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List of Publications by Year in descending order

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Version: 2024-02-01

44
papers

1,652
citations

331670

21
h-index

302126

39
g-index

45
all docs

45
docs citations

45
times ranked

2748
citing authors

#	ARTICLE	IF	CITATIONS
1	The genomic landscape of metastatic breast cancer highlights changes in mutation and signature frequencies. <i>Nature Genetics</i> , 2019, 51, 1450-1458.	21.4	250
2	Methylation-mediated silencing and tumour suppressive function of hsa-miR-124 in cervical cancer. <i>Molecular Cancer</i> , 2010, 9, 167.	19.2	217
3	Gene length corrected trimmed mean of M-values (GeTMM) processing of RNA-seq data performs similarly in intersample analyses while improving intrasample comparisons. <i>BMC Bioinformatics</i> , 2018, 19, 236.	2.6	105
4	The circular RNome of primary breast cancer. <i>Genome Research</i> , 2019, 29, 356-366.	5.5	85
5	Better prediction by use of co-regularized ridge regression. <i>Statistics in Medicine</i> , 2016, 35, 368-381.	1.6	78
6	Genome-wide DNA Methylation Profiling Reveals Methylation Markers Associated with 3q Gain for Detection of Cervical Precancer and Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 3813-3822.	7.0	68
7	Methylation-mediated transcriptional repression of microRNAs during cervical carcinogenesis. <i>Epigenetics</i> , 2013, 8, 220-228.	2.7	67
8	Integrated genomic and transcriptional profiling identifies chromosomal loci with altered gene expression in cervical cancer. <i>Genes Chromosomes and Cancer</i> , 2008, 47, 890-905.	2.8	59
9	Genomic profiling identifies common HPV-associated chromosomal alterations in squamous cell carcinomas of cervix and head and neck. <i>BMC Medical Genomics</i> , 2009, 2, 32.	1.5	56
10	Identification and Validation of a 3-Gene Methylation Classifier for HPV-Based Cervical Screening on Self-Samples. <i>Clinical Cancer Research</i> , 2018, 24, 3456-3464.	7.0	55
11	Chromosomal Signatures of a Subset of High-Grade Premalignant Cervical Lesions Closely Resemble Invasive Carcinomas. <i>Cancer Research</i> , 2009, 69, 647-655.	0.9	53
12	Interplay between promoter methylation and chromosomal loss in gene silencing at 3p11-p14 in cervical cancer. <i>Epigenetics</i> , 2015, 10, 970-980.	2.7	47
13	Molecular events leading to HPV-induced high grade neoplasia. <i>Papillomavirus Research (Amsterdam, Neth)</i> 2014, 1, 1-10. doi:10.1016/j.pvr.2014.01.001	4.5	40
14	Whole genome sequencing of metastatic colorectal cancer reveals prior treatment effects and specific metastasis features. <i>Nature Communications</i> , 2021, 12, 574.	12.8	39
15	Chromosomal profiles of high-grade cervical intraepithelial neoplasia relate to duration of preceding high-risk human papillomavirus infection. <i>International Journal of Cancer</i> , 2012, 131, E579-85.	5.1	37
16	High-throughput isolation of circulating tumor DNA: a comparison of automated platforms. <i>Molecular Oncology</i> , 2019, 13, 392-402.	4.6	37
17	Pharmacological CDK4/6 inhibition reveals a p53-dependent senescent state with restricted toxicity. <i>EMBO Journal</i> , 2022, 41, e108946.	7.8	35
18	Confirmation of a metastasis-specific microRNA signature in primary colon cancer. <i>Scientific Reports</i> , 2018, 8, 5242.	3.3	33

