

# Sampsa Kalervo Hautaniemi

## List of Publications by Year in descending order

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170  
papers

8,779  
citations

36303

51  
h-index

49909

87  
g-index

180  
all docs

180  
docs citations

180  
times ranked

15548  
citing authors

#	ARTICLE	IF	CITATIONS
1	Multiple reaction monitoring for robust quantitative proteomic analysis of cellular signaling networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 5860-5865.	7.1	472
2	Impact of DNA amplification on gene expression patterns in breast cancer. <i>Cancer Research</i> , 2002, 62, 6240-5.	0.9	352
3	PINA v2.0: mining interactome modules. <i>Nucleic Acids Research</i> , 2012, 40, D862-D865.	14.5	321
4	Dual role of FoxA1 in androgen receptor binding to chromatin, androgen signalling and prostate cancer. <i>EMBO Journal</i> , 2011, 30, 3962-3976.	7.8	318
5	Integrated network analysis platform for protein-protein interactions. <i>Nature Methods</i> , 2009, 6, 75-77.	19.0	278
6	Systematic bioinformatic analysis of expression levels of 17,330 human genes across 9,783 samples from 175 types of healthy and pathological tissues. <i>Genome Biology</i> , 2008, 9, R139.	9.6	234
7	Effects of HER2 overexpression on cell signaling networks governing proliferation and migration. <i>Molecular Systems Biology</i> , 2006, 2, 54.	7.2	217
8	FoxA1 Specifies Unique Androgen and Glucocorticoid Receptor Binding Events in Prostate Cancer Cells. <i>Cancer Research</i> , 2013, 73, 1570-1580.	0.9	194
9	Nonsense-mediated decay microarray analysis identifies mutations of EPHB2 in human prostate cancer. <i>Nature Genetics</i> , 2004, 36, 979-983.	21.4	180
10	Are data from different gene expression microarray platforms comparable?. <i>Genomics</i> , 2004, 83, 1164-1168.	2.9	179
11	Immunogenomic profiling determines responses to combined PARP and PD-1 inhibition in ovarian cancer. <i>Nature Communications</i> , 2020, 11, 1459.	12.8	176
12	RNAi Microarray Analysis in Cultured Mammalian Cells. <i>Genome Research</i> , 2003, 13, 2341-2347.	5.5	173
13	Large-scale data integration framework provides a comprehensive view on glioblastoma multiforme. <i>Genome Medicine</i> , 2010, 2, 65.	8.2	145
14	Early recovery from cow's milk allergy is associated with decreasing IgE and increasing IgG4 binding to cow's milk epitopes. <i>Journal of Allergy and Clinical Immunology</i> , 2010, 125, 1315-1321.e9.	2.9	136
15	KSHV-Initiated Notch Activation Leads to Membrane-Type-1 Matrix Metalloproteinase-Dependent Lymphatic Endothelial-to-Mesenchymal Transition. <i>Cell Host and Microbe</i> , 2011, 10, 577-590.	11.0	123
16	Evolutionary history of metastatic breast cancer reveals minimal seeding from axillary lymph nodes. <i>Journal of Clinical Investigation</i> , 2018, 128, 1355-1370.	8.2	123
17	Gene-Expression Profiling Predicts Recurrence in Dukesâ€™ C Colorectal Cancer. <i>Gastroenterology</i> , 2005, 129, 874-884.	1.3	119
18	Characterising metabolically healthy obesity in weight-discordant monozygotic twins. <i>Diabetologia</i> , 2014, 57, 167-176.	6.3	118

