Benedikt Brors

List of Publications by Year
in descending order

235 papers	25,185 citations	10986 71 h-index	8396 147 g-index
250 all docs	250 docs citations	250 times ranked	41293 citing authors

#	Article	IF	Citations
1	circlizeimplements and enhances circular visualization in R. Bioinformatics, 2014, 30, 2811-2812.	4.1	2,736
2	The landscape of genomic alterations across childhood cancers. Nature, 2018, 555, 321-327.	27.8	1,068
3	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. Nature Biotechnology, 2010, 28, 827-838.	17.5	795
4	The whole-genome landscape of medulloblastoma subtypes. Nature, 2017, 547, 311-317.	27.8	787
5	Dissecting the genomic complexity underlying medulloblastoma. Nature, 2012, 488, 100-105.	27.8	765
6	Genome Sequencing of Pediatric Medulloblastoma Links Catastrophic DNA Rearrangements with TP53 Mutations. Cell, 2012, 148, 59-71.	28.9	743
7	Recurrent somatic alterations of FGFR1 and NTRK2 in pilocytic astrocytoma. Nature Genetics, 2013, 45, 927-932.	21.4	674
8	Genome Sequencing of SHH Medulloblastoma Predicts Genotype-Related Response to Smoothened Inhibition. Cancer Cell, 2014, 25, 393-405.	16.8	627
9	Enhancer hijacking activates GFI1 family oncogenes in medulloblastoma. Nature, 2014, 511, 428-434.	27.8	520
10	Promiscuous gene expression in thymic epithelial cells is regulated at multiple levels. Journal of Experimental Medicine, 2005, 202, 33-45.	8.5	498
11	Identification of Regulatory Networks in HSCs and Their Immediate Progeny via Integrated Proteome, Transcriptome, and DNA Methylome Analysis. Cell Stem Cell, 2014, 15, 507-522.	11.1	439
12	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. Nature Genetics, 2020, 52, 331-341.	21.4	431
13	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	28.9	404
14	Recurrent mutation of the ID3 gene in Burkitt lymphoma identified by integrated genome, exome and transcriptome sequencing. Nature Genetics, 2012, 44, 1316-1320.	21.4	389
15	Decoding the regulatory landscape of medulloblastoma using DNA methylation sequencing. Nature, 2014, 510, 537-541.	27.8	378
16	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. Genome Biology, 2015, 16, 133.	8.8	325
17	Medullary Epithelial Cells of the Human Thymus Express a Highly Diverse Selection of Tissue-specific Genes Colocalized in Chromosomal Clusters. Journal of Experimental Medicine, 2004, 199, 155-166.	8.5	317
18	Transient colocalization of X-inactivation centres accompanies the initiation of X inactivation. Nature Cell Biology, 2006, 8, 293-299.	10.3	304

