

Benedikt Brors

List of Publications by Citations

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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.

219
papers

17,254
citations

64
h-index

128
g-index

250
ext. papers

22,026
ext. citations

11.3
avg, IF

6.07
L-index

#	Paper	IF	Citations
219	circize Implements and enhances circular visualization in R. <i>Bioinformatics</i> , 2014 , 30, 2811-2	7.2	1242
218	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. <i>Nature Biotechnology</i> , 2010 , 28, 827-38	44.5	644
217	Dissecting the genomic complexity underlying medulloblastoma. <i>Nature</i> , 2012 , 488, 100-5	50.4	623
216	The landscape of genomic alterations across childhood cancers. <i>Nature</i> , 2018 , 555, 321-327	50.4	603
215	Genome sequencing of pediatric medulloblastoma links catastrophic DNA rearrangements with TP53 mutations. <i>Cell</i> , 2012 , 148, 59-71	56.2	600
214	Recurrent somatic alterations of FGFR1 and NTRK2 in pilocytic astrocytoma. <i>Nature Genetics</i> , 2013 , 45, 927-32	36.3	550
213	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , 2017 , 547, 311-317	50.4	472
212	Genome sequencing of SHH medulloblastoma predicts genotype-related response to smoothed inhibition. <i>Cancer Cell</i> , 2014 , 25, 393-405	24.3	469
211	Promiscuous gene expression in thymic epithelial cells is regulated at multiple levels. <i>Journal of Experimental Medicine</i> , 2005 , 202, 33-45	16.6	431
210	Enhancer hijacking activates GFI1 family oncogenes in medulloblastoma. <i>Nature</i> , 2014 , 511, 428-34	50.4	377
209	Identification of regulatory networks in HSCs and their immediate progeny via integrated proteome, transcriptome, and DNA methylome analysis. <i>Cell Stem Cell</i> , 2014 , 15, 507-522	18	320
208	Recurrent mutation of the ID3 gene in Burkitt lymphoma identified by integrated genome, exome and transcriptome sequencing. <i>Nature Genetics</i> , 2012 , 44, 1316-20	36.3	317
207	Decoding the regulatory landscape of medulloblastoma using DNA methylation sequencing. <i>Nature</i> , 2014 , 510, 537-41	50.4	296
206	Medullary epithelial cells of the human thymus express a highly diverse selection of tissue-specific genes colocalized in chromosomal clusters. <i>Journal of Experimental Medicine</i> , 2004 , 199, 155-66	16.6	293
205	Transient colocalization of X-inactivation centres accompanies the initiation of X inactivation. <i>Nature Cell Biology</i> , 2006 , 8, 293-9	23.4	276
204	Integrative genomic analyses reveal an androgen-driven somatic alteration landscape in early-onset prostate cancer. <i>Cancer Cell</i> , 2013 , 23, 159-70	24.3	259
203	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016 , 167, 1145-1149	56.2	232

