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List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

1,367
citations

471061

17
h-index

344852

36
g-index

43
all docs

43
docs citations

43
times ranked

2487
citing authors

#	ARTICLE	IF	CITATIONS
1	Methylome sequencing in triple-negative breast cancer reveals distinct methylation clusters with prognostic value. <i>Nature Communications</i> , 2015, 6, 5899.	5.8	162
2	Up-regulation of Mcl-1 Is Critical for Survival of Human Melanoma Cells upon Endoplasmic Reticulum Stress. <i>Cancer Research</i> , 2008, 68, 6708-6717.	0.4	129
3	Small Molecular Weight Variants of p53 Are Expressed in Human Melanoma Cells and Are Induced by the DNA-Damaging Agent Cisplatin. <i>Clinical Cancer Research</i> , 2008, 14, 1659-1668.	3.2	112
4	BRIP1, PALB2, and RAD51C mutation analysis reveals their relative importance as genetic susceptibility factors for breast cancer. <i>Breast Cancer Research and Treatment</i> , 2011, 127, 853-859.	1.1	95
5	P53 in human melanoma fails to regulate target genes associated with apoptosis and the cell cycle and may contribute to proliferation. <i>BMC Cancer</i> , 2011, 11, 203.	1.1	88
6	Decreased expression of key tumour suppressor microRNAs is associated with lymph node metastases in triple negative breast cancer. <i>BMC Cancer</i> , 2014, 14, 51.	1.1	73
7	Glucose-regulated protein 78 antagonizes cisplatin and adriamycin in human melanoma cells. <i>Carcinogenesis</i> , 2009, 30, 197-204.	1.3	68
8	The relative mRNA expression of p53 isoforms in breast cancer is associated with clinical features and outcome. <i>Carcinogenesis</i> , 2014, 35, 586-596.	1.3	67
9	Proteotranscriptomic Profiling of 231-BR Breast Cancer Cells: Identification of Potential Biomarkers and Therapeutic Targets for Brain Metastasis. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2316-2330.	2.5	59
10	miRNAs and Other Epigenetic Changes as Biomarkers in Triple Negative Breast Cancer. <i>International Journal of Molecular Sciences</i> , 2015, 16, 28347-28376.	1.8	56
11	DNA methylation profile of triple negative breast cancer-specific genes comparing lymph node positive patients to lymph node negative patients. <i>Scientific Reports</i> , 2016, 6, 33435.	1.6	56
12	Novel genes associated with lymph node metastasis in triple negative breast cancer. <i>Scientific Reports</i> , 2015, 5, 15832.	1.6	48
13	STaRRRT: a table of short tandem repeats in regulatory regions of the human genome. <i>BMC Genomics</i> , 2013, 14, 795.	1.2	33
14	The expression of Dicer and Drosha in matched normal tissues, tumours and lymph node metastases in triple negative breast cancer. <i>BMC Cancer</i> , 2014, 14, 253.	1.1	30
15	Activation of Jun N-terminal kinase is a mediator of vincristine-induced apoptosis of melanoma cells. <i>Anti-Cancer Drugs</i> , 2008, 19, 189-200.	0.7	29
16	Nucleotide Excision Repair Gene Expression after Cisplatin Treatment in Melanoma. <i>Cancer Research</i> , 2010, 70, 7918-7926.	0.4	23
17	Good Cop, Bad Cop: Defining the Roles of p53 in Cancer and Aging. <i>Cancers</i> , 2020, 12, 1659.	1.7	22
18	The Roles of Non-Coding RNAs in Tumor-Associated Lymphangiogenesis. <i>Cancers</i> , 2020, 12, 3290.	1.7	21

