

Markus Ringn  r

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/224539/publications.pdf>

Version: 2024-02-01

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 | Classification and diagnostic prediction of cancers using gene expression profiling and artificial neural networks. <i>Nature Medicine</i> , 2001, 7, 673-679. | 15.2 | 2,352 |
| 2 | Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020, 578, 82-93. | 13.7 | 1,966 |
| 3 | Landscape of somatic mutations in 560 breast cancer whole-genome sequences. <i>Nature</i> , 2016, 534, 47-54. | 13.7 | 1,760 |
| 4 | What is principal component analysis?. <i>Nature Biotechnology</i> , 2008, 26, 303-304. | 9.4 | 1,634 |
| 5 | 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 |
| 6 | A Molecular Taxonomy for Urothelial Carcinoma. <i>Clinical Cancer Research</i> , 2012, 18, 3377-3386. | 3.2 | 729 |
| 7 | 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 |
| 8 | The CD44+/CD24-phenotype is enriched in basal-like breast tumors. <i>Breast Cancer Research</i> , 2008, 10, R53. | 2.2 | 464 |
| 9 | 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 |
| 10 | GOBO: Gene Expression-Based Outcome for Breast Cancer Online. <i>PLoS ONE</i> , 2011, 6, e17911. | 1.1 | 361 |
| 11 | Impact of DNA amplification on gene expression patterns in breast cancer. <i>Cancer Research</i> , 2002, 62, 6240-5. | 0.4 | 352 |
| 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 | Molecular subtypes of breast cancer are associated with characteristic DNA methylation patterns. <i>Breast Cancer Research</i> , 2010, 12, R36. | 2.2 | 251 |
| 14 | 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 |
| 15 | Gene expression profile in multiple sclerosis patients and healthy controls: identifying pathways relevant to disease. <i>Human Molecular Genetics</i> , 2003, 12, 2191-2199. | 1.4 | 191 |
| 16 | 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, 2532-2537. | 3.3 | 182 |
| 17 | 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 |
| 18 | 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 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 19 | Microarray expression profiling in melanoma reveals a BRAF mutation signature. <i>Oncogene</i> , 2004, 23, 4060-4067. | 2.6 | 169 |
| 20 | 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 |
| 21 | 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 |
| 22 | 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 |
| 23 | 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 |
| 24 | Identification of Subtypes in Human Epidermal Growth Factor Receptor 2â€“Positive Breast Cancer Reveals a Gene Signature Prognostic of Outcome. <i>Journal of Clinical Oncology</i> , 2010, 28, 1813-1820. | 0.8 | 145 |
| 25 | An integrative genomics screen uncovers ncRNA T-UCR functions in neuroblastoma tumours. <i>Oncogene</i> , 2010, 29, 3583-3592. | 2.6 | 141 |
| 26 | Global H3K27 trimethylation and EZH2 abundance in breast tumor subtypes. <i>Molecular Oncology</i> , 2012, 6, 494-506. | 2.1 | 136 |
| 27 | 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 |
| 28 | 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 |
| 29 | Breast cancer genome and transcriptome integration implicates specific mutational signatures with immune cell infiltration. <i>Nature Communications</i> , 2016, 7, 12910. | 5.8 | 119 |
| 30 | Genomic profiling of malignant melanoma using tiling-resolution arrayCGH. <i>Oncogene</i> , 2007, 26, 4738-4748. | 2.6 | 118 |
| 31 | Folding Free Energies of 5â€“UTRs Impact Post-Transcriptional Regulation on a Genomic Scale in Yeast. <i>PLoS Computational Biology</i> , 2005, 1, e72. | 1.5 | 116 |
| 32 | 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 |
| 33 | 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 |
| 34 | 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 |
