# Markus Ringnr

## List of Publications by Year in Descending Order

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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.

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|---|---|---|---|
| 92<br>papers | 12,317<br>citations | 42<br>h-index | 101<br>g-index |
| 101<br>ext. papers | 15,022<br>ext. citations | 9.4<br>avg, IF | 7.33<br>L-index |

| # | Paper | IF | Citations |
|---|---|---|---|
| 92 | Environmentally induced DNA methylation is inherited across generations in an aquatic keystone species.. *IScience*, **2022**, 25, 104303 | 6.1 | 1 |
| 91 | Mutational patterns and clonal evolution from diagnosis to relapse in pediatric acute lymphoblastic leukemia. *Scientific Reports*, **2021**, 11, 15988 | 4.9 | 0 |
| 90 | Mitochondrial dysfunction in adult midbrain dopamine neurons triggers an early immune response. *PLoS Genetics*, **2021**, 17, e1009822 | 6 | 0 |
| 89 | Tissue-specific transcriptional imprinting and heterogeneity in human innate lymphoid cells revealed by full-length single-cell RNA-sequencing. *Cell Research*, **2021**, 31, 554-568 | 24.7 | 37 |
| 88 | Analysis of DNA methylation patterns in the tumor immune microenvironment of metastatic melanoma. *Molecular Oncology*, **2020**, 14, 933-950 | 7.9 | 16 |
| 87 | Pan-cancer analysis of whole genomes. *Nature*, **2020**, 578, 82-93 | 50.4 | 840 |
| 86 | Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. *Nature Communications*, **2020**, 11, 4748 | 17.4 | 10 |
| 85 | Sex differences in oncogenic mutational processes. *Nature Communications*, **2020**, 11, 4330 | 17.4 | 23 |
| 84 | Partially methylated domains are hypervariable in breast cancer and fuel widespread CpG island hypermethylation. *Nature Communications*, **2019**, 10, 1749 | 17.4 | 19 |
| 83 | A comprehensive map coupling histone modifications with gene regulation in adult dopaminergic and serotonergic neurons. *Nature Communications*, **2018**, 9, 1226 | 17.4 | 20 |
| 82 | Spatially and functionally distinct subclasses of breast cancer-associated fibroblasts revealed by single cell RNA sequencing. *Nature Communications*, **2018**, 9, 5150 | 17.4 | 271 |
| 81 | Mutational and putative neoantigen load predict clinical benefit of adoptive T cell therapy in melanoma. *Nature Communications*, **2017**, 8, 1738 | 17.4 | 172 |
| 80 | Prognostic and Chemotherapy Predictive Value of Gene-Expression Phenotypes in Primary Lung Adenocarcinoma. *Clinical Cancer Research*, **2016**, 22, 218-29 | 12.9 | 16 |
| 79 | Breast cancer genome and transcriptome integration implicates specific mutational signatures with immune cell infiltration. *Nature Communications*, **2016**, 7, 12910 | 17.4 | 74 |
| 78 | An integrated genomics analysis of epigenetic subtypes in human breast tumors links DNA methylation patterns to chromatin states in normal mammary cells. *Breast Cancer Research*, **2016**, 18, 27 | 8.3 | 51 |
| 77 | Consensus of gene expression phenotypes and prognostic risk predictors in primary lung adenocarcinoma. *Oncotarget*, **2016**, 7, 52957-52973 | 3.3 | 9 |
| 76 | Landscape of somatic mutations in 560 breast cancer whole-genome sequences. *Nature*, **2016**, 534, 47-54 | 50.4 | 1193 |