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19	The gene expression signature of genomic instability in breast cancer is an independent predictor of clinical outcome. <i>International Journal of Cancer</i> , 2009, 124, 1552-1564.	5.1	112
20	ErbB2-Driven Breast Cancer Cell Invasion Depends on a Complex Signaling Network Activating Myeloid Zinc Finger-1-Dependent Cathepsin B Expression. <i>Molecular Cell</i> , 2012, 45, 764-776.	9.7	112
21	Optimized LOWESS normalization parameter selection for DNA microarray data. <i>BMC Bioinformatics</i> , 2004, 5, 194.	2.6	110
22	High-Resolution Analysis of Gene Copy Number Alterations in Human Prostate Cancer Using CGH on cDNA Microarrays: Impact of Copy Number on Gene Expression. <i>Neoplasia</i> , 2004, 6, 240-247.	5.3	110
23	Relationships between probabilistic Boolean networks and dynamic Bayesian networks as models of gene regulatory networks. <i>Signal Processing</i> , 2006, 86, 814-834.	3.7	106
24	High-Resolution Genomic and Expression Profiling Reveals 105 Putative Amplification Target Genes in Pancreatic Cancer. <i>Neoplasia</i> , 2004, 6, 432-439.	5.3	104
25	Global Gene Expression Profile of Human Cord Blood-Derived CD133+Cells. <i>Stem Cells</i> , 2006, 24, 631-641.	3.2	104
26	Tissue-specific pioneer factors associate with androgen receptor cistromes and transcription programs. <i>EMBO Journal</i> , 2014, 33, n/a-n/a.	7.8	100
27	Candidate driver genes in microsatellite-unstable colorectal cancer. <i>International Journal of Cancer</i> , 2012, 130, 1558-1566.	5.1	99
28	CGH-Plotter: MATLAB toolbox for CGH-data analysis. <i>Bioinformatics</i> , 2003, 19, 1714-1715.	4.1	98
29	AIP inactivation leads to pituitary tumorigenesis through defective G $\beta$ i-cAMP signaling. <i>Oncogene</i> , 2015, 34, 1174-1184.	5.9	95
30	CNAmet: an R package for integrating copy number, methylation and expression data. <i>Bioinformatics</i> , 2011, 27, 887-888.	4.1	91
31	A Functional Homologous Recombination Assay Predicts Primary Chemotherapy Response and Long-Term Survival in Ovarian Cancer Patients. <i>Clinical Cancer Research</i> , 2018, 24, 4482-4493.	7.0	91
32	Fast Gene Ontology based clustering for microarray experiments. <i>BioData Mining</i> , 2008, 1, 11.	4.0	89
33	Rapid mobilization of cytotoxic lymphocytes induced by dasatinib therapy. <i>Leukemia</i> , 2013, 27, 914-924.	7.2	84
34	Adipocyte morphology and implications for metabolic derangements in acquired obesity. <i>International Journal of Obesity</i> , 2014, 38, 1423-1431.	3.4	83
35	Dectin-1 Pathway Activates Robust Autophagy-Dependent Unconventional Protein Secretion in Human Macrophages. <i>Journal of Immunology</i> , 2014, 192, 5952-5962.	0.8	82
36	Individual and combined effects of DNA methylation and copy number alterations on miRNA expression in breast tumors. <i>Genome Biology</i> , 2013, 14, R126.	9.6	80

