## Olli Kallioniemi

List of Publications by Year in descending order

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438 papers

52,432 citations

102 h-index

1888

219 g-index

460 all docs

460 docs citations

460 times ranked

50887 citing authors

#	Article	IF	CITATIONS
1	Tissue microarrays for high-throughput molecular profiling of tumor specimens. Nature Medicine, 1998, 4, 844-847.	15.2	3,661
2	Average Risks of Breast and Ovarian Cancer Associated with BRCA1 or BRCA2 Mutations Detected in Case Series Unselected for Family History: A Combined Analysis of 22 Studies. American Journal of Human Genetics, 2003, 72, 1117-1130.	2.6	3,105
3	Comparative genomic hybridization for molecular cytogenetic analysis of solid tumors. Science, 1992, 258, 818-821.	6.0	3,065
4	International network of cancer genome projects. Nature, 2010, 464, 993-998.	13.7	2,114
5	Gene-Expression Profiles in Hereditary Breast Cancer. New England Journal of Medicine, 2001, 344, 539-548.	13.9	1,669
6	High frequency of BRAF mutations in nevi. Nature Genetics, 2003, 33, 19-20.	9.4	1,547
7	AIB1, a Steroid Receptor Coactivator Amplified in Breast and Ovarian Cancer. Science, 1997, 277, 965-968.	6.0	1,514
8	In vivo amplification of the androgen receptor gene and progression of human prostate cancer. Nature Genetics, 1995, 9, 401-406.	9.4	1,316
9	Optimizing comparative genomic hybridization for analysis of DNA sequence copy number changes in solid tumors. Genes Chromosomes and Cancer, 1994, 10, 231-243.	1.5	1,215
10	Major Susceptibility Locus for Prostate Cancer on Chromosome 1 Suggested by a Genome-Wide Search. Science, 1996, 274, 1371-1374.	6.0	717
11	Somatic <i>STAT3</i> Mutations in Large Granular Lymphocytic Leukemia. New England Journal of Medicine, 2012, 366, 1905-1913.	13.9	681
12	Detection and mapping of amplified DNA sequences in breast cancer by comparative genomic hybridization Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 2156-2160.	3.3	661
13	A community effort to assess and improve drug sensitivity prediction algorithms. Nature Biotechnology, 2014, 32, 1202-1212.	9.4	653
14	Evidence for a prostate cancer susceptibility locus on the X chromosome Nature Genetics, 1998, 20, 175-179.	9.4	641
15	Tissue Microarrays for Rapid Linking of Molecular Changes to Clinical Endpoints. American Journal of Pathology, 2001, 159, 2249-2256.	1.9	521
16	Expression of Cytokeratins 17 and 5 Identifies a Group of Breast Carcinomas with Poor Clinical Outcome. American Journal of Pathology, 2002, 161, 1991-1996.	1.9	494
17	ERBB2 amplification in breast cancer analyzed by fluorescence in situ hybridization Proceedings of the National Academy of Sciences of the United States of America, 1992, 89, 5321-5325.	3.3	493
18	Tissue microarray technology for high-throughput molecular profiling of cancer. Human Molecular Genetics, 2001, 10, 657-662.	1.4	479

