Matti Nykter

List of Publications by Year
in descending order

87 papers	5,254 citations	136885 32 h-index	95218 68 g-index
94 all docs	94 docs citations	94 times ranked	10787 citing authors

#	Article	IF	Citations
1	The evolutionary history of lethal metastatic prostate cancer. Nature, 2015, 520, 353-357.	13.7	1,185
2	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	2.9	407
3	Circulating Tumor DNA Genomics Correlate with Resistance to Abiraterone and Enzalutamide in Prostate Cancer. Cancer Discovery, 2018, 8, 444-457.	7.7	376
4	Concordance of Circulating Tumor DNA and Matched Metastatic Tissue Biopsy in Prostate Cancer. Journal of the National Cancer Institute, 2017, 109, .	3.0	288
5	A prostate cancer susceptibility allele at 6q22 increases RFX6 expression by modulating HOXB13 chromatin binding. Nature Genetics, 2014, 46, 126-135.	9.4	182
6	Treatment Outcomes and Tumor Loss of Heterozygosity in Germline DNA Repair–deficient Prostate Cancer. European Urology, 2017, 72, 34-42.	0.9	179
7	Circulating Tumor DNA Abundance and Potential Utility in De Novo Metastatic Prostate Cancer. European Urology, 2019, 75, 667-675.	0.9	131
8	Circulating Tumor DNA Reveals Clinically Actionable Somatic Genome of Metastatic Bladder Cancer. Clinical Cancer Research, 2017, 23, 6487-6497.	3.2	121
9	Integrative proteomics in prostate cancer uncovers robustness against genomic and transcriptomic aberrations during disease progression. Nature Communications, 2018, 9, 1176.	5.8	117
10	Ageing-associated changes in the human DNA methylome: genomic locations and effects on gene expression. BMC Genomics, 2015, 16, 179.	1.2	110
11	Immunogenomic Landscape of Hematological Malignancies. Cancer Cell, 2020, 38, 380-399.e13.	7.7	109
12	Androgen Receptor Deregulation Drives Bromodomain-Mediated Chromatin Alterations in Prostate Cancer. Cell Reports, 2017, 19, 2045-2059.	2.9	99
13	Plasma ctDNA is a tumor tissue surrogate and enables clinical-genomic stratification of metastatic bladder cancer. Nature Communications, 2021, 12, 184.	5.8	85
14	Chromatin accessibility is associated with CRISPR-Cas9 efficiency in the zebrafish (Danio rerio). PLoS ONE, 2018, 13, e0196238.	1.1	82
15	Metagenomics of the faecal virome indicate a cumulative effect of enterovirus and gluten amount on the risk of coeliac disease autoimmunity in genetically at risk children: the TEDDY study. Gut, 2020, 69, 1416-1422.	6.1	82
16	Genetic and Epigenetic Characteristics of Inflammatory Bowel Disease–Associated Colorectal Cancer. Gastroenterology, 2021, 161, 592-607.	0.6	81
17	IGFBP2 potentiates nuclear EGFR–STAT3 signaling. Oncogene, 2016, 35, 738-747.	2.6	70
18	Transcriptome Sequencing Reveals *PCAT5* as a Novel ERG-Regulated Long Noncoding RNA in Prostate Cancer. Cancer Research, 2015, 75, 4026-4031.	0.4	68

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19	Constitutively active androgen receptor splice variants AR-V3, AR-V7 and AR-V9 are co-expressed in castration-resistant prostate cancer metastases. British Journal of Cancer, 2018, 119, 347-356.	2.9	63
20	MicroRNA Expression Profile of Primary Prostate Cancer Stem Cells as a Source of Biomarkers and Therapeutic Targets. European Urology, 2015, 67, 7-10.	0.9	61
21	Nrf2 and SQSTM1/p62 jointly contribute to mesenchymal transition and invasion in glioblastoma. Oncogene, 2019, 38, 7473-7490.	2.6	61
22	Single-cell ATAC and RNA sequencing reveal pre-existing and persistent cells associated with prostate cancer relapse. Nature Communications, 2021, 12, 5307.	5.8	58
23	Computational Characterization of Suppressive Immune Microenvironments in Glioblastoma. Cancer Research, 2018, 78, 5574-5585.	0.4	53
24	Oncogenic K-Ras upregulates ITGA6 expression via FOSL1 to induce anoikis resistance and synergizes with αV-Class integrins to promote EMT. Oncogene, 2017, 36, 5681-5694.	2.6	52
25	Comparison of iTRAQ and SWATH in a clinical study with multiple time points. Clinical Proteomics, 2018, 15, 24.	1.1	50
26	Laminin α5 substrates promote survival, network formation and functional development of human pluripotent stem cell-derived neurons in vitro. Stem Cell Research, 2017, 24, 118-127.	0.3	47
27	Prostate cancer evolution from multilineage primary to single lineage metastases with implications for liquid biopsy. Nature Communications, 2020, 11, 5070.	5.8	44
28	Evolution of Castration-Resistant Prostate Cancer in ctDNA during Sequential Androgen Receptor Pathway Inhibition. Clinical Cancer Research, 2021, 27, 4610-4623.	3.2	41
29	Biological Information as Set-Based Complexity. IEEE Transactions on Information Theory, 2010, 56, 667-677.	1.5	39
30	Epigenetically altered miR‑193b targets cyclin D1 in prostate cancer. Cancer Medicine, 2015, 4, 1417-1425.	1.3	39
31	Cabazitaxel versus abiraterone or enzalutamide in poor prognosis metastatic castration-resistant prostate cancer: a multicentre, randomised, open-label, phase II trial. Annals of Oncology, 2021, 32, 896-905.	0.6	39
32	The expression of AURKA is androgen regulated in castration-resistant prostate cancer. Scientific Reports, 2017, 7, 17978.	1.6	38
33	Metastasis detection from whole slide images using local features and random forests. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2017, 91, 555-565.	1.1	37
34	Genome-wide repression of eRNA and target gene loci by the ETV6-RUNX1 fusion in acute leukemia. Genome Research, 2016, 26, 1468-1477.	2.4	31
35	Mutational Landscapes of Smoking-Related Cancers in Caucasians and African Americans: Precision Oncology Perspectives at Wake Forest Baptist Comprehensive Cancer Center. Theranostics, 2017, 7, 2914-2923.	4.6	31
36	Interleukin 10 mutant zebrafish have an enhanced interferon gamma response and improved survival against a Mycobacterium marinum infection. Scientific Reports, 2018, 8, 10360.	1.6	31