202	Acute myeloid leukemias with reciprocal rearrangements can be distinguished by specific gene expression profiles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 10008-13	11.5	215
201	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. <i>Genome Biology</i> , 2015 , 16, 133	18.3	212
200	Customized oligonucleotide microarray gene expression-based classification of neuroblastoma patients outperforms current clinical risk stratification. <i>Journal of Clinical Oncology</i> , 2006 , 24, 5070-8	2.2	212
199	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. <i>Nature Communications</i> , 2015 , 6, 10001	17.4	199
198	DNA methylation dynamics during B cell maturation underlie a continuum of disease phenotypes in chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2016 , 48, 253-64	36.3	193
197	Next-generation personalised medicine for high-risk paediatric cancer patients - The INFORM pilot study. <i>European Journal of Cancer</i> , 2016 , 65, 91-101	7.5	186
196	Intratumor DNA methylation heterogeneity reflects clonal evolution in aggressive prostate cancer. <i>Cell Reports</i> , 2014 , 8, 798-806	10.6	177
195	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. <i>Nature Genetics</i> , 2020 , 52, 331-341	36.3	168
194	Distinct transcriptional MYCN/c-MYC activities are associated with spontaneous regression or malignant progression in neuroblastomas. <i>Genome Biology</i> , 2008 , 9, R150	18.3	159
193	DNMT and HDAC inhibitors induce cryptic transcription start sites encoded in long terminal repeats. <i>Nature Genetics</i> , 2017 , 49, 1052-1060	36.3	157
192	Cell competition is a tumour suppressor mechanism in the thymus. <i>Nature</i> , 2014 , 509, 465-70	50.4	156
191	Solitary fibrous tumors/hemangiopericytomas with different variants of the NAB2-STAT6 gene fusion are characterized by specific histomorphology and distinct clinicopathological features. <i>American Journal of Pathology</i> , 2014 , 184, 1209-1218	5.8	155
190	Thymic B Cells Are Licensed to Present Self Antigens for Central T Cell Tolerance Induction. <i>Immunity</i> , 2015 , 42, 1048-61	32.3	152
189	Cross-platform analysis of cancer microarray data improves gene expression based classification of phenotypes. <i>BMC Bioinformatics</i> , 2005 , 6, 265	3.6	146
188	Gene expression pattern in biomechanically stretched cardiomyocytes: evidence for a stretch-specific gene program. <i>Hypertension</i> , 2008 , 51, 309-18	8.5	144
187	Seromic profiling of ovarian and pancreatic cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 5088-93	11.5	141
186	Genome-wide association-, replication-, and neuroimaging study implicates HOMER1 in the etiology of major depression. <i>Biological Psychiatry</i> , 2010 , 68, 578-85	7.9	139
185	Recurrent MET fusion genes represent a drug target in pediatric glioblastoma. <i>Nature Medicine</i> , 2016 , 22, 1314-1320	50.5	137

184	Hox-C9 activates the intrinsic pathway of apoptosis and is associated with spontaneous regression in neuroblastoma. <i>Cell Death and Disease</i> , 2013 , 4, e586	9.8	136
183	Genome-wide transcriptional analysis of the human cell cycle identifies genes differentially regulated in normal and cancer cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 955-60	11.5	134
182	Gene expression signature predicting pathologic complete response with gemcitabine, epirubicin, and docetaxel in primary breast cancer. <i>Journal of Clinical Oncology</i> , 2006 , 24, 1839-45	2.2	129
181	Genome-wide DNA-methylation landscape defines specialization of regulatory T cells in tissues. <i>Nature Immunology</i> , 2017 , 18, 1160-1172	19.1	125
180	Group testing for pathway analysis improves comparability of different microarray datasets. <i>Bioinformatics</i> , 2006 , 22, 2500-6	7.2	119
179	Epigenomic Profiling of Human CD4 T Cells Supports a Linear Differentiation Model and Highlights Molecular Regulators of Memory Development. <i>Immunity</i> , 2016 , 45, 1148-1161	32.3	118
178	Integrative genomic and transcriptomic analysis of leiomyosarcoma. <i>Nature Communications</i> , 2018 , 9, 144	17.4	115
177	MicroRNA miR-885-5p targets CDK2 and MCM5, activates p53 and inhibits proliferation and survival. <i>Cell Death and Differentiation</i> , 2011 , 18, 974-84	12.7	113
176	Temporal transcriptomic analysis of the <i>Listeria monocytogenes</i> EGD-e sigmaB regulon. <i>BMC Microbiology</i> , 2008 , 8, 20	4.5	108
175	Prognostic impact of gene expression-based classification for neuroblastoma. <i>Journal of Clinical Oncology</i> , 2010 , 28, 3506-15	2.2	106
174	CD95-ligand on peripheral myeloid cells activates Syk kinase to trigger their recruitment to the inflammatory site. <i>Immunity</i> , 2010 , 32, 240-52	32.3	101
173	Prediction of clinical outcome and biological characterization of neuroblastoma by expression profiling. <i>Oncogene</i> , 2005 , 24, 7902-12	9.2	100
172	BAZ2A (TIP5) is involved in epigenetic alterations in prostate cancer and its overexpression predicts disease recurrence. <i>Nature Genetics</i> , 2015 , 47, 22-30	36.3	99
171	Fusions in Wild-Type Pancreatic Cancer. <i>Cancer Discovery</i> , 2018 , 8, 1087-1095	24.4	99
170	Microarray-based approach identifies microRNAs and their target functional patterns in polycystic kidney disease. <i>BMC Genomics</i> , 2008 , 9, 624	4.5	97
169	Autoantibodies against the exocrine pancreas in autoimmune pancreatitis: gene and protein expression profiling and immunoassays identify pancreatic enzymes as a major target of the inflammatory process. <i>American Journal of Gastroenterology</i> , 2010 , 105, 2060-71	0.7	96
168	Molecular Evolution of Early-Onset Prostate Cancer Identifies Molecular Risk Markers and Clinical Trajectories. <i>Cancer Cell</i> , 2018 , 34, 996-1011.e8	24.3	89
167	High ALK receptor tyrosine kinase expression supersedes ALK mutation as a determining factor of an unfavorable phenotype in primary neuroblastoma. <i>Clinical Cancer Research</i> , 2011 , 17, 5082-92	12.9	83