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37	Novel Proteomics Strategy Brings Insight into the Prevalence of SUMO-2 Target Sites. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1382-1390.	3.8	77
38	Mutations in the Circadian Gene <i>CLOCK</i> in Colorectal Cancer. <i>Molecular Cancer Research</i> , 2010, 8, 952-960.	3.4	77
39	Deciphering downstream gene targets of PI3K/mTOR/p70S6K pathway in breast cancer. <i>BMC Genomics</i> , 2008, 9, 348.	2.8	75
40	Co-evolution of matrisome and adaptive adhesion dynamics drives ovarian cancer chemoresistance. <i>Nature Communications</i> , 2021, 12, 3904.	12.8	74
41	CIP2A signature reveals the MYC dependency of CIP2A-regulated phenotypes and its clinical association with breast cancer subtypes. <i>Oncogene</i> , 2012, 31, 4266-4278.	5.9	72
42	Biclustering Methods: Biological Relevance and Application in Gene Expression Analysis. <i>PLoS ONE</i> , 2014, 9, e90801.	2.5	72
43	Allelic Imbalance at <i>rs6983267</i> Suggests Selection of the Risk Allele in Somatic Colorectal Tumor Evolution. <i>Cancer Research</i> , 2008, 68, 14-17.	0.9	69
44	Genomic profile of pseudomyxoma peritonei analyzed using next-generation sequencing and immunohistochemistry. <i>International Journal of Cancer</i> , 2015, 136, E282-9.	5.1	66
45	Early Maternal Alcohol Consumption Alters Hippocampal DNA Methylation, Gene Expression and Volume in a Mouse Model. <i>PLoS ONE</i> , 2015, 10, e0124931.	2.5	63
46	High-Resolution Analysis of Gene Copy Number Alterations in Human Prostate Cancer Using CGH on cDNA Microarrays: Impact of Copy Number on Gene Expression. <i>Neoplasia</i> , 2004, 6, 240-247.	5.3	62
47	MMP16 Mediates a Proteolytic Switch to Promote Cell-Cell Adhesion, Collagen Alignment, and Lymphatic Invasion in Melanoma. <i>Cancer Research</i> , 2015, 75, 2083-2094.	0.9	61
48	Effects of Herceptin treatment on global gene expression patterns in HER2-amplified and nonamplified breast cancer cell lines. <i>Oncogene</i> , 2004, 23, 1010-1013.	5.9	59
49	Longitudinal single-cell RNA-seq analysis reveals stress-promoted chemoresistance in metastatic ovarian cancer. <i>Science Advances</i> , 2022, 8, eabm1831.	10.3	59
50	Use of IgE and IgG4 epitope binding to predict the outcome of oral immunotherapy in cow's milk allergy. <i>Pediatric Allergy and Immunology</i> , 2014, 25, 227-235.	2.6	58
51	Modeling of signal-response cascades using decision tree analysis. <i>Bioinformatics</i> , 2005, 21, 2027-2035.	4.1	57
52	Defects in mtDNA replication challenge nuclear genome stability through nucleotide depletion and provide a unifying mechanism for mouse progerias. <i>Nature Metabolism</i> , 2019, 1, 958-965.	11.9	57
53	Insulin/IGF-1 Signaling Regulates Proteasome Activity through the Deubiquitinating Enzyme UBH-4. <i>Cell Reports</i> , 2013, 3, 1980-1995.	6.4	56
54	Comparative analysis of methods for identifying somatic copy number alterations from deep sequencing data. <i>Briefings in Bioinformatics</i> , 2015, 16, 242-254.	6.5	56