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19	Germline mutations in the ribonuclease L gene in families showing linkage with HPC1. Nature Genetics, 2002, 30, 181-184.	9.4	470
20	The BOADICEA model of genetic susceptibility to breast and ovarian cancers: updates and extensions. British Journal of Cancer, 2008, 98, 1457-1466.	2.9	461
21	Novel Theranostic Opportunities Offered by Characterization of Altered Membrane Lipid Metabolism in Breast Cancer Progression. Cancer Research, 2011, 71, 3236-3245.	0.4	444
22	Loss of the tight junction protein claudin-7 correlates with histological grade in both ductal carcinoma in situ and invasive ductal carcinoma of the breast. Oncogene, 2003, 22, 2021-2033.	2.6	415
23	A CHEK2 Genetic Variant Contributing to a Substantial Fraction of Familial Breast Cancer. American Journal of Human Genetics, 2002, 71, 432-438.	2.6	402
24	MicroRNA in Prostate, Bladder, and Kidney Cancer: A Systematic Review. European Urology, 2011, 59, 671-681.	0.9	401
25	Break-Induced Replication Repair of Damaged Forks Induces Genomic Duplications in Human Cells. Science, 2014, 343, 88-91.	6.0	387
26	High-Throughput Tissue Microarray Analysis to Evaluate Genes Uncovered by cDNA Microarray Screening in Renal Cell Carcinoma. American Journal of Pathology, 1999, 154, 981-986.	1.9	376
27	Association of C-erbB-2 protein over-expression with high rate of cell proliferation, increased risk of visceral metastasis and poor long-term survival in breast cancer. International Journal of Cancer, 1991, 49, 650-655.	2.3	352
28	Association of Overexpression of Tumor Suppressor Protien p53 With Rapid Cell Proliferation and Poor Prognosis in Node-Negative Breast Cancer Patients. Journal of the National Cancer Institute, 1992, 84, 1109-1114.	3.0	337
29	Individualized Systems Medicine Strategy to Tailor Treatments for Patients with Chemorefractory Acute Myeloid Leukemia. Cancer Discovery, 2013, 3, 1416-1429.	7.7	334
30	Hormone Therapy Failure in Human Prostate Cancer: Analysis by Complementary DNA and Tissue Microarrays. Journal of the National Cancer Institute, 1999, 91, 1758-1764.	3.0	325
31	Dual role of FoxA1 in androgen receptor binding to chromatin, androgen signalling and prostate cancer. EMBO Journal, 2011, 30, 3962-3976.	3.5	318
32	The impact of low-frequency and rare variants on lipid levels. Nature Genetics, 2015, 47, 589-597.	9.4	310
33	Identification of fusion genes in breast cancer by paired-end RNA-sequencing. Genome Biology, 2011, 12, R6.	13.9	301
34	Small Subgroup of Aggressive, Highly Proliferative Prostatic Carcinomas Defined by p53 Accumulation. Journal of the National Cancer Institute, 1992, 84, 883-887.	3.0	299
35	A Comprehensive Panel of Three-Dimensional Models for Studies of Prostate Cancer Growth, Invasion and Drug Responses. PLoS ONE, 2010, 5, e10431.	1.1	299
36	miRNA-mRNA Integrated Analysis Reveals Roles for miRNAs in Primary Breast Tumors. PLoS ONE, 2011, 6, e16915.	1.1	278