166	Precision oncology based on omics data: The NCT Heidelberg experience. <i>International Journal of Cancer</i> , 2017 , 141, 877-886	7.5	82
165	Sarcoma classification by DNA methylation profiling. <i>Nature Communications</i> , 2021 , 12, 498	17.4	74
164	Identification of two tetranuclear FeS clusters on the ferredoxin-type subunit of NADH:ubiquinone oxidoreductase (complex I). <i>Biochemistry</i> , 2001 , 40, 6124-31	3.2	70
163	Accurate outcome prediction in neuroblastoma across independent data sets using a multigene signature. <i>Clinical Cancer Research</i> , 2010 , 16, 1532-41	12.9	69
162	Genome-wide association study of pathological gambling. <i>European Psychiatry</i> , 2016 , 36, 38-46	6	68
161	Oligonucleotide array-based comparative genomic hybridization (aCGH) of 90 neuroblastomas reveals aberration patterns closely associated with relapse pattern and outcome. <i>Genes Chromosomes and Cancer</i> , 2006 , 45, 1130-42	5	68
160	Recurrent CDKN1B (p27) mutations in hairy cell leukemia. <i>Blood</i> , 2015 , 126, 1005-8	2.2	66
159	Combining transcription factor binding affinities with open-chromatin data for accurate gene expression prediction. <i>Nucleic Acids Research</i> , 2017 , 45, 54-66	20.1	66
158	MYC/MIZ1-dependent gene repression inversely coordinates the circadian clock with cell cycle and proliferation. <i>Nature Communications</i> , 2016 , 7, 11807	17.4	65
157	Two genes of the putative mitochondrial fatty acid synthase in the genome of <i>Saccharomyces cerevisiae</i> . <i>Current Genetics</i> , 1997 , 32, 384-8	2.9	65
156	Argonaute--a database for gene regulation by mammalian microRNAs. <i>Nucleic Acids Research</i> , 2006 , 34, D115-8	20.1	64
155	Comparison of normalization methods for Illumina BeadChip HumanHT-12 v3. <i>BMC Genomics</i> , 2010 , 11, 349	4.5	60
154	A highly standardized, robust, and cost-effective method for genome-wide transcriptome analysis of peripheral blood applicable to large-scale clinical trials. <i>Genomics</i> , 2006 , 87, 653-64	4.3	59
153	Integrative DNA methylation and gene expression analysis in high-grade soft tissue sarcomas. <i>Genome Biology</i> , 2013 , 14, r137	18.3	58
152	Coverage bias and sensitivity of variant calling for four whole-genome sequencing technologies. <i>PLoS ONE</i> , 2013 , 8, e66621	3.7	58
151	Comparison of performance of one-color and two-color gene-expression analyses in predicting clinical endpoints of neuroblastoma patients. <i>Pharmacogenomics Journal</i> , 2010 , 10, 258-66	3.5	56
150	Precursors for Nonlymphoid-Tissue Treg Cells Reside in Secondary Lymphoid Organs and Are Programmed by the Transcription Factor BATF. <i>Immunity</i> , 2020 , 52, 295-312.e11	32.3	55
149	N2M2 (NOA-20) phase I/II trial of molecularly matched targeted therapies plus radiotherapy in patients with newly diagnosed non-MGMT hypermethylated glioblastoma. <i>Neuro-Oncology</i> , 2019 , 21, 95-105	1	55