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55	Integrated mechanistic and data-driven modelling for multivariate analysis of signalling pathways. <i>Journal of the Royal Society Interface</i> , 2006, 3, 515-526.	3.4	53
56	A novel strategy for microarray quality control using Bayesian networks. <i>Bioinformatics</i> , 2003, 19, 2031-2038.	4.1	48
57	The Phytoestrogen Genistein Is a Tissue-Specific Androgen Receptor Modulator. <i>Endocrinology</i> , 2011, 152, 4395-4405.	2.8	47
58	Posttranscriptional regulation of angiotensin II type 1 receptor expression by glyceraldehyde 3-phosphate dehydrogenase. <i>Nucleic Acids Research</i> , 2009, 37, 2346-2358.	14.5	45
59	Title is missing!. <i>Machine Learning</i> , 2003, 52, 45-66.	5.4	44
60	Functional Profiling of Precursor MicroRNAs Identifies MicroRNAs Essential for Glioma Proliferation. <i>PLoS ONE</i> , 2013, 8, e60930.	2.5	43
61	Differential gene expression in non-malignant tumour microenvironment is associated with outcome in follicular lymphoma patients treated with rituximab and CHOP. <i>British Journal of Haematology</i> , 2006, 135, 33-42.	2.5	42
62	Complete androgen insensitivity syndrome caused by a deep intronic pseudoexon-activating mutation in the androgen receptor gene. <i>Scientific Reports</i> , 2016, 6, 32819.	3.3	42
63	Jointly Analyzing Gene Expression and Copy Number Data in Breast Cancer Using Data Reduction Models. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2006, 3, 2-16.	3.0	40
64	Identification of a c-Jun N-terminal kinase-2-dependent signal amplification cascade that regulates c-Myc levels in ras transformation. <i>Oncogene</i> , 2012, 31, 390-401.	5.9	40
65	Netrin-4 Promotes Glioblastoma Cell Proliferation through Integrin $\beta$ 24 Signaling. <i>Neoplasia</i> , 2012, 14, 219-IN23.	5.3	40
66	An optimized isolation of biotinylated cell surface proteins reveals novel players in cancer metastasis. <i>Journal of Proteomics</i> , 2012, 77, 87-100.	2.4	39
67	Role of RNA binding protein HuR in ductal carcinoma <i>in situ</i> of the breast. <i>Journal of Pathology</i> , 2011, 224, 529-539.	4.5	38
68	Prognostic value of tumour budding in oesophageal cancer: a meta-analysis. <i>Histopathology</i> , 2016, 68, 173-182.	2.9	38
69	ALDH1A1-related stemness in high-grade serous ovarian cancer is a negative prognostic indicator but potentially targetable by EGFR/mTOR/PI3K/aurora kinase inhibitors. <i>Journal of Pathology</i> , 2020, 250, 159-169.	4.5	37
70	Comparison of Affymetrix data normalization methods using 6,926 experiments across five array generations. <i>BMC Bioinformatics</i> , 2009, 10, S24.	2.6	35
71	Novel Mad2-targeting miR-493-3p controls mitotic fidelity and cancer cells' sensitivity to paclitaxel. <i>Oncotarget</i> , 2016, 7, 12267-12285.	1.8	33
72	Mre11 inhibition by oncolytic adenovirus associates with autophagy and underlies synergy with ionizing radiation. <i>International Journal of Cancer</i> , 2009, 125, 2441-2449.	5.1	32

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73	Potential role of a navigator gene NAV3 in colorectal cancer. <i>British Journal of Cancer</i> , 2012, 106, 517-524.	6.4	31
74	Identification of Prognostic Groups in High-Grade Serous Ovarian Cancer Treated with Platinum+Taxane Chemotherapy. <i>Cancer Research</i> , 2015, 75, 2987-2998.	0.9	31
75	Mathematical Modeling Predicts Response to Chemotherapy and Drug Combinations in Ovarian Cancer. <i>Cancer Research</i> , 2018, 78, 4036-4044.	0.9	31
76	Lymphatic endothelium stimulates melanoma metastasis and invasion via MMP14-dependent Notch3 and $\beta$ 1-integrin activation. <i>ELife</i> , 2018, 7, .	6.0	31
77	Anduril 2: upgraded large-scale data integration framework. <i>Bioinformatics</i> , 2019, 35, 3815-3817.	4.1	31
78	MYC Promotes Bone Marrow Stem Cell Dysfunction in Fanconi Anemia. <i>Cell Stem Cell</i> , 2021, 28, 33-47.e8.	11.1	31
79	Comparative analysis of algorithms for integration of copy number and expression data. <i>Nature Methods</i> , 2012, 9, 351-355.	19.0	30
80	Oncogenic Herpesvirus Utilizes Stress-Induced Cell Cycle Checkpoints for Efficient Lytic Replication. <i>PLoS Pathogens</i> , 2016, 12, e1005424.	4.7	30
81	Therapeutic targets for HIV-1 infection in the host proteome. <i>Retrovirology</i> , 2005, 2, 20.	2.0	29
82	Transcriptional Profiling Reflects Shared and Unique Characters for CD34+and CD133+Cells. <i>Stem Cells and Development</i> , 2006, 15, 839-851.	2.1	29
83	Transmembrane Prostatic Acid Phosphatase (TMPAP) Interacts with Snapin and Deficient Mice Develop Prostate Adenocarcinoma. <i>PLoS ONE</i> , 2013, 8, e73072.	2.5	28
84	Identification of several potential chromatin binding sites of HOXB7 and its downstream target genes in breast cancer. <i>International Journal of Cancer</i> , 2015, 137, 2374-2383.	5.1	28
85	Combined T regulatory cell and Th2 expression profile identifies children with cow's milk allergy. <i>Clinical Immunology</i> , 2010, 136, 16-20.	3.2	26
86	Comprehensive exon array data processing method for quantitative analysis of alternative spliced variants. <i>Nucleic Acids Research</i> , 2011, 39, e123-e123.	14.5	26
87	Plasticity of Blood- and Lymphatic Endothelial Cells and Marker Identification. <i>PLoS ONE</i> , 2013, 8, e74293.	2.5	26
88	MicroRNAs regulate key cell survival pathways and mediate chemosensitivity during progression of diffuse large B-cell lymphoma. <i>Blood Cancer Journal</i> , 2017, 7, 654.	6.2	26
89	PROX1 is a transcriptional regulator of MMP14. <i>Scientific Reports</i> , 2018, 8, 9531.	3.3	26
90	SePIA: RNA and small RNA sequence processing, integration, and analysis. <i>BioData Mining</i> , 2016, 9, 20.	4.0	25