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19	Genome-wide microRNA analysis of HPV-positive self-samples yields novel triage markers for early detection of cervical cancer. <i>International Journal of Cancer</i> , 2019, 144, 372-379.	5.1	29
20	miR-9-5p Exerts a Dual Role in Cervical Cancer and Targets Transcription Factor TWIST1. <i>Cells</i> , 2020, 9, 65.	4.1	25
21	Immortalization capacity of HPV types is inversely related to chromosomal instability. <i>Oncotarget</i> , 2016, 7, 37608-37621.	1.8	25
22	Aberrant methylation-mediated silencing of microRNAs contributes to HPV-induced anchorage independence. <i>Oncotarget</i> , 2016, 7, 43805-43819.	1.8	22
23	A Strategy to Find Suitable Reference Genes for miRNA Quantitative PCR Analysis and Its Application to Cervical Specimens. <i>Journal of Molecular Diagnostics</i> , 2017, 19, 625-637.	2.8	21
24	Molecular heterogeneity in human papillomavirus-dependent and -independent vulvar carcinogenesis. <i>Cancer Medicine</i> , 2018, 7, 4542-4553.	2.8	21
25	Identification of Deregulated Pathways, Key Regulators, and Novel miRNA-mRNA Interactions in HPV-Mediated Transformation. <i>Cancers</i> , 2020, 12, 700.	3.7	20
26	Triage of high-risk HPV-positive women in population-based screening by miRNA expression analysis in cervical scrapes; a feasibility study. <i>Clinical Epigenetics</i> , 2018, 10, 76.	4.1	18
27	Detection of Aneuploidy in Cerebrospinal Fluid from Patients with Breast Cancer Can Improve Diagnosis of Leptomeningeal Metastases. <i>Clinical Cancer Research</i> , 2021, 27, 2798-2806.	7.0	14
28	Validity and utility of HER2/ERBB2 copy number variation assessed in liquid biopsies from breast cancer patients: A systematic review. <i>Cancer Treatment Reviews</i> , 2022, 106, 102384.	7.7	12
29	Better diagnostic signatures from RNAseq data through use of auxiliary co-data. <i>Bioinformatics</i> , 2017, 33, 1572-1574.	4.1	11
30	Improved high-dimensional prediction with Random Forests by the use of co-data. <i>BMC Bioinformatics</i> , 2017, 18, 584.	2.6	11
31	High-throughput and affordable genome-wide methylation profiling of circulating cell-free DNA by methylated DNA sequencing (MeD-seq) of LpnPI digested fragments. <i>Clinical Epigenetics</i> , 2021, 13, 196.	4.1	10
32	Genome-wide aneuploidy detected by mFast-SeqS in circulating cell-free DNA is associated with poor response to pembrolizumab in patients with advanced urothelial cancer. <i>Molecular Oncology</i> , 2022, 16, 2086-2097.	4.6	8
33	Complementarity between miRNA expression analysis and DNA methylation analysis in hrHPV-positive cervical scrapes for the detection of cervical disease. <i>Epigenetics</i> , 2019, 14, 558-567.	2.7	7
34	Ridge estimation of the VAR(1) model and its time series chain graph from multivariate time-course omics data. <i>Biometrical Journal</i> , 2017, 59, 172-191.	1.0	6
35	A Systematic Review of the Use of Circulating Cell-Free DNA Dynamics to Monitor Response to Treatment in Metastatic Breast Cancer Patients. <i>Cancers</i> , 2021, 13, 1811.	3.7	6
36	A pipeline for copy number profiling of single circulating tumour cells to assess inpatient tumour heterogeneity. <i>Molecular Oncology</i> , 2022, 16, 2981-3000.	4.6	6

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37	ESR1 Methylation Measured in Cell-Free DNA to Evaluate Endocrine Resistance in Metastatic Breast Cancer Patients. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5631.	4.1	4
38	A panel of DNA methylation markers for the classification of consensus molecular subtypes 2 and 3 in patients with colorectal cancer. <i>Molecular Oncology</i> , 2021, 15, 3348-3362.	4.6	3
39	Functional Screen for microRNAs Suppressing Anchorage-Independent Growth in Human Cervical Cancer Cells. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4791.	4.1	3
40	Lost by Transcription: Fork Failures, Elevated Expression, and Clinical Consequences Related to Deletions in Metastatic Colorectal Cancer. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5080.	4.1	2
41	Ridge estimation of network models from time-course omics data. <i>Biometrical Journal</i> , 2019, 61, 391-405.	1.0	1
42	Circular RNA in Chemonaive Lymph Node Negative Colon Cancer Patients. <i>Cancers</i> , 2021, 13, 1903.	3.7	1
43	Abstract P2-01-17: Circulating tumor cell count and levels of circulating tumor DNA are complementary prognostic biomarkers in metastatic breast cancer - A pilot study. <i>Cancer Research</i> , 2022, 82, P2-01-17-P2-01-17.	0.9	1
44	A tale on rabbit ears and pan-handles, the rings that rule all. <i>EBioMedicine</i> , 2019, 49, 17-18.	6.1	0