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List of Publications by Year in descending order

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Version: 2024-02-01

86
papers

6,842
citations

117625
34
h-index

66911
78
g-index

94
all docs

94
docs citations

94
times ranked

14902
citing authors

#	ARTICLE	IF	CITATIONS
1	Abstract P1-08-09: High mid-treatment RNA disruption in patients with HER2-negative breast cancer predicts survival benefit after neoadjuvant chemotherapy. Cancer Research, 2022, 82, P1-08-09-P1-08-09.	0.9	3
2	NRF2 drives an oxidative stress response predictive of breast cancer. Free Radical Biology and Medicine, 2022, 184, 170-184.	2.9	8
3	Prognostic Significance of the Loss of Heterozygosity of KRAS in Early-Stage Lung Adenocarcinoma. Frontiers in Oncology, 2022, 12, 873532.	2.8	3
4	Proteome Analysis of Pancreatic Tumors Implicates Extracellular Matrix in Patient Outcome. Cancer Research Communications, 2022, 2, 434-446.	1.7	1
5	Protein Signature Predicts Response to Neoadjuvant Treatment With Chemotherapy and Bevacizumab in HER2-Negative Breast Cancers. JCO Precision Oncology, 2021, 5, 286-306.	3.0	5
6	A Systemic Protein Deviation Score Linked to PD-1+ CD8+ T Cell Expansion That Predicts Overall Survival in Diffuse Large B Cell Lymphoma. Med, 2021, 2, 180-195.e5.	4.4	0
7	miRNA normalization enables joint analysis of several datasets to increase sensitivity and to reveal novel miRNAs differentially expressed in breast cancer. PLoS Computational Biology, 2021, 17, e1008608.	3.2	1
8	Clinicopathological factors associated with tumour-specific mutation detection in plasma of patients with <i>RAS</i> mutated or <i>BRAF</i> mutated metastatic colorectal cancer. International Journal of Cancer, 2021, 149, 1385-1397.	5.1	10
9	Whole genome copy number analyses reveal a highly aberrant genome in TP53 mutant lung adenocarcinoma tumors. BMC Cancer, 2021, 21, 1089.	2.6	3
10	Sample Preparation Approach Influences PAM50 Risk of Recurrence Score in Early Breast Cancer. Cancers, 2021, 13, 6118.	3.7	10
11	Immune phenotype of tumor microenvironment predicts response to bevacizumab in neoadjuvant treatment of <i>ER</i> -positive breast cancer. International Journal of Cancer, 2020, 147, 2515-2525.	5.1	13
12	Mutational dynamics and immune evasion in diffuse large B-cell lymphoma explored in a relapse-enriched patient series. Blood Advances, 2020, 4, 1859-1866.	5.2	7
13	Molecularly matched therapy in the context of sensitivity, resistance, and safety; patient outcomes in end-stage cancer – the MetAction study. Acta Oncologica, 2020, 59, 733-740.	1.8	8
14	Contrasting DCIS and invasive breast cancer by subtype suggests basal-like DCIS as distinct lesions. Npj Breast Cancer, 2020, 6, 26.	5.2	24
15	DNA copy number motifs are strong and independent predictors of survival in breast cancer. Communications Biology, 2020, 3, 153.	4.4	9
16	miRNA expression changes during the course of neoadjuvant bevacizumab and chemotherapy treatment in breast cancer. Molecular Oncology, 2019, 13, 2278-2296.	4.6	30
17	A clinico-molecular predictor identifies follicular lymphoma patients at risk of early transformation after first-line immunotherapy. Haematologica, 2019, 104, e460-e464.	3.5	5
18	The immune microenvironment in non-small cell lung cancer is predictive of prognosis after surgery. Molecular Oncology, 2019, 13, 1166-1179.	4.6	57

