## Adriane F Evangelista

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Comprehensive Molecular Landscape of Cetuximab Resistance in Head and Neck Cancer Cell Lines. Cells, 2022, 11, 154.	1.8	9
2	Transcript Expression Profiles and MicroRNA Regulation Indicate an Upregulation of Processes Linked to Oxidative Stress, DNA Repair, Cell Death, and Inflammation in Type 1 Diabetes Mellitus Patients. Journal of Diabetes Research, 2022, 2022, 1-15.	1.0	6
3	Cutaneous and acral melanoma cross-OMICs reveals prognostic cancer drivers associated with pathobiology and ultraviolet exposure. Nature Communications, 2022, 13, .	5.8	7
4	Analysis of RPL37A, MTSS1, and HTRA1 expression as potential markers for pathologic complete response and survival. Breast Cancer, 2021, 28, 307-320.	1.3	5
5	Simultaneous analysis of ALK, RET, and ROS1 gene fusions by NanoString in Brazilian lung adenocarcinoma patients. Translational Lung Cancer Research, 2021, 10, 292-303.	1.3	4
6	Somatic Copy Number Alterations and Associated Genes in Clear-Cell Renal-Cell Carcinoma in Brazilian Patients. International Journal of Molecular Sciences, 2021, 22, 2265.	1.8	12
7	Bioprospecting of Natural Compounds from Brazilian Cerrado Biome Plants in Human Cervical Cancer Cell Lines. International Journal of Molecular Sciences, 2021, 22, 3383.	1.8	9
8	Role of glioblastoma stem cells in cancer therapeutic resistance: a perspective on antineoplastic agents from natural sources and chemical derivatives. Stem Cell Research and Therapy, 2021, 12, 206.	2.4	91
9	MicroRNA Biomarkers of High-Grade Cervical Intraepithelial Neoplasia in Liquid Biopsy. BioMed Research International, 2021, 2021, 1-9.	0.9	9
10	A 4-Gene Signature Associated With Recurrence in Low- and Intermediate-Risk Endometrial Cancer. Frontiers in Oncology, 2021, 11, 729219.	1.3	7
11	Integrated analysis of mRNA and miRNA profiles revealed the role of miR-193 and miR-210 as potential regulatory biomarkers in different molecular subtypes of breast cancer. BMC Cancer, 2021, 21, 76.	1.1	12
12	Profile of esophageal squamous cell carcinoma mutations in Brazilian patients. Scientific Reports, 2021, 11, 20596.	1.6	2
13	A computational approach for the discovery of significant cancer genes by weighted mutation and asymmetric spreading strength in networks. Scientific Reports, 2021, 11, 23551.	1.6	1
14	Using Co-segregation and Loss of Heterozygosity Analysis to Define the Pathogenicity of Unclassified Variants in Hereditary Breast Cancer Patients. Frontiers in Oncology, 2020, 10, 571330.	1.3	5
15	Pyknon-Containing Transcripts Are Downregulated in Colorectal Cancer Tumors, and Loss of PYK44 Is Associated With Worse Patient Outcome. Frontiers in Genetics, 2020, 11, 581454.	1.1	3
16	The combination of coffee compounds attenuates early fibrosis-associated hepatocarcinogenesis in mice: involvement of miRNA profile modulation. Journal of Nutritional Biochemistry, 2020, 85, 108479.	1.9	13
17	Deregulated microRNAs Are Associated with Patient Survival and Predicted to Target Genes That Modulate Lung Cancer Signaling Pathways. Cancers, 2020, 12, 2711.	1.7	5
18	Approaches for the identification of driver mutations in cancer: A tutorial from a computational perspective. Journal of Bioinformatics and Computational Biology, 2020, 18, 2050016.	0.3	4