# (2012-2015)

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| 75 | Integrative epigenomic analysis of differential DNA methylation in urothelial carcinoma. *Genome Medicine*, **2015**, 7, 23 | 14.4 | 26 |
| 74 | MicroRNA-200c-141 and ▯Np63 are required for breast epithelial differentiation and branching morphogenesis. *Developmental Biology*, **2015**, 403, 150-61 | 3.1 | 17 |
| 73 | DNA methylation subgroups in melanoma are associated with proliferative and immunological processes. *BMC Medical Genomics*, **2015**, 8, 73 | 3.7 | 20 |
| 72 | Genome-Wide DNA Methylation Analysis in Melanoma Reveals the Importance of CpG Methylation in MITF Regulation. *Journal of Investigative Dermatology*, **2015**, 135, 1820-1828 | 4.3 | 39 |
| 71 | Genome methylation patterns in male breast cancer - Identification of an epitype with hypermethylation of polycomb target genes. *Molecular Oncology*, **2015**, 9, 1565-79 | 7.9 | 10 |
| 70 | DNA methylation and histone modifications regulate SOX11 expression in lymphoid and solid cancer cells. *BMC Cancer*, **2015**, 15, 273 | 4.8 | 12 |
| 69 | Molecular stratification of metastatic melanoma using gene expression profiling: Prediction of survival outcome and benefit from molecular targeted therapy. *Oncotarget*, **2015**, 6, 12297-309 | 3.3 | 102 |
| 68 | Primary melanoma tumors from CDKN2A mutation carriers do not belong to a distinct molecular subclass. *Journal of Investigative Dermatology*, **2014**, 134, 3000-3003 | 4.3 | 5 |
| 67 | Genome-wide DNA methylation analysis of lung carcinoma reveals one neuroendocrine and four adenocarcinoma epitypes associated with patient outcome. *Clinical Cancer Research*, **2014**, 20, 6127-40 | 12.9 | 72 |
| 66 | Genomic and transcriptional alterations in lung adenocarcinoma in relation to smoking history. *Clinical Cancer Research*, **2014**, 20, 4912-24 | 12.9 | 21 |
| 65 | Nonfamilial breast cancer subtypes. *Methods in Molecular Biology*, **2013**, 973, 279-95 | 1.4 | 5 |
| 64 | Exosomes reflect the hypoxic status of glioma cells and mediate hypoxia-dependent activation of vascular cells during tumor development. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 7312-7 | 11.5 | 626 |
| 63 | High expression of ZNF703 independent of amplification indicates worse prognosis in patients with luminal B breast cancer. *Cancer Medicine*, **2013**, 2, 437-46 | 4.8 | 33 |
| 62 | Monitoring of technical variation in quantitative high-throughput datasets. *Cancer Informatics*, **2013**, 12, 193-201 | 2.4 | 40 |
| 61 | The landscape of candidate driver genes differs between male and female breast cancer. *PLoS ONE*, **2013**, 8, e78299 | 3.7 | 36 |
| 60 | Gene expression profiling of primary male breast cancers reveals two unique subgroups and identifies N-acetyltransferase-1 (NAT1) as a novel prognostic biomarker. *Breast Cancer Research*, **2012**, 14, R31 | 8.3 | 83 |
| 59 | Global H3K27 trimethylation and EZH2 abundance in breast tumor subtypes. *Molecular Oncology*, **2012**, 6, 494-506 | 7.9 | 114 |
| 58 | The gene expression landscape of breast cancer is shaped by tumor protein p53 status and epithelial-mesenchymal transition. *Breast Cancer Research*, **2012**, 14, R113 | 8.3 | 36 |