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19	Copy number variation in triple-negative breast cancer samples associated with lymph node metastasis. <i>Neoplasia</i> , 2021, 23, 743-753.	2.3	21
20	Regulation of the human placental (pro)renin receptor-prorenin-angiotensin system by microRNAs. <i>Molecular Human Reproduction</i> , 2018, 24, 453-464.	1.3	19
21	The presence of the intron 3 16 bp duplication polymorphism of p53(rs17878362) in breast cancer is associated with a low Δ 40p53:p53 ratio and better outcome. <i>Carcinogenesis</i> , 2016, 37, 81-86.	1.3	16
22	Molecular patterns of cancer colonisation in lymph nodes of breast cancer patients. <i>Breast Cancer Research</i> , 2018, 20, 143.	2.2	16
23	Regulation of the interferon-gamma (IFN- γ) pathway by p63 and Δ 133p53 isoform in different breast cancer subtypes. <i>Oncotarget</i> , 2018, 9, 29146-29161.	0.8	16
24	Effect of p53 and its N-terminally truncated isoform, Δ 40p53, on breast cancer migration and invasion. <i>Molecular Oncology</i> , 2022, 16, 447-465.	2.1	15
25	Low prevalence of germline <i>PALB2</i> mutations in Australian triple-negative breast cancer. <i>International Journal of Cancer</i> , 2014, 134, 301-305.	2.3	13
26	Intronic TP53 Polymorphisms Are Associated with Increased Δ 133TP53 Transcript, Immune Infiltration and Cancer Risk. <i>Cancers</i> , 2020, 12, 2472.	1.7	13
27	Comparison of Three Different Methods for Determining Cell Proliferation in Breast Cancer Cell Lines. <i>Journal of Visualized Experiments</i> , 2016, , .	0.2	9
28	Genome-wide miRNA, gene and methylation analysis of triple negative breast cancer to identify changes associated with lymph node metastases. <i>Genomics Data</i> , 2017, 14, 1-4.	1.3	9
29	Regulators of Global Genome Repair Do Not Respond to DNA Damaging Therapy but Correlate with Survival in Melanoma. <i>PLoS ONE</i> , 2013, 8, e70424.	1.1	8
30	Assessment of Potential Risk Factors and Skin Ultrasound Presentation Associated with Breast Cancer-Related Lymphedema in Long-Term Breast Cancer Survivors. <i>Diagnostics</i> , 2021, 11, 1303.	1.3	8
31	Cross-Cultural Adaptation of the Functional Assessment of Cancer Therapy-Breast (FACT-B) in Malaysian Breast Cancer Survivors. <i>Asian Pacific Journal of Cancer Prevention</i> , 2021, 22, 1055-1061.	0.5	7
32	Cytoplasmic p53 Δ 2 Isoforms Are Associated with Worse Disease-Free Survival in Breast Cancer. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6670.	1.8	7
33	Comparison of the QuantiGene 2.0 Assay and Real-Time RT-PCR in the Detection of p53 Isoform mRNA Expression in Formalin-Fixed Paraffin-Embedded Tissues- A Preliminary Study. <i>PLoS ONE</i> , 2016, 11, e0165930.	1.1	6
34	The intron 3 16bp duplication polymorphism of p53 (rs17878362) is not associated with increased risk of developing triple-negative breast cancer. <i>Breast Cancer Research and Treatment</i> , 2019, 173, 727-733.	1.1	5
35	Crosstalk Between microRNAs and the Pathological Features of Secondary Lymphedema. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 732415.	1.8	3
36	A novel polymorphic repeat in the upstream regulatory region of the estrogen-induced gene EIG121 is not associated with the risk of developing breast or endometrial cancer. <i>BMC Research Notes</i> , 2016, 9, 287.	0.6	1

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37	A polymorphic repeat in the IGF1 promoter influences the risk of endometrial cancer. <i>Endocrine Connections</i> , 2016, 5, 115-122.	0.8	1
38	A Simple Migration/Invasion Workflow Using an Automated Live-cell Imager. <i>Journal of Visualized Experiments</i> , 2019, , .	0.2	1
39	Switching off Cancer: Is There a Role for Epigenetics?. <i>Cancers</i> , 2021, 13, 1272.	1.7	1
40	Verification and Validation of a Four-Gene Panel as a Prognostic Indicator in Triple Negative Breast Cancer. <i>Frontiers in Oncology</i> , 2022, 12, 821334.	1.3	1
41	Genetic insights into breast cancer risk. <i>Hereditary Cancer in Clinical Practice</i> , 2015, 13, .	0.6	0
42	Abstract 3938: Altered nucleotide excision repair gene expression after cisplatin treatment in melanoma. , 2010, , .		0
43	Abstract 3944: Base excision repair and gene expression profiling in malignant melanoma. , 2010, , .		0