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37	Emerging molecular biomarkers—blood-based strategies to detect and monitor cancer. Nature Reviews Clinical Oncology, 2011, 8, 142-150.	12.5	277
38	Genome screening by comparative genomic hybridization. Trends in Genetics, 1997, 13, 405-409.	2.9	272
39	Positional cloning of ZNF217 and NABC1: Genes amplified at 20q13.2 and overexpressed in breast carcinoma. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 8703-8708.	3.3	271
40	Discovery of somatic STAT5b mutations in large granular lymphocytic leukemia. Blood, 2013, 121, 4541-4550.	0.6	252
41	Detecting Activation of Ribosomal Protein S6 Kinase by Complementary DNA and Tissue Microarray Analysis. Journal of the National Cancer Institute, 2000, 92, 1252-1259.	3.0	251
42	Computer image analysis of comparative genomic hybridization. Cytometry, 1995, 19, 10-26.	1.8	250
43	Systematic Analysis of MicroRNAs Targeting the Androgen Receptor in Prostate Cancer Cells. Cancer Research, 2011, 71, 1956-1967.	0.4	244
44	Quantitative scoring of differential drug sensitivity for individually optimized anticancer therapies. Scientific Reports, 2014, 4, 5193.	1.6	243
45	Improving the prognostic value of DNA flow cytometry in breast cancer by combining DNA index and S-phase fraction: A proposed classification of DNA histograms in breast cancer. Cancer, 1988, 62, 2183-2190.	2.0	240
46	Systematic bioinformatic analysis of expression levels of 17,330 human genes across 9,783 samples from 175 types of healthy and pathological tissues. Genome Biology, 2008, 9, R139.	13.9	234
47	High-Throughput Tissue Microarray Analysis of Cyclin E Gene Amplification and Overexpression in Urinary Bladder Cancer. American Journal of Pathology, 2000, 157, 787-794.	1.9	232
48	ProteomeBinders: planning a European resource of affinity reagents for analysis of the human proteome. Nature Methods, 2007, 4, 13-17.	9.0	231
49	<i>FZD4</i> as a Mediator of <i>ERG</i> Oncogeneâ€"Induced WNT Signaling and Epithelial-to-Mesenchymal Transition in Human Prostate Cancer Cells. Cancer Research, 2010, 70, 6735-6745.	0.4	229
50	Comparison of fresh and paraffin-embedded tissue as starting material for DNA flow cytometry and evaluation of intratumor heterogeneity. Cytometry, 1988, 9, 164-169.	1.8	228
51	Enhanced serine production by bone metastatic breast cancer cells stimulates osteoclastogenesis. Breast Cancer Research and Treatment, 2011, 125, 421-430.	1.1	222
52	Tissue microarrays (TMAs) for high-throughput molecular pathology research. International Journal of Cancer, 2001, 94, 1-5.	2.3	220
53	TMPRSS2 Fusions with Oncogenic ETS Factors in Prostate Cancer Involve Unbalanced Genomic Rearrangements and Are Associated with HDAC1 and Epigenetic Reprogramming. Cancer Research, 2006, 66, 10242-10246.	0.4	209
54	SATB2 in Combination With Cytokeratin 20 Identifies Over 95% of all Colorectal Carcinomas. American Journal of Surgical Pathology, 2011, 35, 937-948.	2.1	209

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55	Axitinib effectively inhibits BCR-ABL1(T315I) with a distinct binding conformation. Nature, 2015, 519, 102-105.	13.7	207
56	CIP2A Is Associated with Human Breast Cancer Aggressivity. Clinical Cancer Research, 2009, 15, 5092-5100.	3.2	205
57	Protein lysate microarray analysis to identify microRNAs regulating estrogen receptor signaling in breast cancer cell lines. Oncogene, 2009, 28, 3926-3936.	2.6	205
58	Inferring Tree Models for Oncogenesis from Comparative Genome Hybridization Data. Journal of Computational Biology, 1999, 6, 37-51.	0.8	202
59	Germline Alterations of the RNASEL Gene, a Candidate HPC1 Gene at 1q25, in Patients and Families with Prostate Cancer. American Journal of Human Genetics, 2002, 70, 1299-1304.	2.6	202
60	Identification of gains and losses of DNA sequences in primary bladder cancer by comparative genomic hybridization. Genes Chromosomes and Cancer, 1995, 12, 213-219.	1.5	198
61	Prognostic significance of dna index, multiploidy, and S-phase fraction in ovarian cancer. Cancer, 1988, 61, 334-339.	2.0	197
62	Differentiation of Human Embryonal Carcinomas In vitro and In vivo Reveals Expression Profiles Relevant to Normal Development. Cancer Research, 2005, 65, 5588-5598.	0.4	194
63	A Nuclear Factor, ASC-2, as a Cancer-amplified Transcriptional Coactivator Essential for Ligand-dependent Transactivation by Nuclear Receptors in Vivo. Journal of Biological Chemistry, 1999, 274, 34283-34293.	1.6	190
64	Molecular cytogenetic analysis of 11 new breast cancer cell lines. British Journal of Cancer, 1999, 81, 1328-1334.	2.9	186
65	High-Throughput Cell-Based Screening of 4910 Known Drugs and Drug-like Small Molecules Identifies Disulfiram as an Inhibitor of Prostate Cancer Cell Growth. Clinical Cancer Research, 2009, 15, 6070-6078.	3.2	185
66	SHARPIN is an endogenous inhibitor of $\hat{I}^21$ -integrin activation. Nature Cell Biology, 2011, 13, 1315-1324.	4.6	184
67	Nonsense-mediated decay microarray analysis identifies mutations of EPHB2 in human prostate cancer. Nature Genetics, 2004, 36, 979-983.	9.4	180
68	Are data from different gene expression microarray platforms comparable?. Genomics, 2004, 83, 1164-1168.	1.3	179
69	Integrin Trafficking Regulated by Rab21 Is Necessary for Cytokinesis. Developmental Cell, 2008, 15, 371-385.	3.1	177
70	Colorectal Cancer Consensus Molecular Subtypes Translated to Preclinical Models Uncover Potentially Targetable Cancer Cell Dependencies. Clinical Cancer Research, 2018, 24, 794-806.	3.2	177
71	RNAi Microarray Analysis in Cultured Mammalian Cells. Genome Research, 2003, 13, 2341-2347.	2.4	173
72	Use of cancerâ€specific genomic rearrangements to quantify disease burden in plasma from patients with solid tumors. Genes Chromosomes and Cancer, 2010, 49, 1062-1069.	1.5	172