148	Epigenetic dynamics of monocyte-to-macrophage differentiation. <i>Epigenetics and Chromatin</i> , 2016 , 9, 33	5.8	54
147	Distinct gene expression patterns associated with FLT3- and NRAS-activating mutations in acute myeloid leukemia with normal karyotype. <i>Oncogene</i> , 2005 , 24, 1580-8	9.2	54
146	Revised risk estimation and treatment stratification of low- and intermediate-risk neuroblastoma patients by integrating clinical and molecular prognostic markers. <i>Clinical Cancer Research</i> , 2015 , 21, 1904-15	12.9	53
145	Intratumoral cytokines and tumor cell biology determine spontaneous breast cancer-specific immune responses and their correlation to prognosis. <i>Cancer Research</i> , 2009 , 69, 8420-8	10.1	53
144	CCM2 mediates death signaling by the TrkA receptor tyrosine kinase. <i>Neuron</i> , 2009 , 63, 585-91	13.9	53
143	Reduced expression of CAMTA1 correlates with adverse outcome in neuroblastoma patients. <i>Clinical Cancer Research</i> , 2006 , 12, 131-8	12.9	53
142	Microarray data warehouse allowing for inclusion of experiment annotations in statistical analysis. <i>Bioinformatics</i> , 2002 , 18, 423-33	7.2	53
141	A reductase/isomerase subunit of mitochondrial NADH:ubiquinone oxidoreductase (complex I) carries an NADPH and is involved in the biogenesis of the complex. <i>Journal of Molecular Biology</i> , 1999 , 292, 569-80	6.5	52
140	Whole genome sequencing puts forward hypotheses on metastasis evolution and therapy in colorectal cancer. <i>Nature Communications</i> , 2018 , 9, 4782	17.4	51
139	Hypermethylation of the inactive X chromosome is a frequent event in cancer. <i>Cell</i> , 2013 , 155, 567-81	56.2	50
138	Overlapping gene coexpression patterns in human medullary thymic epithelial cells generate self-antigen diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, E3497-505	11.5	50
137	Mitochondrial fatty acid synthesis: a relic of endosymbiotic origin and a specialized means for respiration. <i>FEBS Letters</i> , 1997 , 407, 249-52	3.8	50
136	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. <i>Nature Communications</i> , 2019 , 10, 1459	17.4	49
135	Integration of genomics and histology revises diagnosis and enables effective therapy of refractory cancer of unknown primary with amplification. <i>Journal of Physical Education and Sports Management</i> , 2016 , 2, a001180	2.8	49
134	An integrated genome research network for studying the genetics of alcohol addiction. <i>Addiction Biology</i> , 2010 , 15, 369-79	4.6	49
133	Differential expression of neuronal genes defines subtypes of disseminated neuroblastoma with favorable and unfavorable outcome. <i>Clinical Cancer Research</i> , 2006 , 12, 5118-28	12.9	49
132	TMPRSS2-ERG fusions are strongly linked to young patient age in low-grade prostate cancer. <i>European Urology</i> , 2014 , 66, 978-81	10.2	48
131	BRAF inhibitor-associated ERK activation drives development of chronic lymphocytic leukemia. <i>Journal of Clinical Investigation</i> , 2014 , 124, 5074-84	15.9	46