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19	Integrative Genomic Analyses Reveal an Androgen-Driven Somatic Alteration Landscape in Early-Onset Prostate Cancer. Cancer Cell, 2013, 23, 159-170.	16.8	292
20	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001.	12.8	266
21	Next-generation personalised medicine for high-risk paediatric cancer patients â€“ The INFORM pilot study. European Journal of Cancer, 2016, 65, 91-101.	2.8	262
22	DNA methylation dynamics during B cell maturation underlie a continuum of disease phenotypes in chronic lymphocytic leukemia. Nature Genetics, 2016, 48, 253-264.	21.4	254
23	Acute myeloid leukemias with reciprocal rearrangements can be distinguished by specific gene expression profiles. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 10008-10013.	7.1	246
24	Customized Oligonucleotide Microarray Gene Expressionâ€“Based Classification of Neuroblastoma Patients Outperforms Current Clinical Risk Stratification. Journal of Clinical Oncology, 2006, 24, 5070-5078.	1.6	243
25	Sarcoma classification by DNA methylation profiling. Nature Communications, 2021, 12, 498.	12.8	237
26	DNMT and HDAC inhibitors induce cryptic transcription start sites encoded in long terminal repeats. Nature Genetics, 2017, 49, 1052-1060.	21.4	235
27	Intratumor DNA Methylation Heterogeneity Reflects Clonal Evolution in Aggressive Prostate Cancer. Cell Reports, 2014, 8, 798-806.	6.4	219
28	Distinct transcriptional MYCN/c-MYC activities are associated with spontaneous regression or malignant progression in neuroblastomas. Genome Biology, 2008, 9, R150.	9.6	215
29	Accurate and efficient detection of gene fusions from RNA sequencing data. Genome Research, 2021, 31, 448-460.	5.5	215
30	Cell competition is a tumour suppressor mechanism in the thymus. Nature, 2014, 509, 465-470.	27.8	209
31	Thymic B Cells Are Licensed to Present Self Antigens for Central T Cell Tolerance Induction. Immunity, 2015, 42, 1048-1061.	14.3	201
32	Solitary Fibrous Tumors/Hemangiopericytomas with Different Variants of the NAB2-STAT6 Gene Fusion Are Characterized by Specific Histomorphology and Distinct Clinicopathological Features. American Journal of Pathology, 2014, 184, 1209-1218.	3.8	198
33	Integrative genomic and transcriptomic analysis of leiomyosarcoma. Nature Communications, 2018, 9, 144.	12.8	197
34	Genome-wide DNA-methylation landscape defines specialization of regulatory T cells in tissues. Nature Immunology, 2017, 18, 1160-1172.	14.5	193
35	Molecular Evolution of Early-Onset Prostate Cancer Identifies Molecular Risk Markers and Clinical Trajectories. Cancer Cell, 2018, 34, 996-1011.e8.	16.8	190
36	NRG1 Fusions in KRAS Wild-Type Pancreatic Cancer. Cancer Discovery, 2018, 8, 1087-1095.	9.4	189

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37	Hox-C9 activates the intrinsic pathway of apoptosis and is associated with spontaneous regression in neuroblastoma. Cell Death and Disease, 2013, 4, e586-e586.	6.3	184
38	Cross-platform analysis of cancer microarray data improves gene expression based classification of phenotypes. BMC Bioinformatics, 2005, 6, 265.	2.6	183
39	Recurrent MET fusion genes represent a drug target in pediatric glioblastoma. Nature Medicine, 2016, 22, 1314-1320.	30.7	183
40	Epigenomic Profiling of Human CD4+ T Cells Supports a Linear Differentiation Model and Highlights Molecular Regulators of Memory Development. Immunity, 2016, 45, 1148-1161.	14.3	174
41	Seromic profiling of ovarian and pancreatic cancer. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 5088-5093.	7.1	163
42	Gene Expression Pattern in Biomechanically Stretched Cardiomyocytes. Hypertension, 2008, 51, 309-318.	2.7	161
43	Genome-Wide Association-, Replication-, and Neuroimaging Study Implicates HOMER1 in the Etiology of Major Depression. Biological Psychiatry, 2010, 68, 578-585.	1.3	156
44	Gene Expression Signature Predicting Pathologic Complete Response With Gemcitabine, Epirubicin, and Docetaxel in Primary Breast Cancer. Journal of Clinical Oncology, 2006, 24, 1839-1845.	1.6	146
45	Genome-wide transcriptional analysis of the human cell cycle identifies genes differentially regulated in normal and cancer cells. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 955-960.	7.1	145
46	BAZ2A (TIP5) is involved in epigenetic alterations in prostate cancer and its overexpression predicts disease recurrence. Nature Genetics, 2015, 47, 22-30.	21.4	141
47	Precursors for Nonlymphoid-Tissue Treg Cells Reside in Secondary Lymphoid Organs and Are Programmed by the Transcription Factor BATF. Immunity, 2020, 52, 295-312.e11.	14.3	140
48	CD95-Ligand on Peripheral Myeloid Cells Activates Syk Kinase to Trigger Their Recruitment to the Inflammatory Site. Immunity, 2010, 32, 240-252.	14.3	134
49	Temporal transcriptomic analysis of the Listeria monocytogenes EGD-e ÏƒB regulon. BMC Microbiology, 2008, 8, 20.	3.3	133
50	MicroRNA miR-885-5p targets CDK2 and MCM5, activates p53 and inhibits proliferation and survival. Cell Death and Differentiation, 2011, 18, 974-984.	11.2	133
51	Precision oncology based on omics data: The NCT Heidelberg experience. International Journal of Cancer, 2017, 141, 877-886.	5.1	133
52	Group testing for pathway analysis improves comparability of different microarray datasets. Bioinformatics, 2006, 22, 2500-2506.	4.1	129
53	Prognostic Impact of Gene Expressionâ€“Based Classification for Neuroblastoma. Journal of Clinical Oncology, 2010, 28, 3506-3515.	1.6	129
54	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. American Journal of Gastroenterology, 2010, 105, 2060-2071.	0.4	126