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73	Application of Active and Kinase-Deficient Kinome Collection for Identification of Kinases Regulating Hedgehog Signaling. Cell, 2008, 133, 537-548.	13.5	171
74	Evaluation of cell proliferation in breast carcinoma. Comparison of Ki-67 immunohistochemical study, DNA flow cytometric analysis, and mitotic count. Cancer, 1990, 65, 1180-1184.	2.0	169
75	Metabolomic Profiling of Extracellular Vesicles and Alternative Normalization Methods Reveal Enriched Metabolites and Strategies to Study Prostate Cancer-Related Changes. Theranostics, 2017, 7, 3824-3841.	4.6	167
76	Tumour DNA ploidy as an independent prognostic factor in breast cancer. British Journal of Cancer, 1987, 56, 637-642.	2.9	163
77	Population-Based Study of BRCA1 and BRCA2 Mutations in 1035 Unselected Finnish Breast Cancer Patients. Journal of the National Cancer Institute, 2000, 92, 1529-1531.	3.0	159
78	Claudin-1 overexpression in melanoma is regulated by PKC and contributes to melanoma cell motility. Oncogene, 2007, 26, 3846-3856.	2.6	155
79	High-Throughput 3D Screening Reveals Differences in Drug Sensitivities between Culture Models of JIMT1 Breast Cancer Cells. PLoS ONE, 2013, 8, e77232.	1.1	154
80	Somatic deletions in hereditary breast cancers implicate 13q21 as a putative novel breast cancer susceptibility locus. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 9603-9608.	3.3	153
81	Highâ€throughput screens identify microRNAs essential for HER2 positive breast cancer cell growth. Molecular Oncology, 2014, 8, 93-104.	2.1	146
82	Androgen regulation of microâ€RNAs in prostate cancer. Prostate, 2011, 71, 604-614.	1.2	144
83	Salinomycin inhibits prostate cancer growth and migration via induction of oxidative stress. British Journal of Cancer, 2012, 106, 99-106.	2.9	141
84	Aneuploid DNA content and high S-phase fraction of tumour cells are related to poor prognosis in patients with primary breast cancer. European Journal of Cancer & Clinical Oncology, 1987, 23, 277-282.	0.9	134
85	ANDROGEN RECEPTOR GENE AMPLIFICATION AT PRIMARY PROGRESSION PREDICTS RESPONSE TO COMBINED ANDROGEN BLOCKADE AS SECOND LINE THERAPY FOR ADVANCED PROSTATE CANCER. Journal of Urology, 2000, 164, 1992-1995.	0.2	134
86	CHEK2 variant I157T may be associated with increased breast cancer risk. International Journal of Cancer, 2004, 111, 543-547.	2.3	134
87	Tissue Microarrays: What Will They Bring to Molecular and Anatomic Pathology?. Advances in Anatomic Pathology, 2001, 8, 14-20.	2.4	133
88	Low proportion of BRCA1 and BRCA2 mutations in Finnish breast cancer families: evidence for additional susceptibility genes. Human Molecular Genetics, 1997, 6, 2309-2315.	1.4	128
89	ANX7, a candidate tumor suppressor gene for prostate cancer. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 4575-4580.	3.3	128
90	MiR-9, -31, and -182 Deregulation Promote Proliferation and Tumor Cell Survival in Colon Cancer. Neoplasia, 2012, 14, 868-IN21.	2.3	124