130	Accurate and efficient detection of gene fusions from RNA sequencing data. <i>Genome Research</i> , 2021 , 31, 448-460	9.7	45
129	A systems biology approach to identify the combination effects of human herpesvirus 8 genes on NF-kappaB activation. <i>Journal of Virology</i> , 2009 , 83, 2563-74	6.6	43
128	Distinct molecular phenotype of malignant CD34(+) hematopoietic stem and progenitor cells in chronic myelogenous leukemia. <i>Oncogene</i> , 2005 , 24, 5313-24	9.2	43
127	Methylation profiling identifies two subclasses of squamous cell carcinoma related to distinct cells of origin. <i>Nature Communications</i> , 2018 , 9, 577	17.4	42
126	Cooperation of BRAF(F595L) and mutant HRAS in histiocytic sarcoma provides new insights into oncogenic BRAF signaling. <i>Leukemia</i> , 2016 , 30, 937-46	10.7	42
125	Molecular profiling of long-term survivors identifies a subgroup of glioblastoma characterized by chromosome 19/20 co-gain. <i>Acta Neuropathologica</i> , 2015 , 130, 419-34	14.3	41
124	PD-L1 (CD274) copy number gain, expression, and immune cell infiltration as candidate predictors for response to immune checkpoint inhibitors in soft-tissue sarcoma. <i>Oncotarget</i> , 2017 , 8, e127977 ²	7.2	40
123	Genomic footprints of activated telomere maintenance mechanisms in cancer. <i>Nature Communications</i> , 2020 , 11, 733	17.4	40
122	Multi-parametric analysis and modeling of relationships between mitochondrial morphology and apoptosis. <i>PLoS ONE</i> , 2012 , 7, e28694	3.7	39
121	Characterization of two novel redox groups in the respiratory NADH:ubiquinone oxidoreductase (complex I). <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2000 , 1459, 305-9	4.6	39
120	HiGHmed - An Open Platform Approach to Enhance Care and Research across Institutional Boundaries. <i>Methods of Information in Medicine</i> , 2018 , 57, e66-e81	1.5	37
119	Monitoring CSF proteome alterations in amyotrophic lateral sclerosis: obstacles and perspectives in translating a novel marker panel to the clinic. <i>PLoS ONE</i> , 2012 , 7, e44401	3.7	36
118	Recurrent mutations within the amino-terminal region of β -catenin are probable key molecular driver events in sinonasal hemangiopericytoma. <i>American Journal of Pathology</i> , 2015 , 185, 563-71	5.8	35
117	Integrated pathway-based approach identifies association between genomic regions at CTCF and CACNB2 and schizophrenia. <i>PLoS Genetics</i> , 2014 , 10, e1004345	6	35
116	Redox components and structure of the respiratory NADH:ubiquinone oxidoreductase (complex I). <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 1998 , 1365, 215-9	4.6	35
115	High Skp2 expression characterizes high-risk neuroblastomas independent of MYCN status. <i>Clinical Cancer Research</i> , 2007 , 13, 4695-703	12.9	35
114	Defective homologous recombination DNA repair as therapeutic target in advanced chordoma. <i>Nature Communications</i> , 2019 , 10, 1635	17.4	33
113	Comparative transcriptome profiling of amyloid precursor protein family members in the adult cortex. <i>BMC Genomics</i> , 2011 , 12, 160	4.5	33

112	The landscape of chromothripsis across adult cancer types. <i>Nature Communications</i> , 2020 , 11, 2320	17.4	32
111	Human resting CD4+ T cells are constitutively inhibited by TGF beta under steady-state conditions. <i>Journal of Immunology</i> , 2007 , 178, 6931-40	5.3	32
110	Identification of DNA methylation changes at cis-regulatory elements during early steps of HSC differentiation using tagmentation-based whole genome bisulfite sequencing. <i>Cell Cycle</i> , 2014 , 13, 3476-87	4.7	31
109	Alterations of microRNA and microRNA-regulated messenger RNA expression in germinal center B-cell lymphomas determined by integrative sequencing analysis. <i>Haematologica</i> , 2016 , 101, 1380-1389	6.6	31
108	Dissecting intratumour heterogeneity of nodal B-cell lymphomas at the transcriptional, genetic and drug-response levels. <i>Nature Cell Biology</i> , 2020 , 22, 896-906	23.4	30
107	MicroRNA profiling of primary high-grade soft tissue sarcomas. <i>Genes Chromosomes and Cancer</i> , 2012 , 51, 982-96	5	30
106	Variant classification in precision oncology. <i>International Journal of Cancer</i> , 2019 , 145, 2996-3010	7.5	28
105	Decreased contractility due to energy deprivation in a transgenic rat model of hypertrophic cardiomyopathy. <i>Journal of Molecular Medicine</i> , 2009 , 87, 411-22	5.5	28
104	Suppression of early hematogenous dissemination of human breast cancer cells to bone marrow by retinoic Acid-induced 2. <i>Cancer Discovery</i> , 2015 , 5, 506-19	24.4	27
103	Feasibility of real-time molecular profiling for patients with newly diagnosed glioblastoma without MGMT promoter hypermethylation-the NCT Neuro Master Match (N2M2) pilot study. <i>Neuro-Oncology</i> , 2018 , 20, 826-837	1	27
102	Translating expression profiling into a clinically feasible test to predict neuroblastoma outcome. <i>Clinical Cancer Research</i> , 2007 , 13, 1459-65	12.9	27
101	Pathways of urothelial cancer progression suggested by Bayesian network analysis of allelotyping data. <i>International Journal of Cancer</i> , 2004 , 110, 850-6	7.5	27
100	Succession of transiently active tumor-initiating cell clones in human pancreatic cancer xenografts. <i>EMBO Molecular Medicine</i> , 2017 , 9, 918-932	12	26
99	Chromosome 17/17q gain and unaltered profiles in high resolution array-CGH are prognostically informative in neuroblastoma. <i>Genes Chromosomes and Cancer</i> , 2014 , 53, 639-49	5	26
98	Autotaxin is expressed in FLT3-ITD positive acute myeloid leukemia and hematopoietic stem cells and promotes cell migration and proliferation. <i>Experimental Hematology</i> , 2013 , 41, 444-461.e4	3.1	25
97	Cross-study analysis of gene expression data for intermediate neuroblastoma identifies two biological subtypes. <i>BMC Cancer</i> , 2007 , 7, 89	4.8	25
96	TelomereHunter - in silico estimation of telomere content and composition from cancer genomes. <i>BMC Bioinformatics</i> , 2019 , 20, 272	3.6	24
95	Comprehensive Genomic and Transcriptomic Analysis for Guiding Therapeutic Decisions in Patients with Rare Cancers. <i>Cancer Discovery</i> , 2021 , 11, 2780-2795	24.4	24