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55	Comprehensive Genomic and Transcriptomic Analysis for Guiding Therapeutic Decisions in Patients with Rare Cancers. Cancer Discovery, 2021, 11, 2780-2795.	9.4	125
56	Prediction of clinical outcome and biological characterization of neuroblastoma by expression profiling. Oncogene, 2005, 24, 7902-7912.	5.9	113
57	Combining transcription factor binding affinities with open-chromatin data for accurate gene expression prediction. Nucleic Acids Research, 2017, 45, 54-66.	14.5	112
58	Microarray-based approach identifies microRNAs and their target functional patterns in polycystic kidney disease. BMC Genomics, 2008, 9, 624.	2.8	107
59	MYC/MIZ1-dependent gene repression inversely coordinates the circadian clock with cell cycle and proliferation. Nature Communications, 2016, 7, 11807.	12.8	103
60	Whole genome sequencing puts forward hypotheses on metastasis evolution and therapy in colorectal cancer. Nature Communications, 2018, 9, 4782.	12.8	103
61	N2M2 (NOA-20) phase I/II trial of molecularly matched targeted therapies plus radiotherapy in patients with newly diagnosed non-MGMT hypermethylated glioblastoma. Neuro-Oncology, 2019, 21, 95-105.	1.2	100
62	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. Nature Communications, 2019, 10, 1459.	12.8	99
63	High ALK Receptor Tyrosine Kinase Expression Supersedes ALK Mutation as a Determining Factor of an Unfavorable Phenotype in Primary Neuroblastoma. Clinical Cancer Research, 2011, 17, 5082-5092.	7.0	95
64	Dissecting intratumour heterogeneity of nodal B-cell lymphomas at the transcriptional, genetic and drug-response levels. Nature Cell Biology, 2020, 22, 896-906.	10.3	93
65	Recurrent CDKN1B (p27) mutations in hairy cell leukemia. Blood, 2015, 126, 1005-1008.	1.4	88
66	Genomic footprints of activated telomere maintenance mechanisms in cancer. Nature Communications, 2020, 11, 733.	12.8	87
67	Accurate Outcome Prediction in Neuroblastoma across Independent Data Sets Using a Multigene Signature. Clinical Cancer Research, 2010, 16, 1532-1541.	7.0	86
68	Genome-wide association study of pathological gambling. European Psychiatry, 2016, 36, 38-46.	0.2	82
69	Revised Risk Estimation and Treatment Stratification of Low- and Intermediate-Risk Neuroblastoma Patients by Integrating Clinical and Molecular Prognostic Markers. Clinical Cancer Research, 2015, 21, 1904-1915.	7.0	80
70	Integrative DNA methylation and gene expression analysis in high-grade soft tissue sarcomas. Genome Biology, 2013, 14, r137.	9.6	78
71	Single-cell chromatin accessibility landscape identifies tissue repair program in human regulatory TÂcells. Immunity, 2021, 54, 702-720.e17.	14.3	78
72	Variant classification in precision oncology. International Journal of Cancer, 2019, 145, 2996-3010.	5.1	76