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37	Estimation of tumor cell total mRNA expression in 15 cancer types predicts disease progression. Nature Biotechnology, 2022, 40, 1624-1633.	9.4	31
38	Comparative analysis of tissue reconstruction algorithms for 3D histology. Bioinformatics, 2018, 34, 3013-3021.	1.8	30
39	Myeloid cell expressed proprotein convertase FURIN attenuates inflammation. Oncotarget, 2016, 7, 54392-54404.	0.8	30
40	Microseminoprotein-Beta Expression in Different Stages of Prostate Cancer. PLoS ONE, 2016, 11, e0150241.	1.1	28
41	Circulating mutational portrait of cancer: manifestation of aggressive clonal events in both early and late stages. Journal of Hematology and Oncology, 2017, 10, 100.	6.9	28
42	Virtual cell imaging: A review on simulation methods employed in image cytometry. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2016, 89, 1057-1072.	1.1	27
43	Integrated clinical, whole-genome, and transcriptome analysis of multisampled lethal metastatic prostate cancer. Journal of Physical Education and Sports Management, 2016, 2, a000752.	0.5	24
44	Data-driven characterization of molecular phenotypes across heterogeneous sample collections. Nucleic Acids Research, 2019, 47, e76-e76.	6.5	23
45	Hemap: An Interactive Online Resource for Characterizing Molecular Phenotypes across Hematologic Malignancies. Cancer Research, 2019, 79, 2466-2479.	0.4	23
46	CD109-GP130 interaction drives glioblastoma stem cell plasticity and chemoresistance through STAT3 activity. JCI Insight, 2021, 6, .	2.3	23
47	Recurrent SKIL-activating rearrangements in ETS-negative prostate cancer. Oncotarget, 2015, 6, 6235-6250.	0.8	23
48	Comparative analysis of osteoblast gene expression profiles and Runx2 genomic occupancy of mouse and human osteoblasts in vitro. Gene, 2017, 626, 119-131.	1.0	22
49	Frequent mutation of the FOXA1 untranslated region in prostate cancer. Communications Biology, 2018, 1, 122.	2.0	21
50	Vipie: web pipeline for parallel characterization of viral populations from multiple NGS samples. BMC Genomics, 2017, 18, 378.	1.2	20
51	Expression Analysis of Platinum Sensitive and Resistant Epithelial Ovarian Cancer Patient Samples Reveals New Candidates for Targeted Therapies. Translational Oncology, 2018, 11, 1160-1170.	1.7	19
52	Extensive reprogramming of the nascent transcriptome during iPSC to hepatocyte differentiation. Scientific Reports, 2019, 9, 3562.	1.6	19
53	Twist predicts poor outcome of patients with astrocytic glioma. Journal of Clinical Pathology, 2015, 68, 905-912.	1.0	17
54	OUP accepted manuscript. Neuro-Oncology, 2017, 19, 1206-1216.	0.6	17