94	Aggressive PDACs Show Hypomethylation of Repetitive Elements and the Execution of an Intrinsic IFN Program Linked to a Ductal Cell of Origin. <i>Cancer Discovery</i> , 2021 , 11, 638-659	24.4	24
93	Genetic subclone architecture of tumor clone-initiating cells in colorectal cancer. <i>Journal of Experimental Medicine</i> , 2017 , 214, 2073-2088	16.6	23
92	Distinct human circulating NKp30Fc ^{hi} CD8 T cell population exhibiting high natural killer-like antitumor potential. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E5980-E5989	11.5	23
91	MetaboDiff: an R package for differential metabolomic analysis. <i>Bioinformatics</i> , 2018 , 34, 3417-3418	7.2	22
90	From somatic variants towards precision oncology: Evidence-driven reporting of treatment options in molecular tumor boards. <i>Genome Medicine</i> , 2018 , 10, 18	14.4	22
89	Classification of neuroblastoma patients by published gene-expression markers reveals a low sensitivity for unfavorable courses of MYCN non-amplified disease. <i>Cancer Letters</i> , 2007 , 250, 250-67	9.9	22
88	Response to olaparib in a germline mutated prostate cancer and genetic events associated with resistance. <i>Journal of Physical Education and Sports Management</i> , 2019 , 5,	2.8	21
87	Between-species differences in gene copy number are enriched among functions critical for adaptive evolution in <i>Arabidopsis halleri</i> . <i>BMC Genomics</i> , 2016 , 17, 1034	4.5	21
86	Linking aberrant chromatin features in chronic lymphocytic leukemia to transcription factor networks. <i>Molecular Systems Biology</i> , 2019 , 15, e8339	12.2	20
85	Mining quasi-bicliques from HIV-1-human protein interaction network: a multiobjective biclustering approach. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013 , 10, 423-35	3	20
84	Subclassification and individual survival time prediction from gene expression data of neuroblastoma patients by using CASPAR. <i>Clinical Cancer Research</i> , 2008 , 14, 6590-601	12.9	20
83	FGFR2 is overexpressed in myxoid liposarcoma and inhibition of FGFR signaling impairs tumor growth in vitro. <i>Oncotarget</i> , 2015 , 6, 20215-30	3.3	20
82	IGF1R upregulation confers resistance to isoform-specific inhibitors of PI3K in PIK3CA-driven ovarian cancer. <i>Cell Death and Disease</i> , 2018 , 9, 944	9.8	19
81	Patient-derived xenografts of gastrointestinal cancers are susceptible to rapid and delayed B-lymphoproliferation. <i>International Journal of Cancer</i> , 2017 , 140, 1356-1363	7.5	18
80	Single-cell chromatin accessibility landscape identifies tissue repair program in human regulatory T cells. <i>Immunity</i> , 2021 , 54, 702-720.e17	32.3	18
79	Revisiting the Road Map of Medullary Thymic Epithelial Cell Differentiation. <i>Journal of Immunology</i> , 2017 , 199, 3488-3503	5.3	17
78	Targeting Fibroblast Growth Factor Receptor 1 for Treatment of Soft-Tissue Sarcoma. <i>Clinical Cancer Research</i> , 2017 , 23, 962-973	12.9	17
77	Identification of the Rage-dependent gene regulatory network in a mouse model of skin inflammation. <i>BMC Genomics</i> , 2010 , 11, 537	4.5	17