| 35 | Molecular Profiling Reveals Low- and High-Grade Forms of Primary Melanoma. <i>Clinical Cancer Research</i> , 2012, 18, 4026-4036. | 3.2 | 96 |
| 36 | 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 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 37 | Endothelial Induced EMT in Breast Epithelial Cells with Stem Cell Properties. PLoS ONE, 2011, 6, e23833. | 1.1 | 87 |
| 38 | 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, 747-760. | 1.1 | 70 |
| 39 | Detection and Identification of Protein Isoforms Using Cluster Analysis of MALDI-MS Mass Spectra. Journal of Proteome Research, 2006, 5, 785-792. | 1.8 | 68 |
| 40 | Analyzing array data using supervised methods. Pharmacogenomics, 2002, 3, 403-415. | 0.6 | 67 |
| 41 | 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. | 2.2 | 67 |
| 42 | Sex differences in oncogenic mutational processes. Nature Communications, 2020, 11, 4330. | 5.8 | 60 |
| 43 | Normalization of array-CGH data: influence of copy number imbalances. BMC Genomics, 2007, 8, 382. | 1.2 | 57 |
| 44 | Osteopontin is a downstream effector of the PI3-kinase pathway in melanomas that is inversely correlated with functional PTEN. Carcinogenesis, 2006, 27, 1778-1786. | 1.3 | 55 |
| 45 | The gene expression landscape of breast cancer is shaped by tumor protein p53 status and epithelial-mesenchymal transition. Breast Cancer Research, 2012, 14, R113. | 2.2 | 49 |
| 46 | Monitoring of Technical Variation in Quantitative High-Throughput Datasets. Cancer Informatics, 2013, 12, CIN.S12862. | 0.9 | 47 |
| 47 | Genome-Wide DNA Methylation Analysis in Melanoma Reveals the Importance of CpG Methylation in MITF Regulation. Journal of Investigative Dermatology, 2015, 135, 1820-1828. | 0.3 | 46 |
| 48 | Partially methylated domains are hypervariable in breast cancer and fuel widespread CpG island hypermethylation. Nature Communications, 2019, 10, 1749. | 5.8 | 46 |
| 49 | The Landscape of Candidate Driver Genes Differs between Male and Female Breast Cancer. PLoS ONE, 2013, 8, e78299. | 1.1 | 46 |
| 50 | Gene expression in inherited breast cancer. Advances in Cancer Research, 2002, 84, 1-34. | 1.9 | 44 |
| 51 | DNA methylation analyses of urothelial carcinoma reveal distinct epigenetic subtypes and an association between gene copy number and methylation status. Epigenetics, 2012, 7, 858-867. | 1.3 | 44 |
| 52 | 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, 583-594. | 1.1 | 44 |
| 53 | Analyzing tumor gene expression profiles. Artificial Intelligence in Medicine, 2003, 28, 59-74. | 3.8 | 43 |
| 54 | Integrative epigenomic analysis of differential DNA methylation in urothelial carcinoma. Genome Medicine, 2015, 7, 23. | 3.6 | 42 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 55 | 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 |
| 56 | 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 |
| 57 | Microarray-Based Cancer Diagnosis with Artificial Neural Networks. <i>BioTechniques</i> , 2003, 34, S30-S35. | 0.8 | 37 |
| 58 | 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 |
| 59 | Expression profiling to predict outcome in breast cancer: the influence of sample selection. <i>Breast Cancer Research</i> , 2002, 5, 23-6. | 2.2 | 35 |
| 60 | 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 |
| 61 | Gene expression profiling demonstrates that $TGF-\beta 1$ signals exclusively through receptor complexes involving <i>Alk5</i> and identifies targets of $TGF-\beta 2$ signaling. <i>Physiological Genomics</i> , 2005, 21, 396-403. | 1.0 | 33 |
| 62 | 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 |
| 63 | 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 |
| 64 | Matching protein structures with fuzzy alignments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 11936-11940. | 3.3 | 29 |
| 65 | DNA methylation subgroups in melanoma are associated with proliferative and immunological processes. <i>BMC Medical Genomics</i> , 2015, 8, 73. | 0.7 | 29 |