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73	The landscape of chromothripsis across adult cancer types. Nature Communications, 2020, 11, 2320.	12.8	75
74	Two genes of the putative mitochondrial fatty acid synthase in the genome of Saccharomyces cerevisiae. Current Genetics, 1997, 32, 384-388.	1.7	74
75	Coverage Bias and Sensitivity of Variant Calling for Four Whole-genome Sequencing Technologies. PLoS ONE, 2013, 8, e66621.	2.5	74
76	Molecular profiling of long-term survivors identifies a subgroup of glioblastoma characterized by chromosome 19/20 co-gain. Acta Neuropathologica, 2015, 130, 419-434.	7.7	74
77	Epigenetic dynamics of monocyte-to-macrophage differentiation. Epigenetics and Chromatin, 2016, 9, 33.	3.9	73
78	Identification of Two Tetranuclear FeS Clusters on the Ferredoxin-Type Subunit of NADH:Ubiquinone Oxidoreductase (Complex I). Biochemistry, 2001, 40, 6124-6131.	2.5	72
79	Oligonucleotide arrayâ€based comparative genomic hybridization (aCGH) of 90 neuroblastomas reveals aberration patterns closely associated with relapse pattern and outcome. Genes Chromosomes and Cancer, 2006, 45, 1130-1142.	2.8	72
80	Argonaute--a database for gene regulation by mammalian microRNAs. Nucleic Acids Research, 2006, 34, D115-D118.	14.5	72
81	Overlapping gene coexpression patterns in human medullary thymic epithelial cells generate self-antigen diversity. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E3497-505.	7.1	70
82	A highly standardized, robust, and cost-effective method for genome-wide transcriptome analysis of peripheral blood applicable to large-scale clinical trials. Genomics, 2006, 87, 653-664.	2.9	68
83	Comparison of normalization methods for Illumina BeadChip HumanHT-12 v3. BMC Genomics, 2010, 11, 349.	2.8	68
84	Reduced Expression of CAMTA1 Correlates with Adverse Outcome in Neuroblastoma Patients. Clinical Cancer Research, 2006, 12, 131-138.	7.0	67
85	Hypermutation of the Inactive X Chromosome Is a Frequent Event in Cancer. Cell, 2013, 155, 567-581.	28.9	67
86	Distinct gene expression patterns associated with FLT3- and NRAS-activating mutations in acute myeloid leukemia with normal karyotype. Oncogene, 2005, 24, 1580-1588.	5.9	65
87	Aggressive PDACs Show Hypomethylation of Repetitive Elements and the Execution of an Intrinsic IFN Program Linked to a Ductal Cell of Origin. Cancer Discovery, 2021, 11, 638-659.	9.4	65
88	Methylation profiling identifies two subclasses of squamous cell carcinoma related to distinct cells of origin. Nature Communications, 2018, 9, 577.	12.8	64
89	HiGHmed â€“ An Open Platform Approach to Enhance Care and Research across Institutional Boundaries. Methods of Information in Medicine, 2018, 57, e66-e81.	1.2	64
90	Defective homologous recombination DNA repair as therapeutic target in advanced chordoma. Nature Communications, 2019, 10, 1635.	12.8	64