76	Search for novel redox groups in mitochondrial NADH:ubiquinone oxidoreductase (complex I) by diode array UV/VIS spectroscopy. <i>BioFactors</i> , 1998 , 8, 177-86	6.1	17
75	ACEseq Allele specific copy number estimation from whole genome sequencing		17
74	Homology Modelling and Molecular Docking Studies of Selected Substituted Benzo[imidazol-1-yl)methyl)benzimidamide Scaffolds on Adenylosuccinate Lyase Receptor. <i>Bioinformatics and Biology Insights</i> , 2019 , 13, 1177932219865533	5.3	16
73	Mutant KIT as imatinib-sensitive target in metastatic sinonasal carcinoma. <i>Annals of Oncology</i> , 2017 , 28, 142-148	10.3	16
72	Macrophages/Microglia Represent the Major Source of Indolamine 2,3-Dioxygenase Expression in Melanoma Metastases of the Brain. <i>Frontiers in Immunology</i> , 2020 , 11, 120	8.4	15
71	Drug-based perturbation screen uncovers synergistic drug combinations in Burkitt lymphoma. <i>Scientific Reports</i> , 2018 , 8, 12046	4.9	15
70	KIT-Dependent and KIT-Independent Genomic Heterogeneity of Resistance in Gastrointestinal Stromal Tumors - TORC1/2 Inhibition as Salvage Strategy. <i>Molecular Cancer Therapeutics</i> , 2019 , 18, 1985-1996	6.1	15
69	Investigation of manic and euthymic episodes identifies state- and trait-specific gene expression and STAB1 as a new candidate gene for bipolar disorder. <i>Translational Psychiatry</i> , 2014 , 4, e426	8.6	15
68	Discovery of transcriptional programs in cerebral ischemia by in silico promoter analysis. <i>Brain Research</i> , 2009 , 1272, 3-13	3.7	15
67	gene rearrangement: a powerful driver of β -catenin activation in liver tumours. <i>Gut</i> , 2019 , 68, 1287-1296	19.2	15
66	Whole-genome analysis of gene expression associates the ubiquitin-proteasome system with the cardiomyopathy phenotype in disease-sensitized congenic mouse strains. <i>Cardiovascular Research</i> , 2012 , 94, 87-95	9.9	14
65	Computational identification of signalling pathways in Plasmodium falciparum. <i>Infection, Genetics and Evolution</i> , 2011 , 11, 755-64	4.5	13
64	A cut-off based approach for gene expression analysis of formalin-fixed and paraffin-embedded tissue samples. <i>Genomics</i> , 2008 , 91, 522-9	4.3	13
63	XRCC5 as a risk gene for alcohol dependence: evidence from a genome-wide gene-set-based analysis and follow-up studies in Drosophila and humans. <i>Neuropsychopharmacology</i> , 2015 , 40, 361-71	8.7	12
62	Bronchoalveolar lavage fluid of lung cancer patients: mapping the uncharted waters using proteomics technology. <i>Lung Cancer</i> , 2011 , 72, 136-8	5.9	12
61	Alternative lengthening of telomeres in childhood neuroblastoma from genome to proteome. <i>Nature Communications</i> , 2021 , 12, 1269	17.4	12
60	Evolutionary conserved gene co-expression drives generation of self-antigen diversity in medullary thymic epithelial cells. <i>Journal of Autoimmunity</i> , 2016 , 67, 65-75	15.5	11
59	Molecular Classification Substitutes for the Prognostic Variables Stage, Age, and MYCN Status in Neuroblastoma Risk Assessment. <i>Neoplasia</i> , 2017 , 19, 982-990	6.4	11

58	Proteomic bronchiolitis obliterans syndrome risk monitoring in lung transplant recipients. <i>Transplantation</i> , 2011 , 92, 477-85	1.8	11
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