

Markus Ringnr

List of Publications by Citations

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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.

92
papers

12,317
citations

42
h-index

101
g-index

101
ext. papers

15,022
ext. citations

9.4
avg, IF

7.33
L-index

#	Paper	IF	Citations
92	Classification and diagnostic prediction of cancers using gene expression profiling and artificial neural networks. <i>Nature Medicine</i> , 2001 , 7, 673-9	50.5	1928
91	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. <i>Nature</i> , 2016 , 534, 47-54	50.4	1193
90	What is principal component analysis?. <i>Nature Biotechnology</i> , 2008 , 26, 303-4	44.5	1029
89	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020 , 578, 82-93	50.4	840
88	Exosomes reflect the hypoxic status of glioma cells and mediate hypoxia-dependent activation of vascular cells during tumor development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 7312-7	11.5	626
87	A molecular taxonomy for urothelial carcinoma. <i>Clinical Cancer Research</i> , 2012 , 18, 3377-86	12.9	506
86	The CD44+/CD24- phenotype is enriched in basal-like breast tumors. <i>Breast Cancer Research</i> , 2008 , 10, R53	8.3	408
85	Poor prognosis in carcinoma is associated with a gene expression signature of aberrant PTEN tumor suppressor pathway activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 7564-9	11.5	397
84	Impact of DNA amplification on gene expression patterns in breast cancer. <i>Cancer Research</i> , 2002 , 62, 6240-5	10.1	304
83	GOBO: gene expression-based outcome for breast cancer online. <i>PLoS ONE</i> , 2011 , 6, e17911	3.7	295
82	Spatially and functionally distinct subclasses of breast cancer-associated fibroblasts revealed by single cell RNA sequencing. <i>Nature Communications</i> , 2018 , 9, 5150	17.4	271
81	Molecular subtypes of breast cancer are associated with characteristic DNA methylation patterns. <i>Breast Cancer Research</i> , 2010 , 12, R36	8.3	216
80	Gene expression profiling-based identification of molecular subtypes in stage IV melanomas with different clinical outcome. <i>Clinical Cancer Research</i> , 2010 , 16, 3356-67	12.9	185
79	Gene expression profile in multiple sclerosis patients and healthy controls: identifying pathways relevant to disease. <i>Human Molecular Genetics</i> , 2003 , 12, 2191-9	5.6	175
78	Mutational and putative neoantigen load predict clinical benefit of adoptive T cell therapy in melanoma. <i>Nature Communications</i> , 2017 , 8, 1738	17.4	172
77	High-resolution genomic profiles of breast cancer cell lines assessed by tiling BAC array comparative genomic hybridization. <i>Genes Chromosomes and Cancer</i> , 2007 , 46, 543-58	5	162
76	Microarray expression profiling in melanoma reveals a BRAF mutation signature. <i>Oncogene</i> , 2004 , 23, 4060-7	9.2	159