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19	Breast cancer quantitative proteome and proteogenomic landscape. <i>Nature Communications</i> , 2019, 10, 1600.	12.8	152
20	PathTracer: High-sensitivity detection of differential pathway activity in tumours. <i>Scientific Reports</i> , 2019, 9, 16332.	3.3	2
21	Convergence of risk prediction models in follicular lymphoma. <i>Haematologica</i> , 2019, 104, e252-e255.	3.5	9
22	Human ectoparasites and the spread of plague in Europe during the Second Pandemic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1304-1309.	7.1	110
23	N-glycan signatures identified in tumor interstitial fluid and serum of breast cancer patients: association with tumor biology and clinical outcome. <i>Molecular Oncology</i> , 2018, 12, 972-990.	4.6	24
24	T Cells Expressing Checkpoint Receptor TIGIT Are Enriched in Follicular Lymphoma Tumors and Characterized by Reversible Suppression of T-cell Receptor Signaling. <i>Clinical Cancer Research</i> , 2018, 24, 870-881.	7.0	75
25	Time series analysis of neoadjuvant chemotherapy and bevacizumab-treated breast carcinomas reveals a systemic shift in genomic aberrations. <i>Genome Medicine</i> , 2018, 10, 92.	8.2	17
26	Neutral tumor evolution?. <i>Nature Genetics</i> , 2018, 50, 1630-1633.	21.4	59
27	Reply to Park et al.: Human ectoparasite transmission of plague during the Second Pandemic is still plausible. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E7894-E7895.	7.1	0
28	Intratumor heterogeneity defines treatment-resistant HER2+ breast tumors. <i>Molecular Oncology</i> , 2018, 12, 1838-1855.	4.6	74
29	The Longitudinal Transcriptional Response to Neoadjuvant Chemotherapy with and without Bevacizumab in Breast Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 4662-4670.	7.0	31
30	Integrative clustering reveals a novel split in the luminal A subtype of breast cancer with impact on outcome. <i>Breast Cancer Research</i> , 2017, 19, 44.	5.0	85
31	Patterns of constitutively phosphorylated kinases in B cells are associated with disease severity in common variable immunodeficiency. <i>Clinical Immunology</i> , 2017, 175, 69-74.	3.2	6
32	Pan-cancer analysis of homozygous deletions in primary tumours uncovers rare tumour suppressors. <i>Nature Communications</i> , 2017, 8, 1221.	12.8	75
33	Breast Cancer Molecular Stratification. <i>American Journal of Pathology</i> , 2017, 187, 2152-2162.	3.8	198
34	Implementing precision cancer medicine in the public health services of Norway: the diagnostic infrastructure and a cost estimate. <i>ESMO Open</i> , 2017, 2, e000158.	4.5	8
35	The tumour microenvironment influences survival and time to transformation in follicular lymphoma in the rituximab era. <i>British Journal of Haematology</i> , 2016, 175, 102-114.	2.5	56
36	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. <i>Nature</i> , 2016, 534, 47-54.	27.8	1,760

