

# Markus RingnÃ©r

## List of Publications by Year in descending order

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95  
papers

16,943  
citations

53660

45  
h-index

40881

93  
g-index

101  
all docs

101  
docs citations

101  
times ranked

28703  
citing authors

#	ARTICLE	IF	CITATIONS
1	Environmentally induced DNA methylation is inherited across generations in an aquatic keystone species. <i>IScience</i> , 2022, 25, 104303.	1.9	11
2	Mutational patterns and clonal evolution from diagnosis to relapse in pediatric acute lymphoblastic leukemia. <i>Scientific Reports</i> , 2021, 11, 15988.	1.6	6
3	Mitochondrial dysfunction in adult midbrain dopamine neurons triggers an early immune response. <i>PLoS Genetics</i> , 2021, 17, e1009822.	1.5	8
4	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.	5.7	97
5	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. <i>Nature Communications</i> , 2020, 11, 4748.	5.8	27
6	Sex differences in oncogenic mutational processes. <i>Nature Communications</i> , 2020, 11, 4330.	5.8	60
7	Analysis of DNA methylation patterns in the tumor immune microenvironment of metastatic melanoma. <i>Molecular Oncology</i> , 2020, 14, 933-950.	2.1	29
8	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020, 578, 82-93.	13.7	1,966
9	Partially methylated domains are hypervariable in breast cancer and fuel widespread CpG island hypermethylation. <i>Nature Communications</i> , 2019, 10, 1749.	5.8	46
10	A comprehensive map coupling histone modifications with gene regulation in adult dopaminergic and serotonergic neurons. <i>Nature Communications</i> , 2018, 9, 1226.	5.8	35
11	Spatially and functionally distinct subclasses of breast cancer-associated fibroblasts revealed by single cell RNA sequencing. <i>Nature Communications</i> , 2018, 9, 5150.	5.8	496
12	Mutational and putative neoantigen load predict clinical benefit of adoptive T cell therapy in melanoma. <i>Nature Communications</i> , 2017, 8, 1738.	5.8	310
13	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. <i>Nature</i> , 2016, 534, 47-54.	13.7	1,760
14	Breast cancer genome and transcriptome integration implicates specific mutational signatures with immune cell infiltration. <i>Nature Communications</i> , 2016, 7, 12910.	5.8	119
15	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.	2.2	67
16	Prognostic and Chemotherapy Predictive Value of Gene-Expression Phenotypes in Primary Lung Adenocarcinoma. <i>Clinical Cancer Research</i> , 2016, 22, 218-229.	3.2	29
17	Consensus of gene expression phenotypes and prognostic risk predictors in primary lung adenocarcinoma. <i>Oncotarget</i> , 2016, 7, 52957-52973.	0.8	11
18	DNA methylation subgroups in melanoma are associated with proliferative and immunological processes. <i>BMC Medical Genomics</i> , 2015, 8, 73.	0.7	29

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19	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.	0.3	46
20	Genome methylation patterns in male breast cancer – Identification of an epitype with hypermethylation of polycomb target genes. <i>Molecular Oncology</i> , 2015, 9, 1565-1579.	2.1	14
21	DNA methylation and histone modifications regulate SOX11 expression in lymphoid and solid cancer cells. <i>BMC Cancer</i> , 2015, 15, 273.	1.1	14
22	Integrative epigenomic analysis of differential DNA methylation in urothelial carcinoma. <i>Genome Medicine</i> , 2015, 7, 23.	3.6	42
23	MicroRNA-200c-141 and $\beta$ 6 are required for breast epithelial differentiation and branching morphogenesis. <i>Developmental Biology</i> , 2015, 403, 150-161.	0.9	23
24	Molecular stratification of metastatic melanoma using gene expression profiling : Prediction of survival outcome and benefit from molecular targeted therapy. <i>Oncotarget</i> , 2015, 6, 12297-12309.	0.8	148
25	Making Breast Cancer Molecular Subtypes Robust?. <i>Journal of the National Cancer Institute</i> , 2014, 107, dju386-dju386.	3.0	10
26	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, 6127-6140.	3.2	91
27	Genomic and Transcriptional Alterations in Lung Adenocarcinoma in Relation to Smoking History. <i>Clinical Cancer Research</i> , 2014, 20, 4912-4924.	3.2	24
28	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.	0.3	8
29	Nonfamilial Breast Cancer Subtypes. <i>Methods in Molecular Biology</i> , 2013, 973, 279-295.	0.4	5
30	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, 7312-7317.	3.3	768
31	High expression of <i>ZNF703</i> independent of amplification indicates worse prognosis in patients with luminal B breast cancer. <i>Cancer Medicine</i> , 2013, 2, 437-446.	1.3	39
32	Monitoring of Technical Variation in Quantitative High-Throughput Datasets. <i>Cancer Informatics</i> , 2013, 12, CIN.S12862.	0.9	47
33	The Landscape of Candidate Driver Genes Differs between Male and Female Breast Cancer. <i>PLoS ONE</i> , 2013, 8, e78299.	1.1	46
34	A Molecular Taxonomy for Urothelial Carcinoma. <i>Clinical Cancer Research</i> , 2012, 18, 3377-3386.	3.2	729
35	The Retinoblastoma Gene Undergoes Rearrangements in <i>BRCA1</i> -Deficient Basal-like Breast Cancer. <i>Cancer Research</i> , 2012, 72, 4028-4036.	0.4	41
36	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, 858-867.	1.3	44