75	Molecular classification of familial non-BRCA1/BRCA2 breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 2532-7	11.5	157
74	CD44 isoforms are heterogeneously expressed in breast cancer and correlate with tumor subtypes and cancer stem cell markers. <i>BMC Cancer</i> , 2011 , 11, 418	4.8	148
73	Genomic subtypes of breast cancer identified by array-comparative genomic hybridization display distinct molecular and clinical characteristics. <i>Breast Cancer Research</i> , 2010 , 12, R42	8.3	141
72	Distinct genomic profiles in hereditary breast tumors identified by array-based comparative genomic hybridization. <i>Cancer Research</i> , 2005 , 65, 7612-21	10.1	141
71	High Myc pathway activity and low stage of neuronal differentiation associate with poor outcome in neuroblastoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 14094-9	11.5	133
70	Identification of subtypes in human epidermal growth factor receptor 2-positive breast cancer reveals a gene signature prognostic of outcome. <i>Journal of Clinical Oncology</i> , 2010 , 28, 1813-20	2.2	130
69	An integrative genomics screen uncovers ncRNA T-UCR functions in neuroblastoma tumours. <i>Oncogene</i> , 2010 , 29, 3583-92	9.2	125
68	Global H3K27 trimethylation and EZH2 abundance in breast tumor subtypes. <i>Molecular Oncology</i> , 2012 , 6, 494-506	7.9	114
67	Segmentation-based detection of allelic imbalance and loss-of-heterozygosity in cancer cells using whole genome SNP arrays. <i>Genome Biology</i> , 2008 , 9, R136	18.3	111
66	Normalization of Illumina Infinium whole-genome SNP data improves copy number estimates and allelic intensity ratios. <i>BMC Bioinformatics</i> , 2008 , 9, 409	3.6	108
65	Genomic profiling of malignant melanoma using tiling-resolution arrayCGH. <i>Oncogene</i> , 2007 , 26, 4738-48	9.2	104
64	High-resolution genomic and expression analyses of copy number alterations in HER2-amplified breast cancer. <i>Breast Cancer Research</i> , 2010 , 12, R25	8.3	103
63	Molecular stratification of metastatic melanoma using gene expression profiling: Prediction of survival outcome and benefit from molecular targeted therapy. <i>Oncotarget</i> , 2015 , 6, 12297-309	3.3	102
62	Folding free energies of 5SUTRs impact post-transcriptional regulation on a genomic scale in yeast. <i>PLoS Computational Biology</i> , 2005 , 1, e72	5	97
61	Gene expression profiling of primary male breast cancers reveals two unique subgroups and identifies N-acetyltransferase-1 (NAT1) as a novel prognostic biomarker. <i>Breast Cancer Research</i> , 2012 , 14, R31	8.3	83
60	Molecular profiling reveals low- and high-grade forms of primary melanoma. <i>Clinical Cancer Research</i> , 2012 , 18, 4026-36	12.9	81
59	Breast cancer genome and transcriptome integration implicates specific mutational signatures with immune cell infiltration. <i>Nature Communications</i> , 2016 , 7, 12910	17.4	74
58	Genome-wide DNA methylation analysis of lung carcinoma reveals one neuroendocrine and four adenocarcinoma epitypes associated with patient outcome. <i>Clinical Cancer Research</i> , 2014 , 20, 6127-40	12.9	72

57	Endothelial induced EMT in breast epithelial cells with stem cell properties. <i>PLoS ONE</i> , 2011 , 6, e23833	3.7	71
56	High-resolution genomic profiling of male breast cancer reveals differences hidden behind the similarities with female breast cancer. <i>Breast Cancer Research and Treatment</i> , 2011 , 129, 747-60	4.4	63
55	Detection and identification of protein isoforms using cluster analysis of MALDI-MS mass spectra. <i>Journal of Proteome Research</i> , 2006 , 5, 785-92	5.6	60
54	Analyzing array data using supervised methods. <i>Pharmacogenomics</i> , 2002 , 3, 403-15	2.6	59
53	Normalization of array-CGH data: influence of copy number imbalances. <i>BMC Genomics</i> , 2007 , 8, 382	4.5	56
52	An integrated genomics analysis of epigenetic subtypes in human breast tumors links DNA methylation patterns to chromatin states in normal mammary cells. <i>Breast Cancer Research</i> , 2016 , 18, 27	8.3	51
51	Osteopontin is a downstream effector of the PI3-kinase pathway in melanomas that is inversely correlated with functional PTEN. <i>Carcinogenesis</i> , 2006 , 27, 1778-86	4.6	49
50	Monitoring of technical variation in quantitative high-throughput datasets. <i>Cancer Informatics</i> , 2013 , 12, 193-201	2.4	40
49	Genome-Wide DNA Methylation Analysis in Melanoma Reveals the Importance of CpG Methylation in MITF Regulation. <i>Journal of Investigative Dermatology</i> , 2015 , 135, 1820-1828	4.3	39
48	DNA methylation analyses of urothelial carcinoma reveal distinct epigenetic subtypes and an association between gene copy number and methylation status. <i>Epigenetics</i> , 2012 , 7, 858-67	5.7	38
47	Characterisation of amplification patterns and target genes at chromosome 11q13 in CCND1-amplified sporadic and familial breast tumours. <i>Breast Cancer Research and Treatment</i> , 2012 , 133, 583-94	4.4	37
46	The retinoblastoma gene undergoes rearrangements in BRCA1-deficient basal-like breast cancer. <i>Cancer Research</i> , 2012 , 72, 4028-36	10.1	37
45	Tissue-specific transcriptional imprinting and heterogeneity in human innate lymphoid cells revealed by full-length single-cell RNA-sequencing. <i>Cell Research</i> , 2021 , 31, 554-568	24.7	37
44	The gene expression landscape of breast cancer is shaped by tumor protein p53 status and epithelial-mesenchymal transition. <i>Breast Cancer Research</i> , 2012 , 14, R113	8.3	36
43	The landscape of candidate driver genes differs between male and female breast cancer. <i>PLoS ONE</i> , 2013 , 8, e78299	3.7	36
42	Gene expression in inherited breast cancer. <i>Advances in Cancer Research</i> , 2002 , 84, 1-34	5.9	34
41	High expression of ZNF703 independent of amplification indicates worse prognosis in patients with luminal B breast cancer. <i>Cancer Medicine</i> , 2013 , 2, 437-46	4.8	33
40	Prediction of stage, grade, and survival in bladder cancer using genome-wide expression data: a validation study. <i>Clinical Cancer Research</i> , 2010 , 16, 4421-33	12.9	33