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91	Failure of hormone therapy in prostate cancer involves systematic restoration of androgen responsive genes and activation of rapamycin sensitive signaling. Oncogene, 2001, 20, 6718-6723.	2.6	122
92	Breast and ovarian cancer risks to carriers of the BRCA1 5382insC and 185delAG and BRCA2 6174delT mutations: a combined analysis of 22 population based studies. Journal of Medical Genetics, 2005, 42, 602-603.	1.5	121
93	Role of ErbB4 in Breast Cancer. Journal of Mammary Gland Biology and Neoplasia, 2008, 13, 259-268.	1.0	121
94	Non-canonical Notch signaling activates IL-6/JAK/STAT signaling in breast tumor cells and is controlled by p53 and IKK $\hat{l}$ ±/IKK $\hat{l}$ 2. Oncogene, 2013, 32, 4892-4902.	2.6	121
95	Consensus review of the clinical utility of dna content cytometry in prostate cancer. Cytometry, 1993, 14, 497-500.	1.8	120
96	Systems pathology by multiplexed immunohistochemistry and whole-slide digital image analysis. Scientific Reports, 2017, 7, 15580.	1.6	120
97	Improved technique for analysis of formalin-fixed, paraffin-embedded tumors by fluorescence in situ hybridization. Cytometry, 1994, 16, 93-99.	1.8	116
98	Association of tamoxifen resistance and lipid reprogramming in breast cancer. BMC Cancer, 2018, 18, 850.	1.1	113
99	Systematic knockdown of epigenetic enzymes identifies a novel histone demethylase PHF8 overexpressed in prostate cancer with an impact on cell proliferation, migration and invasion. Oncogene, 2012, 31, 3444-3456.	2.6	112
100	An integrated genomic approach identifies ARID1A as a candidate tumor-suppressor gene in breast cancer. Oncogene, 2012, 31, 2090-2100.	2.6	111
101	Cathepsin D expression detected by immunohistochemistry has independent prognostic value in axillary node-negative breast cancer Journal of Clinical Oncology, 1993, 11, 36-43.	0.8	110
102	High-Resolution Analysis of Gene Copy Number Alterations in Human Prostate Cancer Using CGH on cDNA Microarrays: Impact of Copy Number on Gene Expression. Neoplasia, 2004, 6, 240-247.	2.3	110
103	Comparative genomic hybridization reveals frequent gains of 20q, 8q, 11q, 12p, and 17q, and losses of 18q, 9p, and 15q in pancreatic cancer. Genes Chromosomes and Cancer, 1997, 20, 383-391.	1.5	106
104	Arachidonic Acid Pathway Members PLA2G7, HPGD, EPHX2, and CYP4F8 Identified as Putative Novel Therapeutic Targets in Prostate Cancer. American Journal of Pathology, 2011, 178, 525-536.	1.9	102
105	Integrative and Personalized QSAR Analysis in Cancer by Kernelized Bayesian Matrix Factorization. Journal of Chemical Information and Modeling, 2014, 54, 2347-2359.	2.5	101
106	Cloning ofBCAS3(17q23) andBCAS4(20q13) genes that undergo amplification, overexpression, and fusion in breast cancerâ€. Genes Chromosomes and Cancer, 2002, 35, 311-317.	1.5	100
107	ElevatederbB-2 oncoprotein levels in preoperative and follow-up serum samples define an aggressive disease course in patients with breast cancer. Cancer, 1994, 73, 652-658.	2.0	98
108	Genotyping of Adrenocortical Tumors: Very Frequent Deletions of the MEN1 Locus in 11q13 and of a 1-Centimorgan Region in 2p161. Journal of Clinical Endocrinology and Metabolism, 1999, 84, 730-735.	1.8	97