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91	Decision tree modeling predicts effects of inhibiting contractility signaling on cell motility. BMC Systems Biology, 2007, 1, 9.	3.0	24
92	Characterization of the colorectal cancer-associated enhancer MYC-335 at 8q24: the role of rs67491583. Cancer Genetics, 2012, 205, 25-33.	0.4	24
93	Distinct subtypes of diffuse large B-cell lymphoma defined by hypermutated genes. Leukemia, 2019, 33, 2662-2672.	7.2	24
94	Deltex-1 mutations predict poor survival in diffuse large B-cell lymphoma. Haematologica, 2017, 102, e195-e198.	3.5	23
95	Integrative platform to translate gene sets to networks. Bioinformatics, 2010, 26, 1802-1803.	4.1	22
96	Analysis of BMP4 and BMP7 signaling in breast cancer cells unveils time-dependent transcription patterns and highlights a common synexpression group of genes. BMC Medical Genomics, 2011, 4, 80.	1.5	22
97	Neuron navigator 3 alterations in nervous system tumors associate with tumor malignancy grade and prognosis. Genes Chromosomes and Cancer, 2013, 52, 191-201.	2.8	22
98	Netrin-1 induced activation of Notch signaling mediates glioblastoma cell invasion. Journal of Cell Science, 2013, 126, 2459-69.	2.0	22
99	Par6G suppresses cell proliferation and is targeted by loss-of-function mutations in multiple cancers. Oncogene, 2016, 35, 1386-1398.	5.9	22
100	A strategy for identifying putative causes of gene expression variation in human cancers. Journal of the Franklin Institute, 2004, 341, 77-88.	3.4	21
101	Let-7 microRNA controls invasion-promoting lysosomal changes via the oncogenic transcription factor myeloid zinc finger-1. Oncogenesis, 2018, 7, 14.	4.9	20
102	Prospective Longitudinal ctDNA Workflow Reveals Clinically Actionable Alterations in Ovarian Cancer. JCO Precision Oncology, 2019, 3, 1-12.	3.0	20
103	Genomic instability influences the transcriptome and proteome in endometrial cancer subtypes. Molecular Cancer, 2011, 10, 132.	19.2	19
104	Deregulation of COMMD1 Is Associated with Poor Prognosis in Diffuse Large B-cell Lymphoma. PLoS ONE, 2014, 9, e91031.	2.5	19
105	Rituximab regulates signaling pathways and alters gene expression associated with cell death and survival in diffuse large B-cell lymphoma. Oncology Reports, 2011, 25, 1183-90.	2.6	17
106	Heterogeneity and Clonal Evolution of Acquired PARP Inhibitor Resistance in TP53- and BRCA1-Deficient Cells. Cancer Research, 2021, 81, 2774-2787.	0.9	17
107	PRISM: recovering cell-type-specific expression profiles from individual composite RNA-seq samples. Bioinformatics, 2021, 37, 2882-2888.	4.1	17
108	NAV3 copy number changes and target genes in basal and squamous cell cancers. Experimental Dermatology, 2011, 20, 926-931.	2.9	16