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37	Molecular Profiling Reveals Low- and High-Grade Forms of Primary Melanoma. <i>Clinical Cancer Research</i> , 2012, 18, 4026-4036.	3.2	96
38	Global H3K27 trimethylation and EZH2 abundance in breast tumor subtypes. <i>Molecular Oncology</i> , 2012, 6, 494-506.	2.1	136
39	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.	2.2	49
40	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, 583-594.	1.1	44
41	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.	2.2	100
42	Landscape of somatic allelic imbalances and copy number alterations in HER2-amplified breast cancer. <i>Breast Cancer Research</i> , 2011, 13, R129.	2.2	25
43	GOBO: Gene Expression-Based Outcome for Breast Cancer Online. <i>PLoS ONE</i> , 2011, 6, e17911.	1.1	361
44	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.	1.1	173
45	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, 747-760.	1.1	70
46	Endothelial Induced EMT in Breast Epithelial Cells with Stem Cell Properties. <i>PLoS ONE</i> , 2011, 6, e23833.	1.1	87
47	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.	1.2	31
48	An integrative genomics screen uncovers ncRNA T-UCR functions in neuroblastoma tumours. <i>Oncogene</i> , 2010, 29, 3583-3592.	2.6	141
49	Gene Expression Profiling-Based Identification of Molecular Subtypes in Stage IV Melanomas with Different Clinical Outcome. <i>Clinical Cancer Research</i> , 2010, 16, 3356-3367.	3.2	235
50	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, 1813-1820.	0.8	145
51	Prediction of Stage, Grade, and Survival in Bladder Cancer Using Genome-wide Expression Data: A Validation Study. <i>Clinical Cancer Research</i> , 2010, 16, 4421-4433.	3.2	36
52	High-resolution genomic and expression analyses of copy number alterations in HER2-amplified breast cancer. <i>Breast Cancer Research</i> , 2010, 12, R25.	2.2	123
53	Molecular subtypes of breast cancer are associated with characteristic DNA methylation patterns. <i>Breast Cancer Research</i> , 2010, 12, R36.	2.2	251
54	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.	2.2	167