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19	miRNA expression profiling of hereditary breast tumors from BRCA1- and BRCA2-germline mutation carriers in Brazil. BMC Cancer, 2020, 20, 143.	1.1	10
20	Expression of GNAS, TP53, and PTEN Improves the Patient Prognostication in Sonic Hedgehog (SHH) Medulloblastoma Subgroup. Journal of Molecular Diagnostics, 2020, 22, 957-966.	1.2	11
21	Combining Mutation and Gene Network Data in a Machine Learning Approach for False-Positive Cancer Driver Gene Discovery. Lecture Notes in Computer Science, 2020, , 81-92.	1.0	2
22	Euphol, a tetracyclic triterpene, from Euphorbia tirucalli induces autophagy and sensitizes temozolomide cytotoxicity on glioblastoma cells. Investigational New Drugs, 2019, 37, 223-237.	1.2	33
23	Identification of Cell-Free Circulating MicroRNAs for the Detection of Early Breast Cancer and Molecular Subtyping. Journal of Oncology, 2019, 2019, 1-11.	0.6	30
24	The role of single-nucleotide polymorphism (SNPs) in toxicity of induction chemotherapy based on cisplatin and paclitaxel in patients with advanced head and neck cancer. Oral Oncology, 2019, 98, 48-52.	0.8	8
25	Mutation profiling of cancer drivers in Brazilian colorectal cancer. Scientific Reports, 2019, 9, 13687.	1.6	31
26	Identification and performance evaluation of housekeeping genes for microRNA expression normalization by reverse transcription‑quantitative PCR using liquid‑based cervical cytology samples. Oncology Letters, 2019, 18, 4753-4761.	0.8	6
27	Establishment, molecular and biological characterization of HCB-514: a novel human cervical cancer cell line. Scientific Reports, 2019, 9, 1913.	1.6	14
28	Semi-Synthetic Ingenol Derivative from Euphorbia tirucalli Inhibits Protein Kinase C Isotypes and Promotes Autophagy and S-phase Arrest on Glioma Cell Lines. Molecules, 2019, 24, 4265.	1.7	8
29	MicroRNA-27a-5p regulation by promoter methylation and MYC signaling in prostate carcinogenesis. Cell Death and Disease, 2018, 9, 167.	2.7	48
30	Changes in Expression Profiles Revealed by Transcriptomic Analysis in Peripheral Blood Mononuclear Cells of Alzheimer's Disease Patients. Journal of Alzheimer's Disease, 2018, 66, 1483-1495.	1.2	28
31	Reproducibility of the NanoString 22â€gene molecular subgroup assay for improved prognostic prediction of medulloblastoma. Neuropathology, 2018, 38, 475-483.	0.7	26
32	<b>Behavior of α-tomatine and tomatidine against several genera of trypanosomatids from insects and plants and <i>Trypanosoma cruzi. Acta Scientiarum - Biological Sciences, 2018, 40, 41853.</i></b>	0.3	3
33	Expression of tumor suppressors miR-195 and let-7a as potential biomarkers of invasive breast cancer. Clinics, 2018, 73, e184.	0.6	24
34	Genetic alterations detected by comparative genomic hybridization in BRCAX breast and ovarian cancers of Brazilian population. Oncotarget, 2018, 9, 27525-27534.	0.8	4
35	Abstract A33: Molecular classification of Brazilian medulloblastoma by a NanoString gene panel. , 2018, , .		0
36	Abstract A34: SNPs as predictors in the tailoring of treatment for HNSCC patients undergoing organ		0

preservation protocols., 2018,,.

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37	Abstract A29: Omics profile of two immortalized Brazilian glioblastoma cell cultures. , 2018, , .		0
38	Abstract A35: Somatic mutation profile of a panel of oncogenes and tumor suppressor genes in colorectal cancer in a Brazilian population. , 2018, , .		0
39	Abstract 5380: Whole-exome sequencing of Brazilian non-small cell lung cancer. , 2018, , .		Ο
40	Abstract 3998: Integrative molecular analysis uncovers key molecules and signaling pathways regulated by RKIP in gastrointestinal stromal tumors (GISTs). , 2018, , .		0
41	Molecular characterization of breast cancer cell lines by clinical immunohistochemical markers. Oncology Letters, 2017, 13, 4708-4712.	0.8	40
42	Overexpression of mir-183 and mir-494 promotes proliferation and migration in human breast cancer cell lines. Oncology Letters, 2017, 14, 1054-1060.	0.8	40
43	Detection of ALK fusion transcripts in FFPE lung cancer samples by NanoString technology. BMC Pulmonary Medicine, 2017, 17, 86.	0.8	30
44	HER Family Receptors are Important Theranostic Biomarkers for Cervical Cancer: Blocking Glucose Metabolism Enhances the Therapeutic Effect of HER Inhibitors. Theranostics, 2017, 7, 717-732.	4.6	31
45	MiR-21 as prognostic biomarker in head and neck squamous cell carcinoma patients undergoing an organ preservation protocol. Oncotarget, 2017, 8, 9911-9921.	0.8	48
46	Abstract 3386: Brazilian melanoma genome project: mutational landscape based on whole-genome sequencing. , 2017, , .		2
47	Correction, article no. 3671: Importance of the patient's clinical questionnaire for the diagnosis of skin cancer through teledermatology in remote areas of Brazil. Rural and Remote Health, 2017, 17, 4496.	0.4	1
48	MicroRNA profiling in human breast cancer cell lines exposed to the anti-neoplastic drug cediranib. Oncology Reports, 2016, 36, 3197-3206.	1.2	7
49	Vemurafenib resistance increases melanoma invasiveness and modulates the tumor microenvironment by MMP-2 upregulation. Pharmacological Research, 2016, 111, 523-533.	3.1	70
50	PO41 Serum and tissue expression of tumor suppressors miR-195 and let-7A in breast cancer. Breast, 2015, 24, S40.	0.9	0
51	Assessment of DNA damage and mRNA/miRNA transcriptional expression profiles in hyperglycemic versus non-hyperglycemic patients with type 2 diabetes mellitus. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2015, 776, 98-110.	0.4	22
52	Accuracy of microRNAs as markers for the detection of neck lymph node metastases in patients with head and neck squamous cell carcinoma. BMC Medicine, 2015, 13, 108.	2.3	33
53	Multiple myeloma cell lines and primary tumors proteome: protein biosynthesis and Immune system as potential therapeutic targets. Genes and Cancer, 2015, 6, 462-471.	0.6	16
54	MicroRNA expression as risk biomarker of breast cancer metastasis: a pilot retrospective case-cohort study. BMC Cancer, 2014, 14, 739.	1.1	45