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109	Phosphoprotein profiling predicts response to tyrosine kinase inhibitor therapy in chronic myeloid leukemia patients. <i>Experimental Hematology</i> , 2012, 40, 705-714.e3.	0.4	16
110	Molecular characterization of subcutaneous panniculitis-like T-cell lymphoma reveals upregulation of immunosuppression- and autoimmunity-associated genes. <i>Orphanet Journal of Rare Diseases</i> , 2014, 9, 160.	2.7	16
111	DNA methylation signature (SAM40) identifies subgroups of the Luminal A breast cancer samples with distinct survival. <i>Oncotarget</i> , 2017, 8, 1074-1082.	1.8	16
112	Genomic Region Operation Kit for Flexible Processing of Deep Sequencing Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 200-206.	3.0	15
113	Multiple components of PKA and TGF- $\beta$ 2 pathways are mutated in pseudomyxoma peritonei. <i>PLoS ONE</i> , 2017, 12, e0174898.	2.5	15
114	High frequency of TTK mutations in microsatellite-unstable colorectal cancer and evaluation of their effect on spindle assembly checkpoint. <i>Carcinogenesis</i> , 2011, 32, 305-311.	2.8	14
115	Prostatic acid phosphatase is the main acid phosphatase with 5'-ectonucleotidase activity in the male mouse saliva and regulates salivation. <i>American Journal of Physiology - Cell Physiology</i> , 2014, 306, C1017-C1027.	4.6	14
116	Data integration to prioritize drugs using genomics and curated data. <i>BioData Mining</i> , 2016, 9, 21.	4.0	14
117	Alternative splicing discriminates molecular subtypes and has prognostic impact in diffuse large B-cell lymphoma. <i>Blood Cancer Journal</i> , 2017, 7, e596-e596.	6.2	14
118	Anagrelide for Gastrointestinal Stromal Tumor. <i>Clinical Cancer Research</i> , 2019, 25, 1676-1687.	7.0	14
119	Network-guided identification of cancer-selective combinatorial therapies in ovarian cancer. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	13
120	Anima: Modular Workflow System for Comprehensive Image Data Analysis. <i>Frontiers in Bioengineering and Biotechnology</i> , 2014, 2, 25.	4.1	12
121	Human cell transformation by combined lineage conversion and oncogene expression. <i>Oncogene</i> , 2021, 40, 5533-5547.	5.9	12
122	Germline variation in TP53 regulatory network genes associates with breast cancer survival and treatment outcome. <i>International Journal of Cancer</i> , 2013, 132, 2044-2055.	5.1	11
123	Integrative Analysis of Deep Sequencing Data Identifies Estrogen Receptor Early Response Genes and Links ATAD3B to Poor Survival in Breast Cancer. <i>PLoS Computational Biology</i> , 2013, 9, e1003100.	3.2	11
124	Aneuploidy-Associated Gene Expression Signatures Characterize Malignant Transformation in Ulcerative Colitis. <i>Inflammatory Bowel Diseases</i> , 2013, 19, 691-703.	1.9	11
125	Identification of sample-specific regulations using integrative network level analysis. <i>BMC Cancer</i> , 2015, 15, 319.	2.6	11
126	Virtual clinical trials identify effective combination therapies in ovarian cancer. <i>Scientific Reports</i> , 2019, 9, 18678.	3.3	11