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55	RNA Polymerase III Subunit POLR3G Regulates Specific Subsets of PolyA+ and SmallRNA Transcriptomes and Splicing in Human Pluripotent Stem Cells. Stem Cell Reports, 2017, 8, 1442-1454.	2.3	16
56	Inherited DNA Repair Gene Mutations in Men with Lethal Prostate Cancer. Genes, 2020, 11, 314.	1.0	16
57	Assessment of PARP protein expression in epithelial ovarian cancer by ELISA pharmacodynamic assay and immunohistochemistry. Tumor Biology, 2016, 37, 11991-11999.	0.8	14
58	Chromatin and Epigenetic Dysregulation of Prostate Cancer Development, Progression, and Therapeutic Response. Cancers, 2021, 13, 3325.	1.7	14
59	Characterization of immune response against Mycobacterium marinum infection in the main hematopoietic organ of adult zebrafish (Danio rerio). Developmental and Comparative Immunology, 2020, 103, 103523.	1.0	13
60	Prostateâ€specific membrane antigen expression in the vasculature of primary lung carcinomas associates with faster metastatic dissemination toÂthe brain. Journal of Cellular and Molecular Medicine, 2020, 24, 6916-6927.	1.6	12
61	Bone morphogenetic protein 4 regulates micro<scp>RNA</scp> expression in breast cancer cell lines in diverse fashion. Genes Chromosomes and Cancer, 2016, 55, 227-236.	1.5	11
62	Independent and cumulative coeliac disease-susceptibility loci are associated with distinct disease phenotypes. Journal of Human Genetics, 2021, 66, 613-623.	1.1	11
63	Analysis of spatial heterogeneity in normal epithelium and preneoplastic alterations in mouse prostate tumor models. Scientific Reports, 2017, 7, 44831.	1.6	10
64	Essential Physiological Differences Characterize Short- and Long-Lived Strains of Drosophila melanogaster. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2019, 74, 1835-1843.	1.7	9
65	NRF2, DJ1 and SNRX1 and their prognostic impact in astrocytic gliomas. Histology and Histopathology, 2018, 33, 791-801.	0.5	9
66	Construction of therapeutically relevant human prostate epithelial fate map by utilising miRNA and mRNA microarray expression data. British Journal of Cancer, 2015, 113, 611-615.	2.9	8
67	Feature-based analysis of mouse prostatic intraepithelial neoplasia in histological tissue sections. Journal of Pathology Informatics, 2016, 7, 5.	0.8	8
68	A Data Integration Framework for Prediction of Transcription Factor Targets. Annals of the New York Academy of Sciences, 2009, 1158, 205-214.	1.8	7
69	Segmentum: a tool for copy number analysis of cancer genomes. BMC Bioinformatics, 2017, 18, 215.	1.2	7
70	Supervised pathway analysis of blood gene expression profiles in Alzheimer's disease. Neurobiology of Aging, 2019, 84, 98-108.	1.5	7
71	Proprotein convertase subtilisin/kexin type 9 regulates the production of acuteâ€phase reactants from the liver. Liver International, 2021, 41, 2511-2522.	1.9	7
72	Subclone Eradication Analysis Identifies Targets for Enhanced Cancer Therapy and Reveals L1 Retrotransposition as a Dynamic Source of Cancer Heterogeneity. Cancer Research, 2021, 81, 4901-4909.	0.4	6

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73	Spatial analysis of histology in 3D: quantification and visualization of organ and tumor level tissue environment. Heliyon, 2022, 8, e08762.	1.4	6
74	Whole-exome sequencing identifies germline mutation in *TP53* and *ATRX* in a child with genomically aberrant AT/RT and her mother with anaplastic astrocytoma. Journal of Physical Education and Sports Management, 2018, 4, a002246.	0.5	5
75	Proteomics of prostate cancer â€" revealing how cancer cells master their messy genomes. Oncoscience, 2018, 5, 216-217.	0.9	5
76	Modes of immunosuppression in glioblastoma microenvironment. Oncotarget, 2019, 10, 920-921.	0.8	5
77	Overexpression of PTP4A3 in ETV6-RUNX1 acute lymphoblastic leukemia. Leukemia Research, 2017, 54, 1-6.	0.4	4
78	AR and ERG drive the expression of prostate cancer specific long noncoding RNAs. Oncogene, 2020, 39, 5241-5251.	2.6	4
79	Moderate-to-strong expression of FGFR3 and TP53 alterations in a subpopulation of choroid plexus tumors. Histology and Histopathology, 2020, 35, 673-680.	0.5	3
80	Bioinformatics Assembling and Assessment of Novel Coxsackievirus B1 Genome. Methods in Molecular Biology, 2018, 1838, 261-272.	0.4	2
81	Combined Longitudinal Clinical and Autopsy Phenomic Assessment in Lethal Metastatic Prostate Cancer: Recommendations for Advancing Precision Medicine. European Urology Open Science, 2021, 30, 47-62.	0.2	2
82	The transcription factor network of *E. coli* steers global responses to shifts in RNAP concentration. Nucleic Acids Research, 0, , .	6.5	2
83	Identification of Novel Drug Targets in T-Cell Acute Lymphoblastic Leukemia. Blood, 2015, 126, 3646-3646.	0.6	1
84	Novel ZNF414 activity characterized by integrative analysis of ChIP-exo, ATAC-seq and RNA-seq data. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2022, 1865, 194811.	0.9	1
85	Mapping dynamical states to structural classes for Boolean networks using a classification algorithm. , 2015, , .		0
86	P01.143 Unravelling the immune response components landscape in diffuse gliomas using immunophenotyping approach. Neuro-Oncology, 2018, 20, iii265-iii265.	0.6	0
87	Pan-Hematopoietic Cancer Gene Expression Analysis Identifies Immunologically Active Acute Myeloid Leukemia Subtypes. Blood, 2016, 128, 1725-1725.	0.6	0