <i>Breast Cancer Research</i> , 2018 , 20, 143	8.3	10
54	Dual Mechanisms of LYN Kinase Dysregulation Drive Aggressive Behavior in Breast Cancer Cells. <i>Cell Reports</i> , 2018 , 25, 3674-3692.e10	10.6	31
53	Systematic identification of functionally relevant risk alleles to stratify aggressive versus indolent prostate cancer. <i>Oncotarget</i> , 2018 , 9, 12812-12824	3.3	7
52	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	4.9	8
51	ROR β Innate Lymphoid Cells Promote Lymph Node Metastasis of Breast Cancers. <i>Cancer Research</i> , 2017 , 77, 1083-1096	10.1	71
50	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	8.3	3
49	PIK3CA mutations are common in lobular carcinoma in situ, but are not a biomarker of progression. <i>Breast Cancer Research</i> , 2017 , 19, 7	8.3	13
48	Functional and prognostic significance of the genomic amplification of frizzled 6 (FZD6) in breast cancer. <i>Journal of Pathology</i> , 2017 , 241, 350-361	9.4	49
47	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	11.5	6
46	PIM1 kinase regulates cell death, tumor growth and chemotherapy response in triple-negative breast cancer. <i>Nature Medicine</i> , 2016 , 22, 1303-1313	50.5	127
45	Mutation Processes in 293-Based Clones Overexpressing the DNA Cytosine Deaminase APOBEC3B. <i>PLoS ONE</i> , 2016 , 11, e0155391	3.7	24
44	Targeting folate receptor alpha for cancer treatment. <i>Oncotarget</i> , 2016 , 7, 52553-52574	3.3	202
43	Mouse mammary stem cells express prognostic markers for triple-negative breast cancer. <i>Breast Cancer Research</i> , 2015 , 17, 31	8.3	26
42	Genomic Complexity Profiling Reveals That HORMAD1 Overexpression Contributes to Homologous Recombination Deficiency in Triple-Negative Breast Cancers. <i>Cancer Discovery</i> , 2015 , 5, 488-505	24.4	76
41	Robust BRCA1-like classification of copy number profiles of samples repeated across different datasets and platforms. <i>Molecular Oncology</i> , 2015 , 9, 1274-86	7.9	20
40	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, 101-21	4.4	15
39	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	4.8	21
38	Big Data: the challenge for small research groups in the era of cancer genomics. <i>British Journal of Cancer</i> , 2015 , 113, 1405-12	8.7	34

37	Genomic scars as biomarkers of homologous recombination deficiency and drug response in breast and ovarian cancers. <i>Breast Cancer Research</i> , 2014 , 16, 211	8.3	183
36	Identification of a gene regulatory network associated with prion replication. <i>EMBO Journal</i> , 2014 , 33, 1527-47	13	27
35	Immunological visibility: posttranscriptional regulation of human NKG2D ligands by the EGF receptor pathway. <i>Science Translational Medicine</i> , 2014 , 6, 231ra49	17.5	38
34	IL15RA drives antagonistic mechanisms of cancer development and immune control in lymphocyte-enriched triple-negative breast cancers. <i>Cancer Research</i> , 2014 , 74, 4908-21	10.1	25
33	Comparison of basal-like triple-negative breast cancer defined by morphology, immunohistochemistry and transcriptional profiles. <i>Modern Pathology</i> , 2013 , 26, 955-66	9.8	63
32	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	4.5	68
31	Prognostic signatures in breast cancer: correlation does not imply causation. <i>Breast Cancer Research</i> , 2012 , 14, 313	8.3	4
30	Molecular characterisation of cell line models for triple-negative breast cancers. <i>BMC Genomics</i> , 2012 , 13, 619	4.5	60
29	A whole-genome massively parallel sequencing analysis of BRCA1 mutant oestrogen receptor-negative and -positive breast cancers. <i>Journal of Pathology</i> , 2012 , 227, 29-41	9.4	44
28	Profiling the immune stromal interface in breast cancer and its potential for clinical impact. <i>Breast Care</i> , 2012 , 7, 273-80	2.4	6
27	The ForeSee (4C) approach for integrative analysis in gene discovery. <i>Methods in Molecular Biology</i> , 2011 , 760, 53-71	1.4	
26	Selectin ligand sialyl-Lewis x antigen drives metastasis of hormone-dependent breast cancers. <i>Cancer Research</i> , 2011 , 71, 7683-93	10.1	126
25	DART: Denoising Algorithm based on Relevance network Topology improves molecular pathway activity inference. <i>BMC Bioinformatics</i> , 2011 , 12, 403	3.6	22
24	IDH1 and IDH2 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, 334-43	9.4	690
23	Microarray-based class discovery for molecular classification of breast cancer: analysis of interobserver agreement. <i>Journal of the National Cancer Institute</i> , 2011 , 103, 662-73	9.7	105
22	FGFR1 amplification drives endocrine therapy resistance and is a therapeutic target in breast cancer. <i>Cancer Research</i> , 2010 , 70, 2085-94	10.1	533
21	GDN 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, 1526-35	6.6	52
20	BRCA1 basal-like breast cancers originate from luminal epithelial progenitors and not from basal stem cells. <i>Cell Stem Cell</i> , 2010 , 7, 403-17	18	518

19	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, 575-89	4.4	132
18	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	3.5	9
17	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	9.4	29
16	Comparative Membranome expression analysis in primary tumors and derived cell lines. <i>PLoS ONE</i> , 2010 , 5, e11742	3.7	14
15	Integrated functional, gene expression and genomic analysis for the identification of cancer targets. <i>PLoS ONE</i> , 2009 , 4, e5120	3.7	85
14	Molecular and phenotypic characterisation of paediatric glioma cell lines as models for preclinical drug development. <i>PLoS ONE</i> , 2009 , 4, e5209	3.7	88
13	Tiling path genomic profiling of grade 3 invasive ductal breast cancers. <i>Clinical Cancer Research</i> , 2009 , 15, 2711-22	12.9	138
12	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, 13493-8	11.5	78
11	Identification of differentially expressed sense and antisense transcript pairs in breast epithelial tissues. <i>BMC Genomics</i> , 2009 , 10, 324	4.5	25
10	A high-resolution integrated analysis of genetic and expression profiles of breast cancer cell lines. <i>Breast Cancer Research and Treatment</i> , 2009 , 118, 481-98	4.4	55
9	Genome-wide transcriptomic profiling of microdissected human breast tissue reveals differential expression of KIT (c-Kit, CD117) and oestrogen receptor-alpha (ERalpha) in response to therapeutic radiation. <i>Journal of Pathology</i> , 2009 , 219, 131-40	9.4	32
8	Conditional deletion of the Lkb1 gene in the mouse mammary gland induces tumour formation. <i>Journal of Pathology</i> , 2009 , 219, 306-16	9.4	27
7	Transcriptome analysis of mammary epithelial subpopulations identifies novel determinants of lineage commitment and cell fate. <i>BMC Genomics</i> , 2008 , 9, 591	4.5	132
6	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, 7635-44	12.9	22
5	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, 607-15	5	18
4	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	8.3	24
3	FGFR1 emerges as a potential therapeutic target for lobular breast carcinomas. <i>Clinical Cancer Research</i> , 2006 , 12, 6652-62	12.9	228
2	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	8.3	103

- 1 Expression profiling of purified normal human luminal and myoepithelial breast cells: identification of novel prognostic markers for breast cancer. *Cancer Research*, **2004**, 64, 3037-45 10.1 208