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55	Differential Transcript Profiles of MHC Class Ib(Qa-1, Qa-2, and Qa-10) and <i>Aire</i> Genes during the Ontogeny of Thymus and Other Tissues. Journal of Immunology Research, 2014, 2014, 1-12.	0.9	12
56	MicroRNA expression profiling and functional annotation analysis of their targets in patients with type 1 diabetes mellitus. Gene, 2014, 539, 213-223.	1.0	65
57	Integrative analysis of the transcriptome profiles observed in type 1, type 2 and gestational diabetes mellitus reveals the role of inflammation. BMC Medical Genomics, 2014, 7, 28.	0.7	28
58	P102. Human Immunology, 2014, 75, 122.	1.2	0
59	A microRNA signature profile in EBV+ diffuse large B-cell lymphoma of the elderly. Oncotarget, 2014, 5, 11813-11826.	0.8	32
60	MicroRNAs in Cancer. , 2014, , 181-193.		0
61	Transcriptome Analysis During Normal Human Mesenchymal Stem Cell Differentiation. , 2014, , 109-119.		1
62	Differential expression profile of microRNAs associated with human breast cancer progression. BMC Proceedings, 2013, 7, .	1.8	1
63	MicroRNAs from peripheral blood mononuclear cells as biomarkers for detection of preclinical fibrosarcoma. BMC Proceedings, 2013, 7, P2.	1.8	1
64	Autoimmune regulator (Aire) controls the expression of microRNAs in medullary thymic epithelial cells. Immunobiology, 2013, 218, 554-560.	0.8	57
65	Transcriptome meta-analysis of peripheral lymphomononuclear cells indicates that gestational diabetes is closer to type 1 diabetes than to type 2 diabetes mellitus. Molecular Biology Reports, 2013, 40, 5351-5358.	1.0	24
66	Identifying common and specific microRNAs expressed in peripheral blood mononuclear cell of type 1, type 2, and gestational diabetes mellitus patients. BMC Research Notes, 2013, 6, 491.	0.6	132
67	Phospholipase gene expression during Paracoccidioides brasiliensis morphological transition and infection. Memorias Do Instituto Oswaldo Cruz, 2013, 108, 808-811.	0.8	7
68	Micro-RNA Expression Profile Reveals MiR-222 As a Potential Biomarker For EBV-Positive Diffuse Large B-Cell Lymphoma. Blood, 2013, 122, 4269-4269.	0.6	1
69	Gene expression profiles displayed by peripheral blood mononuclear cells from patients with type 2 diabetes mellitus focusing on biological processes implicated on the pathogenesis of the disease. Gene, 2012, 511, 151-160.	1.0	54
70	Expression of genes related to apoptosis, cell cycle and signaling pathways are independent of TP53 status in urinary bladder cancer cells. Molecular Biology Reports, 2011, 38, 4159-4170.	1.0	21
71	Transcriptome Metanalysis of Peripheral Blood Mononuclear Cells of Type 1, Type 2 and Gestational Diabetes Mellitus Patients Features Modulated Immune System and Metabolism Genes. , 2011, , P3-463-P3-463.		0
72	Evidence for a network transcriptional control of promiscuous gene expression in medullary thymic epithelial cells. Molecular Immunology, 2009, 46, 3240-3244.	1.0	26

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73	Gene Expression Profiles Stratified according to Type 1 Diabetes Mellitus Susceptibility Regions. Annals of the New York Academy of Sciences, 2008, 1150, 282-289.	1.8	13

A proposal of a graph-based computational method for ranking significant set of related genes in cancer. , 0, , .