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| 57 | Characterisation of amplification patterns and target genes at chromosome 11q13 in CCND1-amplified sporadic and familial breast tumours. *Breast Cancer Research and Treatment*, **2012**, 133, 583-94 | 4.4 | 37 |
| 56 | A molecular taxonomy for urothelial carcinoma. *Clinical Cancer Research*, **2012**, 18, 3377-86 | 12.9 | 506 |
| 55 | The retinoblastoma gene undergoes rearrangements in BRCA1-deficient basal-like breast cancer. *Cancer Research*, **2012**, 72, 4028-36 | 10.1 | 37 |
| 54 | DNA methylation analyses of urothelial carcinoma reveal distinct epigenetic subtypes and an association between gene copy number and methylation status. *Epigenetics*, **2012**, 7, 858-67 | 5.7 | 38 |
| 53 | Molecular profiling reveals low- and high-grade forms of primary melanoma. *Clinical Cancer Research*, **2012**, 18, 4026-36 | 12.9 | 81 |
| 52 | Landscape of somatic allelic imbalances and copy number alterations in HER2-amplified breast cancer. *Breast Cancer Research*, **2011**, 13, R129 | 8.3 | 19 |
| 51 | GOBO: gene expression-based outcome for breast cancer online. *PLoS ONE*, **2011**, 6, e17911 | 3.7 | 295 |
| 50 | CD44 isoforms are heterogeneously expressed in breast cancer and correlate with tumor subtypes and cancer stem cell markers. *BMC Cancer*, **2011**, 11, 418 | 4.8 | 148 |
| 49 | High-resolution genomic profiling of male breast cancer reveals differences hidden behind the similarities with female breast cancer. *Breast Cancer Research and Treatment*, **2011**, 129, 747-60 | 4.4 | 63 |
| 48 | Endothelial induced EMT in breast epithelial cells with stem cell properties. *PLoS ONE*, **2011**, 6, e23833 | 3.7 | 71 |
| 47 | An integrative genomics screen uncovers ncRNA T-UCR functions in neuroblastoma tumours. *Oncogene*, **2010**, 29, 3583-92 | 9.2 | 125 |
| 46 | Gene expression profiling-based identification of molecular subtypes in stage IV melanomas with different clinical outcome. *Clinical Cancer Research*, **2010**, 16, 3356-67 | 12.9 | 185 |
| 45 | Identification of subtypes in human epidermal growth factor receptor 2--positive breast cancer reveals a gene signature prognostic of outcome. *Journal of Clinical Oncology*, **2010**, 28, 1813-20 | 2.2 | 130 |
| 44 | Prediction of stage, grade, and survival in bladder cancer using genome-wide expression data: a validation study. *Clinical Cancer Research*, **2010**, 16, 4421-33 | 12.9 | 33 |
| 43 | High-resolution genomic and expression analyses of copy number alterations in HER2-amplified breast cancer. *Breast Cancer Research*, **2010**, 12, R25 | 8.3 | 103 |
| 42 | Molecular subtypes of breast cancer are associated with characteristic DNA methylation patterns. *Breast Cancer Research*, **2010**, 12, R36 | 8.3 | 216 |
| 41 | Genomic subtypes of breast cancer identified by array-comparative genomic hybridization display distinct molecular and clinical characteristics. *Breast Cancer Research*, **2010**, 12, R42 | 8.3 | 141 |
| 40 | Genome-wide transcription factor binding site/promoter databases for the analysis of gene sets and co-occurrence of transcription factor binding motifs. *BMC Genomics*, **2010**, 11, 145 | 4.5 | 28 |

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| 39 | Multiple metastases from cutaneous malignant melanoma patients may display heterogeneous genomic and epigenomic patterns. *Melanoma Research*, **2010**, 20, 381-391 | 3.3 | 27 |
| 38 | What is principal component analysis?. *Nature Biotechnology*, **2008**, 26, 303-4 | 44.5 | 1029 |
| 37 | Normalization of Illumina Infinium whole-genome SNP data improves copy number estimates and allelic intensity ratios. *BMC Bioinformatics*, **2008**, 9, 409 | 3.6 | 108 |
| 36 | The CD44+/CD24- phenotype is enriched in basal-like breast tumors. *Breast Cancer Research*, **2008**, 10, R53 | 8.3 | 408 |
| 35 | Segmentation-based detection of allelic imbalance and loss-of-heterozygosity in cancer cells using whole genome SNP arrays. *Genome Biology*, **2008**, 9, R136 | 18.3 | 111 |
| 34 | High Myc pathway activity and low stage of neuronal differentiation associate with poor outcome in neuroblastoma. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 14094-9 | 11.5 | 133 |
| 33 | Tiling array-CGH for the assessment of genomic similarities among synchronous unilateral and bilateral invasive breast cancer tumor pairs. *BMC Clinical Pathology*, **2008**, 8, 6 | 3 | 24 |
| 32 | High-resolution genomic profiles of breast cancer cell lines assessed by tiling BAC array comparative genomic hybridization. *Genes Chromosomes and Cancer*, **2007**, 46, 543-58 | 5 | 162 |
| 31 | Genomic profiling of malignant melanoma using tiling-resolution arrayCGH. *Oncogene*, **2007**, 26, 4738-48 | 9.2 | 104 |
| 30 | Normalization of array-CGH data: influence of copy number imbalances. *BMC Genomics*, **2007**, 8, 382 | 4.5 | 56 |
| 29 | Poor prognosis in carcinoma is associated with a gene expression signature of aberrant PTEN tumor suppressor pathway activity. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 7564-9 | 11.5 | 397 |
| 28 | Revealing signaling pathway deregulation by using gene expression signatures and regulatory motif analysis. *Genome Biology*, **2007**, 8, R77 | 18.3 | 18 |
| 27 | Classification of Genomic and Proteomic Data Using Support Vector Machines **2007**, 187-202 | | 4 |
| 26 | Osteopontin is a downstream effector of the PI3-kinase pathway in melanomas that is inversely correlated with functional PTEN. *Carcinogenesis*, **2006**, 27, 1778-86 | 4.6 | 49 |
| 25 | Detection and identification of protein isoforms using cluster analysis of MALDI-MS mass spectra. *Journal of Proteome Research*, **2006**, 5, 785-92 | 5.6 | 60 |
| 24 | Distinct genomic profiles in hereditary breast tumors identified by array-based comparative genomic hybridization. *Cancer Research*, **2005**, 65, 7612-21 | 10.1 | 141 |
| 23 | Gene expression profiling demonstrates that TGF-beta1 signals exclusively through receptor complexes involving Alk5 and identifies targets of TGF-beta signaling. *Physiological Genomics*, **2005**, 21, 396-403 | 3.6 | 30 |
| 22 | Folding free energies of 5SUTRs impact post-transcriptional regulation on a genomic scale in yeast. *PLoS Computational Biology*, **2005**, 1, e72 | 5 | 97 |