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109	Correlation of CHEK2 protein expression and c.1100delC mutation status with tumor characteristics among unselected breast cancer patients. International Journal of Cancer, 2005, 113, 575-580.	2.3	97
110	Distance-Based Reconstruction of Tree Models for Oncogenesis. Journal of Computational Biology, 2000, 7, 789-803.	0.8	96
111	High-throughput RNAi screening for novel modulators of vimentin expression identifies MTHFD2 as a regulator of breast cancer cell migration and invasion. Oncotarget, 2013, 4, 48-63.	0.8	95
112	Novel activating STAT5B mutations as putative drivers of T-cell acute lymphoblastic leukemia. Leukemia, 2014, 28, 1738-1742.	3.3	90
113	JAK1/2 and BCL2 inhibitors synergize to counteract bone marrow stromal cell–induced protection of AML. Blood, 2017, 130, 789-802.	0.6	90
114	Identification of target genes in laryngeal squamous cell carcinoma by high-resolution copy number and gene expression microarray analyses. Oncogene, 2006, 25, 6997-7008.	2.6	88
115	Novel Human Vascular Endothelial Growth Factor Genes VEGF-B and VEGF-C Localize to Chromosomes 11q13 and 4q34, Respectively. Circulation, 1996, 93, 1079-1082.	1.6	88
116	Drug response prediction by inferring pathway-response associations with kernelized Bayesian matrix factorization. Bioinformatics, 2016, 32, i455-i463.	1.8	87
117	Hardware and software requirements for quantitative analysis of comparative genomic hybridization. Cytometry, 1995, 19, 4-9.	1.8	86
118	Expression of Bcl-2 Family Member Bid in Normal and Malignant Tissues. Neoplasia, 2002, 4, 129-140.	2.3	82
119	Prognostic factors in recurrent breast cancer: relationships to site of recurrence, disease-free interval, female sex steroid receptors, ploidy and histological malignancy grading. British Journal of Cancer, 1990, 62, 142-146.	2.9	81
120	EphB2 Expression across 138 Human Tumor Types in a Tissue Microarray: High Levels of Expression in Gastrointestinal Cancers. Clinical Cancer Research, 2005, 11, 6450-6458.	3.2	81
121	Visual Mapping by Fiber-FISH. Genomics, 1995, 30, 31-36.	1.3	80
122	Monensin Is a Potent Inducer of Oxidative Stress and Inhibitor of Androgen Signaling Leading to Apoptosis in Prostate Cancer Cells. Molecular Cancer Therapeutics, 2010, 9, 3175-3185.	1.9	80
123	The HER2 amplicon includes several genes required for the growth and survival of HER2 positive breast cancer cells. Molecular Oncology, 2013, 7, 392-401.	2.1	80
124	Biochip technologies in cancer research. Annals of Medicine, 2001, 33, 142-147.	1.5	79
125	The transcription factor $Sox11$ is a prognostic factor for improved recurrence-free survival in epithelial ovarian cancer. European Journal of Cancer, 2009, 45, 1510-1517.	1.3	79
126	Different opinions on classification of DNA histograms produced from paraffin-embedded tissue. Cytometry, 1989, 10, 711-717.	1.8	77