39	Analyzing tumor gene expression profiles. <i>Artificial Intelligence in Medicine</i> , 2003 , 28, 59-74	7.4	32
38	Expression profiling to predict outcome in breast cancer: the influence of sample selection. <i>Breast Cancer Research</i> , 2003 , 5, 23-6	8.3	32
37	Gene expression profiling demonstrates that TGF-beta1 signals exclusively through receptor complexes involving Alk5 and identifies targets of TGF-beta signaling. <i>Physiological Genomics</i> , 2005 , 21, 396-403	3.6	30
36	Genome-wide transcription factor binding site/promoter databases for the analysis of gene sets and co-occurrence of transcription factor binding motifs. <i>BMC Genomics</i> , 2010 , 11, 145	4.5	28
35	Microarray-Based Cancer Diagnosis with Artificial Neural Networks. <i>BioTechniques</i> , 2003 , 34, S30-S35	2.5	28
34	Multiple metastases from cutaneous malignant melanoma patients may display heterogeneous genomic and epigenomic patterns. <i>Melanoma Research</i> , 2010 , 20, 381-391	3.3	27
33	Integrative epigenomic analysis of differential DNA methylation in urothelial carcinoma. <i>Genome Medicine</i> , 2015 , 7, 23	14.4	26
32	Bose-Einstein correlations in the Lund model. <i>Nuclear Physics B</i> , 1998 , 513, 627-644	2.8	25
31	Tiling array-CGH for the assessment of genomic similarities among synchronous unilateral and bilateral invasive breast cancer tumor pairs. <i>BMC Clinical Pathology</i> , 2008 , 8, 6	3	24
30	Matching protein structures with fuzzy alignments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 11936-40	11.5	24
29	Sex differences in oncogenic mutational processes. <i>Nature Communications</i> , 2020 , 11, 4330	17.4	23
28	Genomic and transcriptional alterations in lung adenocarcinoma in relation to smoking history. <i>Clinical Cancer Research</i> , 2014 , 20, 4912-24	12.9	21
27	A comprehensive map coupling histone modifications with gene regulation in adult dopaminergic and serotonergic neurons. <i>Nature Communications</i> , 2018 , 9, 1226	17.4	20
26	DNA methylation subgroups in melanoma are associated with proliferative and immunological processes. <i>BMC Medical Genomics</i> , 2015 , 8, 73	3.7	20
25	Partially methylated domains are hypervariable in breast cancer and fuel widespread CpG island hypermethylation. <i>Nature Communications</i> , 2019 , 10, 1749	17.4	19
24	Landscape of somatic allelic imbalances and copy number alterations in HER2-amplified breast cancer. <i>Breast Cancer Research</i> , 2011 , 13, R129	8.3	19
23	Transverse and longitudinal Bose-Einstein correlations. <i>Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics</i> , 1998 , 421, 283-288	4.2	19
22	Revealing signaling pathway deregulation by using gene expression signatures and regulatory motif analysis. <i>Genome Biology</i> , 2007 , 8, R77	18.3	18