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55	Multiple metastases from cutaneous malignant melanoma patients may display heterogeneous genomic and epigenomic patterns. <i>Melanoma Research</i> , 2010, 20, 381-391.	0.6	30
56	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.	1.8	28
57	What is principal component analysis?. <i>Nature Biotechnology</i> , 2008, 26, 303-304.	9.4	1,634
58	Normalization of Illumina Infinium whole-genome SNP data improves copy number estimates and allelic intensity ratios. <i>BMC Bioinformatics</i> , 2008, 9, 409.	1.2	114
59	The CD44+/CD24-phenotype is enriched in basal-like breast tumors. <i>Breast Cancer Research</i> , 2008, 10, R53.	2.2	464
60	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.	13.9	127
61	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, 14094-14099.	3.3	149
62	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, 7564-7569.	3.3	445
63	Revealing signaling pathway deregulation by using gene expression signatures and regulatory motif analysis. <i>Genome Biology</i> , 2007, 8, R77.	13.9	18
64	Classification of Genomic and Proteomic Data Using Support Vector Machines. , 2007, , 187-202.		4
65	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, 543-558.	1.5	176
66	Genomic profiling of malignant melanoma using tiling-resolution arrayCGH. <i>Oncogene</i> , 2007, 26, 4738-4748.	2.6	118
67	Normalization of array-CGH data: influence of copy number imbalances. <i>BMC Genomics</i> , 2007, 8, 382.	1.2	57
68	Detection and Identification of Protein Isoforms Using Cluster Analysis of MALDI-MS Mass Spectra. <i>Journal of Proteome Research</i> , 2006, 5, 785-792.	1.8	68
69	Osteopontin is a downstream effector of the PI3-kinase pathway in melanomas that is inversely correlated with functional PTEN. <i>Carcinogenesis</i> , 2006, 27, 1778-1786.	1.3	55
70	Distinct Genomic Profiles in Hereditary Breast Tumors Identified by Array-Based Comparative Genomic Hybridization. <i>Cancer Research</i> , 2005, 65, 7612-7621.	0.4	147
71	Gene expression profiling demonstrates that TGF- $\beta$ 1 signals exclusively through receptor complexes involving Alk5 and identifies targets of TGF- $\beta$ 2 signaling. <i>Physiological Genomics</i> , 2005, 21, 396-403.	1.0	33
72	Folding Free Energies of 5'-UTRs Impact Post-Transcriptional Regulation on a Genomic Scale in Yeast. <i>PLoS Computational Biology</i> , 2005, 1, e72.	1.5	116

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73	Folding free energies of 5'-UTRs impact post-transcriptional regulation on a genomic scale in yeast. PLoS Computational Biology, 2005, preprint, e72.	1.5	0
74	ACID: a database for microarray clone information. Bioinformatics, 2004, 20, 2305-2306.	1.8	18
75	Microarray expression profiling in melanoma reveals a BRAF mutation signature. Oncogene, 2004, 23, 4060-4067.	2.6	169
76	Multiclass discovery in array data. BMC Bioinformatics, 2004, 5, 70.	1.2	11
77	A strategy for identifying putative causes of gene expression variation in human cancers. Journal of the Franklin Institute, 2004, 341, 77-88.	1.9	21
78	Analyzing tumor gene expression profiles. Artificial Intelligence in Medicine, 2003, 28, 59-74.	3.8	43
79	Gene expression profile in multiple sclerosis patients and healthy controls: identifying pathways relevant to disease. Human Molecular Genetics, 2003, 12, 2191-2199.	1.4	191
80	Matching protein structures with fuzzy alignments. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 11936-11940.	3.3	29
81	Molecular classification of familial non-BRCA1/BRCA2 breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 2532-2537.	3.3	182
82	Classification of Expression Patterns Using Artificial Neural Networks. , 2003, , 201-215.		3
83	Microarray-Based Cancer Diagnosis with Artificial Neural Networks. BioTechniques, 2003, 34, S30-S35.	0.8	37
84	Microarray-based cancer diagnosis with artificial neural networks. BioTechniques, 2003, Suppl, 30-5.	0.8	10
85	Gene expression in inherited breast cancer. Advances in Cancer Research, 2002, 84, 1-34.	1.9	44
86	Analyzing array data using supervised methods. Pharmacogenomics, 2002, 3, 403-415.	0.6	67
87	Expression profiling to predict outcome in breast cancer: the influence of sample selection. Breast Cancer Research, 2002, 5, 23-6.	2.2	35
88	Impact of DNA amplification on gene expression patterns in breast cancer. Cancer Research, 2002, 62, 6240-5.	0.4	352
89	Classification and diagnostic prediction of cancers using gene expression profiling and artificial neural networks. Nature Medicine, 2001, 7, 673-679.	15.2	2,352
90	Transverse and Longitudinal Bose-Einstein Correlations in $e + e \rightarrow e \gamma$ Annihilation. , 1999, , 425-428.		0

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91	The Feynman-Wilson gas and the Lund model. European Physical Journal C, 1999, 7, 251.	1.4	0
92	Transverse and longitudinal Bose-Einstein correlations. Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics, 1998, 421, 283-288.	1.5	19
93	Bose-Einstein correlations in the Lund model. Nuclear Physics B, 1998, 513, 627-644.	0.9	27
94	Is there screwiness at the end of the QCD cascades?. Journal of High Energy Physics, 1998, 1998, 014-014.	1.6	10
95	Bose-Einstein and colour interference in W-pair decays. European Physical Journal C, 1998, 5, 275.	1.4	3