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127	Phospholipase PLA2G7, associated with aggressive prostate cancer, promotes prostate cancer cell migration and invasion and is inhibited by statins. Oncotarget, 2011, 2, 1176-1190.	0.8	77
128	Immunohistochemical determination of estrogen and progesterone receptors in human breast carcinoma. Correlation with histopathology and dna flow cytometry. Cancer, 1990, 63, 1761-1767.	2.0	76
129	Consistency in drug response profiling. Nature, 2016, 540, E5-E6.	13.7	76
130	Genotyping of Adrenocortical Tumors: Very Frequent Deletions of the MEN1 Locus in 11q13 and of a 1-Centimorgan Region in 2p16. Journal of Clinical Endocrinology and Metabolism, 1999, 84, 730-735.	1.8	76
131	Multiple founder effects and geographical clustering of BRCA1 and BRCA2 families in Finland. European Journal of Human Genetics, 2000, 8, 757-763.	1.4	<b>7</b> 5
132	Discovery of novel drug sensitivities in T-PLL by high-throughput ex vivo drug testing and mutation profiling. Leukemia, 2018, 32, 774-787.	3.3	75
133	Immune cell contexture in the bone marrow tumor microenvironment impacts therapy response in CML. Leukemia, 2018, 32, 1643-1656.	3.3	<b>7</b> 5
134	Increased copy number at 17q22-q24 by CGH in breast cancer is due to high-level amplification of two separate regions., 1997, 20, 372-376.		74
135	Topoisomerase-Ill $\hat{\mathbf{I}}$ Is Upregulated in Malignant Peripheral Nerve Sheath Tumors and Associated With Clinical Outcome. Journal of Clinical Oncology, 2003, 21, 4586-4591.	0.8	74
136	Comprehensive Drug Testing of Patient-derived Conditionally Reprogrammed Cells from Castration-resistant Prostate Cancer. European Urology, 2017, 71, 319-327.	0.9	74
137	Steroid receptors and Ki-67 reactivity in ovarian cancer and in normal ovary: Correlation with dna flow cytometry, biochemical receptor assay, and patient survival. Journal of Pathology, 1990, 162, 295-301.	2.1	73
138	Implementing a Functional Precision Medicine Tumor Board for Acute Myeloid Leukemia. Cancer Discovery, 2022, 12, 388-401.	7.7	73
139	Identification of MicroRNAs Inhibiting TGF- $\hat{l}^2$ -Induced IL-11 Production in Bone Metastatic Breast Cancer Cells. PLoS ONE, 2012, 7, e37361.	1.1	72
140	Reanalysis of RNA-Sequencing Data Reveals Several Additional Fusion Genes with Multiple Isoforms. PLoS ONE, 2012, 7, e48745.	1.1	72
141	Generation and analysis of melanoma SAGE libraries: SAGE advice on the melanoma transcriptome. Oncogene, 2004, 23, 2264-2274.	2.6	71
142	Improved prognostic impact of S-phase values from paraffin-embedded breast and prostate carcinomas after correcting for nuclear slicing. Cytometry, 1991, 12, 413-421.	1.8	68
143	c-Jun N-Terminal Kinase Phosphorylation of MARCKSL1 Determines Actin Stability and Migration in Neurons and in Cancer Cells. Molecular and Cellular Biology, 2012, 32, 3513-3526.	1.1	68
144	Integration of Metabolomics and Expression of Glycerol-3-phosphate Acyltransferase (GPAM) in Breast Cancer—Link to Patient Survival, Hormone Receptor Status, and Metabolic Profiling. Journal of Proteome Research, 2012, 11, 850-860.	1.8	68