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127	Comprehensive evaluation of coding region point mutations in microsatellite-unstable colorectal cancer. <i>EMBO Molecular Medicine</i> , 2018, 10, .	6.9	10
128	PerPAS: Topology-Based Single Sample Pathway Analysis Method. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1022-1027.	3.0	9
129	Glycomic Profiling Highlights Increased Fucosylation in Pseudomyxoma Peritonei. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2107-2118.	3.8	8
130	Agile workflow for interactive analysis of mass cytometry data. <i>Bioinformatics</i> , 2021, 37, 1263-1268.	4.1	8
131	Integrated data management and validation platform for phosphorylated tandem mass spectrometry data. <i>Proteomics</i> , 2010, 10, 3515-3524.	2.2	7
132	Integrative transcriptional analysis between human and mouse cancer cells provides a common set of transformation associated genes. <i>Biotechnology Advances</i> , 2012, 30, 16-29.	11.7	7
133	Characterization of the Microrna Expression Profiles of Paired Primary and Relapsed Diffuse Large B-Cell Lymphoma (DLBCL) By Next-Generation Sequencing. <i>Blood</i> , 2014, 124, 1626-1626.	1.4	7
134	Transmembrane prostatic acid phosphatase (TMPAP) delays cells in G1 phase of the cell cycle. <i>Prostate</i> , 2016, 76, 151-162.	2.3	6
135	Dasatinib Induces a Rapid, Dose-Controllable Mobilization of Cytotoxic Lymphocytes: A Novel Immunomodulatory Effect Associated with Prolonged Therapy Responses In Advanced Leukemia.. <i>Blood</i> , 2010, 116, 1204-1204.	1.4	6
136	Dynamic visualization of multi-level molecular data: The Director package in R. <i>Computer Methods and Programs in Biomedicine</i> , 2018, 153, 129-136.	4.7	5
137	Open Source Infrastructure for Health Care Data Integration and Machine Learning Analyses. <i>JCO Clinical Cancer Informatics</i> , 2019, 3, 1-16.	2.1	5
138	Advanced analysis and visualization of gene copy number and expression data. <i>BMC Bioinformatics</i> , 2009, 10, S70.	2.6	4
139	Signal Transducers and Activators of Transcription 5a-Dependent Cross-talk between Follicular Lymphoma Cells and Tumor Microenvironment Characterizes a Group of Patients with Improved Outcome after R-CHOP. <i>Clinical Cancer Research</i> , 2010, 16, 2615-2623.	7.0	4
140	Data Integration Workflow for Search of Disease Driving Genes and Genetic Variants. <i>PLoS ONE</i> , 2011, 6, e18636.	2.5	4
141	Identifying differentially methylated sites in samples with varying tumor purity. <i>Bioinformatics</i> , 2018, 34, 3078-3085.	4.1	3
142	qSNE: quadratic rate t-SNE optimizer with automatic parameter tuning for large datasets. <i>Bioinformatics</i> , 2020, 36, 5086-5092.	4.1	3
143	Low Expression and Somatic Mutations of the KLHL6 Gene Predict Poor Survival in Patients with Activated B-Cell like Diffuse Large B-Cell Lymphoma. <i>Blood</i> , 2016, 128, 2926-2926.	1.4	3
144	POIBM: batch correction of heterogeneous RNA-seq datasets through latent sample matching. <i>Bioinformatics</i> , 2022, 38, 2474-2480.	4.1	3