21	ACID: a database for microarray clone information. <i>Bioinformatics</i> , 2004 , 20, 2305-6	7.2	18
20	A strategy for identifying putative causes of gene expression variation in human cancers. <i>Journal of the Franklin Institute</i> , 2004 , 341, 77-88	4	18
19	MicroRNA-200c-141 and Np63 are required for breast epithelial differentiation and branching morphogenesis. <i>Developmental Biology</i> , 2015 , 403, 150-61	3.1	17
18	Prognostic and Chemotherapy Predictive Value of Gene-Expression Phenotypes in Primary Lung Adenocarcinoma. <i>Clinical Cancer Research</i> , 2016 , 22, 218-29	12.9	16
17	Analysis of DNA methylation patterns in the tumor immune microenvironment of metastatic melanoma. <i>Molecular Oncology</i> , 2020 , 14, 933-950	7.9	16
16	DNA methylation and histone modifications regulate SOX11 expression in lymphoid and solid cancer cells. <i>BMC Cancer</i> , 2015 , 15, 273	4.8	12
15	Genome methylation patterns in male breast cancer - Identification of an epitope with hypermethylation of polycomb target genes. <i>Molecular Oncology</i> , 2015 , 9, 1565-79	7.9	10
14	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. <i>Nature Communications</i> , 2020 , 11, 4748	17.4	10
13	Multiclass discovery in array data. <i>BMC Bioinformatics</i> , 2004 , 5, 70	3.6	9
12	Consensus of gene expression phenotypes and prognostic risk predictors in primary lung adenocarcinoma. <i>Oncotarget</i> , 2016 , 7, 52957-52973	3.3	9
11	Microarray-based cancer diagnosis with artificial neural networks. <i>BioTechniques</i> , 2003 , Suppl, 30-5	2.5	9
10	Is there screwiness at the end of the QCD cascades?. <i>Journal of High Energy Physics</i> , 1998 , 1998, 014-014	5.4	7
9	Primary melanoma tumors from CDKN2A mutation carriers do not belong to a distinct molecular subclass. <i>Journal of Investigative Dermatology</i> , 2014 , 134, 3000-3003	4.3	5
8	Nonfamilial breast cancer subtypes. <i>Methods in Molecular Biology</i> , 2013 , 973, 279-95	1.4	5
7	Classification of Genomic and Proteomic Data Using Support Vector Machines 2007 , 187-202		4
6	Classification of Expression Patterns Using Artificial Neural Networks 2003 , 201-215		1
5	Partially methylated domains are hypervariable in breast cancer and fuel widespread CpG island hypermethylation		
4	Environmentally induced DNA methylation is inherited across generations in an aquatic keystone species.. <i>Science</i> , 2022 , 25, 104303	6.1	1

- 3 Mutational patterns and clonal evolution from diagnosis to relapse in pediatric acute lymphoblastic leukemia. *Scientific Reports*, **2021**, 11, 15988 4.9 ○
- 2 Mitochondrial dysfunction in adult midbrain dopamine neurons triggers an early immune response. *PLoS Genetics*, **2021**, 17, e1009822 6 ○
- 1 Transverse and Longitudinal Bose-Einstein Correlations in $e+e^-$ Annihilation **1999**, 425-428