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37	The Genomic Landscape of Pancreatic and Periampullary Adenocarcinoma. <i>Cancer Research</i> , 2016, 76, 5092-5102.	0.9	33
38	A systematic comparison of copy number alterations in four types of female cancer. <i>BMC Cancer</i> , 2016, 16, 913.	2.6	13
39	Differential expression of miRNAs in pancreatobiliary type of periampullary adenocarcinoma and its associated stroma. <i>Molecular Oncology</i> , 2016, 10, 303-316.	4.6	17
40	AGXT and ERCC2 polymorphisms are associated with clinical outcome in metastatic colorectal cancer patients treated with 5-FU/oxaliplatin. <i>Pharmacogenomics Journal</i> , 2016, 16, 272-279.	2.0	16
41	Intra-patient Inter-metastatic Genetic Heterogeneity in Colorectal Cancer as a Key Determinant of Survival after Curative Liver Resection. <i>PLoS Genetics</i> , 2016, 12, e1006225.	3.5	64
42	Tumor expression, plasma levels and genetic polymorphisms of the coagulation inhibitor TFPI are associated with clinicopathological parameters and survival in breast cancer, in contrast to the coagulation initiator TF. <i>Breast Cancer Research</i> , 2015, 17, 44.	5.0	24
43	Serum N -Glycome Characterization in Patients with Resectable Periampullary Adenocarcinoma. <i>Journal of Proteome Research</i> , 2015, 14, 5144-5156.	3.7	10
44	Molecular signatures of mRNAs and miRNAs as prognostic biomarkers in pancreatobiliary and intestinal types of periampullary adenocarcinomas. <i>Molecular Oncology</i> , 2015, 9, 758-771.	4.6	35
45	A tumor DNA complex aberration index is an independent predictor of survival in breast and ovarian cancer. <i>Molecular Oncology</i> , 2015, 9, 115-127.	4.6	38
46	Integrated analysis reveals microRNA networks coordinately expressed with key proteins in breast cancer. <i>Genome Medicine</i> , 2015, 7, 21.	8.2	34
47	Canine Mammary Tumours Are Affected by Frequent Copy Number Aberrations, including Amplification of MYC and Loss of PTEN. <i>PLoS ONE</i> , 2015, 10, e0126371.	2.5	28
48	Whole-genome integrative analysis reveals expression signatures predicting transformation in follicular lymphoma. <i>Blood</i> , 2014, 123, 1051-1054.	1.4	49
49	Principles and methods of integrative genomic analyses in cancer. <i>Nature Reviews Cancer</i> , 2014, 14, 299-313.	28.4	337
50	Plasma microRNAs predicting clinical outcome in metastatic colorectal cancer patients receiving first-line oxaliplatin-based treatment. <i>Molecular Oncology</i> , 2014, 8, 59-67.	4.6	132
51	Systematic assessment of prognostic gene signatures for breast cancer shows distinct influence of time and ER status. <i>BMC Cancer</i> , 2014, 14, 211.	2.6	34
52	Subtype-specific response to bevacizumab is reflected in the metabolome and transcriptome of breast cancer xenografts. <i>Molecular Oncology</i> , 2013, 7, 130-142.	4.6	26
53	Influence of DNA copy number and mRNA levels on the expression of breast cancer related proteins. <i>Molecular Oncology</i> , 2013, 7, 704-718.	4.6	77
54	Identifying clusters in genomics data by recursive partitioning. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2013, 12, 637-52.	0.6	33