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| 21 | ACID: a database for microarray clone information. *Bioinformatics*, **2004**, 20, 2305-6 | 7.2 | 18 |
| 20 | Microarray expression profiling in melanoma reveals a BRAF mutation signature. *Oncogene*, **2004**, 23, 4060-7 | 9.2 | 159 |
| 19 | Multiclass discovery in array data. *BMC Bioinformatics*, **2004**, 5, 70 | 3.6 | 9 |
| 18 | A strategy for identifying putative causes of gene expression variation in human cancers. *Journal of the Franklin Institute*, **2004**, 341, 77-88 | 4 | 18 |
| 17 | Molecular classification of familial non-BRCA1/BRCA2 breast cancer. *Proceedings of the National Academy of Sciences of the United States of America*, **2003**, 100, 2532-7 | 11.5 | 157 |
| 16 | Classification of Expression Patterns Using Artificial Neural Networks **2003**, 201-215 | | 1 |
| 15 | Microarray-Based Cancer Diagnosis with Artificial Neural Networks. *BioTechniques*, **2003**, 34, S30-S35 | 2.5 | 28 |
| 14 | Analyzing tumor gene expression profiles. *Artificial Intelligence in Medicine*, **2003**, 28, 59-74 | 7.4 | 32 |
| 13 | Gene expression profile in multiple sclerosis patients and healthy controls: identifying pathways relevant to disease. *Human Molecular Genetics*, **2003**, 12, 2191-9 | 5.6 | 175 |
| 12 | Matching protein structures with fuzzy alignments. *Proceedings of the National Academy of Sciences of the United States of America*, **2003**, 100, 11936-40 | 11.5 | 24 |
| 11 | Expression profiling to predict outcome in breast cancer: the influence of sample selection. *Breast Cancer Research*, **2003**, 5, 23-6 | 8.3 | 32 |
| 10 | Microarray-based cancer diagnosis with artificial neural networks. *BioTechniques*, **2003**, Suppl, 30-5 | 2.5 | 9 |
| 9 | Gene expression in inherited breast cancer. *Advances in Cancer Research*, **2002**, 84, 1-34 | 5.9 | 34 |
| 8 | Analyzing array data using supervised methods. *Pharmacogenomics*, **2002**, 3, 403-15 | 2.6 | 59 |
| 7 | Impact of DNA amplification on gene expression patterns in breast cancer. *Cancer Research*, **2002**, 62, 6240-5 | 10.1 | 304 |
| 6 | Classification and diagnostic prediction of cancers using gene expression profiling and artificial neural networks. *Nature Medicine*, **2001**, 7, 673-9 | 50.5 | 1928 |
| 5 | Transverse and Longitudinal Bose-Einstein Correlations in e+e Annihilation **1999**, 425-428 | | |
| 4 | Transverse and longitudinal Bose-Einstein correlations. *Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics*, **1998**, 421, 283-288 | 4.2 | 19 |

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| 3 | Bose-Einstein correlations in the Lund model. *Nuclear Physics B*, **1998**, 513, 627-644 | 2.8 | 25 |
| 2 | Is there screwiness at the end of the QCD cascades?. *Journal of High Energy Physics*, **1998**, 1998, 014-014 | 5.4 | 7 |
| 1 | Partially methylated domains are hypervariable in breast cancer and fuel widespread CpG island hypermethylation | | 1 |