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145	Breeze: an integrated quality control and data analysis application for high-throughput drug screening. Bioinformatics, 2020, 36, 3602-3604.	1.8	68
146	Quality control of CGH: Impact of metaphase chromosomes and the dynamic range of hybridization. Cytometry, 1997, 28, 198-205.	1.8	66
147	A genomic map of a 6-Mb region at 13q21-q22 implicated in cancer development: identification and characterization of candidate genes. Human Genetics, 2002, 110, 111-121.	1.8	66
148	Serum CA 15-3 assay in the diagnosis and follow-up of breast cancer. British Journal of Cancer, 1988, 58, 213-215.	2.9	64
149	Androgen Receptor Gene Amplification in a Recurrent Prostate Cancer after Monotherapy with the Nonsteroidal Potent Antiandrogen Casodex (Bicalutamide) with a Subsequent Favorable Response to Maximal Androgen Blockade. European Urology, 1997, 31, 216-219.	0.9	64
150	PD-L1 <sup>+</sup> tumor-associated macrophages and PD-1 <sup>+</sup> tumor-infiltrating lymphocytes predict survival in primary testicular lymphoma. Haematologica, 2018, 103, 1908-1914.	1.7	64
151	New Paraoxonase 1 Polymorphism I102V and the Risk of Prostate Cancer in Finnish Men. Journal of the National Cancer Institute, 2003, 95, 812-818.	3.0	62
152	Androgen receptor CAG polymorphism and prostate cancer risk. Human Genetics, 2002, 111, 166-171.	1.8	61
153	Functional evidence implicating S100P in prostate cancer progression. International Journal of Cancer, 2008, 123, 330-339.	2.3	61
154	HOX gene expression predicts response to BCL-2 inhibition in acute myeloid leukemia. Leukemia, 2017, 31, 301-309.	3.3	61
155	Genetic changes associated with the acquisition of androgen-independent growth, tumorigenicity and metastatic potential in a prostate cancer model. British Journal of Cancer, 1997, 75, 190-195.	2.9	60
156	Novel findings in gene expression detected in human osteosarcoma by cDNA microarray. Cancer Genetics and Cytogenetics, 2000, 123, 128-132.	1.0	60
157	CGH, cDNA and Tissue Microarray Analyses Implicate <i>FGFR2 </i> Amplification in a Small Subset of Breast Tumors. Analytical Cellular Pathology, 2001, 22, 229-234.	2.1	60
158	Defining the molecular action of HDAC inhibitors and synergism with androgen deprivation in ERGâ€positive prostate cancer. International Journal of Cancer, 2008, 123, 2774-2781.	2.3	60
159	Identification of miR-193b Targets in Breast Cancer Cells and Systems Biological Analysis of Their Functional Impact. Molecular and Cellular Proteomics, 2011, 10, M110.005322.	2.5	60
160	KeepEX, a simple dilution protocol for improving extracellular vesicle yields from urine. European Journal of Pharmaceutical Sciences, 2017, 98, 30-39.	1.9	59
161	Novel somatic mutations in large granular lymphocytic leukemia affecting the STAT-pathway and T-cell activation. Blood Cancer Journal, 2013, 3, e168-e168.	2.8	56
162	Genetic Basis and Clonal Evolution of Human Prostate Cancer. Advances in Cancer Research, 1996, 68, 225-255.	1.9	55

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163	CHEK2 1100delC is not a risk factor for male breast cancer population. International Journal of Cancer, 2004, 108, 475-476.	2.3	55
164	Profiling Genetic Variation along the Androgen Biosynthesis and Metabolism Pathways Implicates Several Single Nucleotide Polymorphisms and Their Combinations as Prostate Cancer Risk Factors. Cancer Research, 2006, 66, 743-747.	0.4	54
165	High-Throughput Transcriptomic and RNAi Analysis Identifies AIM1, ERGIC1, TMED3 and TPX2 as Potential Drug Targets in Prostate Cancer. PLoS ONE, 2012, 7, e39801.	1.1	54
166	Novel Genomic Aberrations in Testicular Germ Cell Tumors by Array-CGH, and Associated Gene Expression Changes. Analytical Cellular Pathology, 2006, 28, 315-326.	0.7	54
167	Frequent loss of the 11q14-24 region in chronic lymphocytic leukemia: A study by comparative genomic hybridization., 1997, 19, 286-290.		53
168	Systematic Identification of MicroRNAs That Impact on Proliferation of Prostate Cancer Cells and Display Changed Expression in Tumor Tissue. European Urology, 2016, 69, 1120-1128.	0.9	53
169	Amplification and overexpression of PRUNE in human sarcomas and breast carcinomas–a possible mechanism for altering the nm23-H1 activity. Oncogene, 2001, 20, 6881-6890.	2.6	52
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