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145	QuantISH: RNA in situ hybridization image analysis framework for quantifying cell type-specific target RNA expression and variability. <i>Laboratory Investigation</i> , 2022, 102, 753-761.	3.7	3
146	Computational identification of candidate loci for recessively inherited mutation using high-throughput SNP arrays. <i>Bioinformatics</i> , 2007, 23, 1952-1961.	4.1	2
147	Circulating tumor DNA (ctDNA) in precision oncology of ovarian cancer. <i>Pharmacogenomics</i> , 2019, 20, 1251-1253.	1.3	2
148	Editorial: Multi-omic Data Integration in Oncology. <i>Frontiers in Oncology</i> , 2020, 10, 1768.	2.8	2
149	Reply to: Proofreading deficiency in mitochondrial DNA polymerase does not affect total dNTP pools in mouse embryos. <i>Nature Metabolism</i> , 2020, 2, 676-677.	11.9	2
150	Low Expression of the CIITA Gene Predicts Poor Outcome in Diffuse Large B-Cell Lymphoma. <i>Blood</i> , 2016, 128, 2948-2948.	1.4	2
151	Identification of genetic markers with synergistic survival effect in cancer. <i>BMC Systems Biology</i> , 2013, 7, S2.	3.0	1
152	High-performance computing in biomedicine. , 2013, , .		1
153	Early <i>Trichinella spiralis</i> and <i>Trichinella nativa</i> infections induce similar gene expression profiles in rat jejunal mucosa. <i>Experimental Parasitology</i> , 2013, 135, 363-369.	1.2	1
154	Systematic use of computational methods allows stratification of treatment responders in glioblastoma multiforme. <i>Systems Biomedicine (Austin, Tex)</i> , 2013, 1, 130-136.	0.7	1
155	Language-Agnostic Reproducible Data Analysis Using Literate Programming. <i>PLoS ONE</i> , 2016, 11, e0164023.	2.5	1
156	Drug screening approach combines epigenetic sensitization with immunochemotherapy in cancer. <i>Clinical Epigenetics</i> , 2019, 11, 192.	4.1	1
157	FUNGI: FUsioN Gene Integration toolset. <i>Bioinformatics</i> , 2021, 37, 3353-3355.	4.1	1
158	The expression and prognostic relevance of CDH3 in tongue squamous cell carcinoma. <i>Apmis</i> , 2021, 129, 717-728.	2.0	1
159	Alternative Splicing and Expression of Class II Tubulin Beta (TUBB2B) Are Associated with Outcome in Diffuse Large B-Cell Lymphoma. <i>Blood</i> , 2012, 120, 1557-1557.	1.4	1
160	Rule-based induction method for haplotype comparison and identification of candidate disease loci. <i>Genome Medicine</i> , 2012, 4, 21.	8.2	0
161	Workflow for automated quantification of cerebrovascular gelatinase activity. <i>Microvascular Research</i> , 2015, 97, 19-24.	2.5	0
162	STAT5 Signaling Is Associated with the Outcome of Follicular and Mantle Cell Lymphoma Patients Treated with Immunochemotherapy.. <i>Blood</i> , 2007, 110, 2626-2626.	1.4	0

#	ARTICLE	IF	CITATIONS
163	Computational Identification of Cancer Susceptibility Loci. <i>Methods in Molecular Biology</i> , 2010, 653, 87-103.	0.9	0
164	Exon-Based Transcriptome Profiling Reveals Genes That Have Prognostic Impact on the Survival of Young High Risk Diffuse Large B-Cell/Follicular Grade 3 Lymphoma Patients Treated with Dose-Dense Chemoimmunotherapy and CNS Prophylaxis. Results From a Nordic Lymphoma Group Phase II Study. <i>Blood</i> , 2010, 116, 3107-3107.	1.4	0
165	Phosphoprotein Profiling Predicts Response to Tyrosine Kinase Inhibitor Therapy in Chronic Myeloid Leukemia Patients. <i>Blood</i> , 2011, 118, 4427-4427.	1.4	0
166	Global Profiling Of Outcome Associated Alternative Splicing Events and Gene Expression In Diffuse Large B-Cell Lymphoma. <i>Blood</i> , 2013, 122, 75-75.	1.4	0
167	Somatic Mutations in E3 Ubiquitin Ligase Deltex 1 Are Associated with Survival in Diffuse Large B-Cell Lymphoma. <i>Blood</i> , 2014, 124, 1688-1688.	1.4	0
168	Abstract 4383: Inferring transcription activity changes from copy-number and expression data of longitudinally sampled high-grade serous ovarian cancer tumors. , 2020, , .		0
169	Abstract 192: Ex vivo screening and analysis of novel effective treatments for ovarian cancer. <i>Cancer Research</i> , 2022, 82, 192-192.	0.9	0
170	Image Processing Pipeline to Compute Homologous Recombination Score. , 2022, , .		0