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55	Individual and combined effects of DNA methylation and copy number alterations on miRNA expression in breast tumors. <i>Genome Biology</i> , 2013, 14, R126.	9.6	80
56	Identifying In-Trans Process Associated Genes in Breast Cancer by Integrated Analysis of Copy Number and Expression Data. <i>PLoS ONE</i> , 2013, 8, e53014.	2.5	54
57	High Levels of Genomic Aberrations in Serous Ovarian Cancers Are Associated with Better Survival. <i>PLoS ONE</i> , 2013, 8, e54356.	2.5	22
58	Copynumber: Efficient algorithms for single- and multi-track copy number segmentation. <i>BMC Genomics</i> , 2012, 13, 591.	2.8	251
59	High-resolution analyses of copy number changes in disseminated tumor cells of patients with breast cancer. <i>International Journal of Cancer</i> , 2012, 131, E405-15.	5.1	48
60	Analyzing Cancer Samples with SNP Arrays. <i>Methods in Molecular Biology</i> , 2012, 802, 57-72.	0.9	34
61	Ischemia caused by time to freezing induces systematic microRNA and mRNA responses in cancer tissue. <i>Molecular Oncology</i> , 2011, 5, 564-576.	4.6	29
62	Combining Gene Signatures Improves Prediction of Breast Cancer Survival. <i>PLoS ONE</i> , 2011, 6, e17845.	2.5	38
63	Gene expression profiles of breast biopsies from healthy women identify a group with claudin-low features. <i>BMC Medical Genomics</i> , 2011, 4, 77.	1.5	38
64	Linear and non-linear dependencies between copy number aberrations and mRNA expression reveal distinct molecular pathways in breast cancer. <i>BMC Bioinformatics</i> , 2011, 12, 197.	2.6	32
65	Genomic alterations reveal potential for higher grade transformation in follicular lymphoma and confirm parallel evolution of tumor cell clones. <i>Blood</i> , 2010, 116, 1489-1497.	1.4	58
66	Merging transcriptomics and metabolomics - advances in breast cancer profiling. <i>BMC Cancer</i> , 2010, 10, 628.	2.6	101
67	Allele-specific copy number analysis of tumors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 16910-16915.	7.1	979
68	Genomic Architecture Characterizes Tumor Progression Paths and Fate in Breast Cancer Patients. <i>Science Translational Medicine</i> , 2010, 2, 38ra47.	12.4	138
69	Glycan gene expression signatures in normal and malignant breast tissue; possible role in diagnosis and progression. <i>Molecular Oncology</i> , 2010, 4, 98-118.	4.6	147
70	Corrigendum to "Presence of bone marrow micrometastasis is associated with different recurrence risk within molecular subtypes of breast cancer" [Mol. Oncol. 1 (2007) 160-171]. <i>Molecular Oncology</i> , 2010, 4, 169-169.	4.6	0
71	The importance of gene-centring microarray data. <i>Lancet Oncology</i> , The, 2010, 11, 719-720.	10.7	42
72	Expression levels of uridine 5'-diphospho-glucuronosyltransferase genes in breast tissue from healthy women are associated with mammographic density. <i>Breast Cancer Research</i> , 2010, 12, R65.	5.0	37

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73	Partial least squares Cox regression for genome-wide data. Lifetime Data Analysis, 2008, 14, 179-195.	0.9	27
74	Pathway based analysis of SNPs with relevance to 5-FU therapy: Relation to intratumoral mRNA expression and survival. International Journal of Cancer, 2008, 123, 577-585.	5.1	20
75	ESR1 gene amplification in breast cancer: a common phenomenon?. Nature Genetics, 2008, 40, 807-808.	21.4	53
76	Presence of bone marrow micrometastasis is associated with different recurrence risk within molecular subtypes of breast cancer. Molecular Oncology, 2007, 1, 160-171.	4.6	128
77	Multilocus analysis of SNP and metabolic data within a given pathway. BMC Genomics, 2006, 7, 5.	2.8	6
78	Statistical dissection of genetic pathways involved in prostate carcinogenesis. Genes Chromosomes and Cancer, 2006, 45, 154-163.	2.8	44
79	Severity of illness and the use of paracetamol in febrile preschool children; a case simulation study of parents' assessments. Family Practice, 2006, 23, 618-623.	1.9	10
80	Spatio-temporal variability of richness estimators: coastal marine fish communities as examples. Oecologia, 2005, 144, 308-317.	2.0	5
81	CGH-Explorer: a program for analysis of array-CGH data. Bioinformatics, 2005, 21, 821-822.	4.1	291
82	From The Cover: The effect of climatic forcing on population synchrony and genetic structuring of the Canadian lynx. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 6056-6061.	7.1	50
83	Snow conditions may create an invisible barrier for lynx. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 10632-10634.	7.1	71
84	Richness dependence and climatic forcing as regulating processes of coastal fish-species richness. Ecology Letters, 2003, 6, 428-439.	6.4	11
85	Adaptive weighted least squares method for the estimation of DNA fragment lengths from agarose gels. Electrophoresis, 2002, 23, 176-181.	2.4	4
86	Gene-Expression Profiles in Hereditary Breast Cancer. New England Journal of Medicine, 2001, 344, 2028-2029.	27.0	28