| 66 | 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 |
| 67 | Analysis of DNA methylation patterns in the tumor immune microenvironment of metastatic melanoma. <i>Molecular Oncology</i> , 2020, 14, 933-950. | 2.1 | 29 |
| 68 | 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 |
| 69 | Bose-Einstein correlations in the Lund model. <i>Nuclear Physics B</i> , 1998, 513, 627-644. | 0.9 | 27 |
| 70 | Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. <i>Nature Communications</i> , 2020, 11, 4748. | 5.8 | 27 |
| 71 | 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 |
| 72 | Genomic and Transcriptional Alterations in Lung Adenocarcinoma in Relation to Smoking History. <i>Clinical Cancer Research</i> , 2014, 20, 4912-4924. | 3.2 | 24 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 73 | MicroRNA-200c-141 and β -catenin are required for breast epithelial differentiation and branching morphogenesis. <i>Developmental Biology</i> , 2015, 403, 150-161. | 0.9 | 23 |
| 74 | A strategy for identifying putative causes of gene expression variation in human cancers. <i>Journal of the Franklin Institute</i> , 2004, 341, 77-88. | 1.9 | 21 |
| 75 | Transverse and longitudinal Bose-Einstein correlations. <i>Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics</i> , 1998, 421, 283-288. | 1.5 | 19 |
| 76 | ACID: a database for microarray clone information. <i>Bioinformatics</i> , 2004, 20, 2305-2306. | 1.8 | 18 |
| 77 | Revealing signaling pathway deregulation by using gene expression signatures and regulatory motif analysis. <i>Genome Biology</i> , 2007, 8, R77. | 13.9 | 18 |
| 78 | 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 |
| 79 | DNA methylation and histone modifications regulate SOX11 expression in lymphoid and solid cancer cells. <i>BMC Cancer</i> , 2015, 15, 273. | 1.1 | 14 |
| 80 | Multiclass discovery in array data. <i>BMC Bioinformatics</i> , 2004, 5, 70. | 1.2 | 11 |
| 81 | Consensus of gene expression phenotypes and prognostic risk predictors in primary lung adenocarcinoma. <i>Oncotarget</i> , 2016, 7, 52957-52973. | 0.8 | 11 |
| 82 | Environmentally induced DNA methylation is inherited across generations in an aquatic keystone species. <i>IScience</i> , 2022, 25, 104303. | 1.9 | 11 |
| 83 | Is there screwiness at the end of the QCD cascades?. <i>Journal of High Energy Physics</i> , 1998, 1998, 014-014. | 1.6 | 10 |
| 84 | Making Breast Cancer Molecular Subtypes Robust?. <i>Journal of the National Cancer Institute</i> , 2014, 107, dju386-dju386. | 3.0 | 10 |
| 85 | Microarray-based cancer diagnosis with artificial neural networks. <i>BioTechniques</i> , 2003, Suppl, 30-5. | 0.8 | 10 |
| 86 | 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 |
| 87 | Mitochondrial dysfunction in adult midbrain dopamine neurons triggers an early immune response. <i>PLoS Genetics</i> , 2021, 17, e1009822. | 1.5 | 8 |
| 88 | Mutational patterns and clonal evolution from diagnosis to relapse in pediatric acute lymphoblastic leukemia. <i>Scientific Reports</i> , 2021, 11, 15988. | 1.6 | 6 |
| 89 | Nonfamilial Breast Cancer Subtypes. <i>Methods in Molecular Biology</i> , 2013, 973, 279-295. | 0.4 | 5 |
| 90 | Classification of Genomic and Proteomic Data Using Support Vector Machines. , 2007, , 187-202. | | 4 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 91 | Classification of Expression Patterns Using Artificial Neural Networks. , 2003, , 201-215. | | 3 |
| 92 | Bose-Einstein and colour interference in W-pair decays. European Physical Journal C, 1998, 5, 275. | 1.4 | 3 |
| 93 | 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 |
| 94 | Transverse and Longitudinal Bose-Einstein Correlations in $e + e \rightarrow \gamma \gamma$ Annihilation. , 1999, , 425-428. | | 0 |
| 95 | The Feynman-Wilson gas and the Lund model. European Physical Journal C, 1999, 7, 251. | 1.4 | 0 |