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91	Mitochondrial fatty acid synthesis: a relic of endosymbiontic origin and a specialized means for respiration. FEBS Letters, 1997, 407, 249-252.	2.8	62
92	Comparison of performance of one-color and two-color gene-expression analyses in predicting clinical endpoints of neuroblastoma patients. Pharmacogenomics Journal, 2010, 10, 258-266.	2.0	62
93	Differential Expression of Neuronal Genes Defines Subtypes of Disseminated Neuroblastoma with Favorable and Unfavorable Outcome. Clinical Cancer Research, 2006, 12, 5118-5128.	7.0	60
94	Microarray data warehouse allowing for inclusion of experiment annotations in statistical analysis. Bioinformatics, 2002, 18, 423-433.	4.1	59
95	CCM2 Mediates Death Signaling by the TrkA Receptor Tyrosine Kinase. Neuron, 2009, 63, 585-591.	8.1	58
96	An integrated genome research network for studying the genetics of alcohol addiction. Addiction Biology, 2010, 15, 369-379.	2.6	57
97	Integration of genomics and histology revises diagnosis and enables effective therapy of refractory cancer of unknown primary with PDL1 amplification. Journal of Physical Education and Sports Management, 2016, 2, a001180.	1.2	57
98	A Reductase/Isomerase Subunit of Mitochondrial NADH:Ubiquinone Oxidoreductase (complex I) Carries an NADPH and is Involved in the Biogenesis of the Complex. Journal of Molecular Biology, 1999, 292, 569-580.	4.2	56
99	BRAF inhibitorâ€“associated ERK activation drives development of chronic lymphocytic leukemia. Journal of Clinical Investigation, 2014, 124, 5074-5084.	8.2	56
100	TelomereHunter â€“ in silico estimation of telomere content and composition from cancer genomes. BMC Bioinformatics, 2019, 20, 272.	2.6	56
101	Intratumoral Cytokines and Tumor Cell Biology Determine Spontaneous Breast Cancerâ€“Specific Immune Responses and Their Correlation to Prognosis. Cancer Research, 2009, 69, 8420-8428.	0.9	55
102	TMPRSS2-ERG Fusions Are Strongly Linked to Young Patient Age in Low-grade Prostate Cancer. European Urology, 2014, 66, 978-981.	1.9	54
103	Cooperation of BRAFF595L and mutant HRAS in histiocytic sarcoma provides new insights into oncogenic BRAF signaling. Leukemia, 2016, 30, 937-946.	7.2	52
104	The genomic and transcriptional landscape of primary central nervous system lymphoma. Nature Communications, 2022, 13, 2558.	12.8	52
105	High Skp2 Expression Characterizes High-Risk Neuroblastomas Independent of MYCN Status. Clinical Cancer Research, 2007, 13, 4695-4703.	7.0	50
106	PD-L1 (CD274) copy number gain, expression, and immune cell infiltration as candidate predictors for response to immune checkpoint inhibitors in soft-tissue sarcoma. OncoImmunology, 2017, 6, e1279777.	4.6	50
107	Recurrent Mutations within the Amino-Terminal Region of Î²-Catenin Are Probable Key Molecular Driver Events in Sinonasal Hemangiopericytoma. American Journal of Pathology, 2015, 185, 563-571.	3.8	49
108	A Systems Biology Approach To Identify the Combination Effects of Human Herpesvirus 8 Genes on NF-ÎºB Activation. Journal of Virology, 2009, 83, 2563-2574.	3.4	47

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109	Distinct molecular phenotype of malignant CD34+ hematopoietic stem and progenitor cells in chronic myelogenous leukemia. Oncogene, 2005, 24, 5313-5324.	5.9	46
110	Alternative lengthening of telomeres in childhood neuroblastoma from genome to proteome. Nature Communications, 2021, 12, 1269.	12.8	46
111	Suppression of Early Hematogenous Dissemination of Human Breast Cancer Cells to Bone Marrow by Retinoic Acidâ€“Induced 2. Cancer Discovery, 2015, 5, 506-519.	9.4	45
112	Multi-Parametric Analysis and Modeling of Relationships between Mitochondrial Morphology and Apoptosis. PLoS ONE, 2012, 7, e28694.	2.5	44
113	Integrated Pathway-Based Approach Identifies Association between Genomic Regions at CTCF and CACNB2 and Schizophrenia. PLoS Genetics, 2014, 10, e1004345.	3.5	44
114	Monitoring CSF Proteome Alterations in Amyotrophic Lateral Sclerosis: Obstacles and Perspectives in Translating a Novel Marker Panel to the Clinic. PLoS ONE, 2012, 7, e44401.	2.5	44
115	Characterization of two novel redox groups in the respiratory NADH:ubiquinone oxidoreductase (complex I). Biochimica Et Biophysica Acta - Bioenergetics, 2000, 1459, 305-309.	1.0	43
116	Alterations of microRNA and microRNA-regulated messenger RNA expression in germinal center B-cell lymphomas determined by integrative sequencing analysis. Haematologica, 2016, 101, 1380-1389.	3.5	43
117	Distinct human circulating NKp30 ⁺ FcÎµRIÎ³ ⁺ CD8 ⁺ T cell population exhibiting high natural killer-like antitumor potential. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E5980-E5989.	7.1	43
118	Redox components and structure of the respiratory NADH:ubiquinone oxidoreductase (complex I). Biochimica Et Biophysica Acta - Bioenergetics, 1998, 1365, 215-219.	1.0	41
119	MetaboDiff: an R package for differential metabolomic analysis. Bioinformatics, 2018, 34, 3417-3418.	4.1	41
120	Comparative transcriptome profiling of amyloid precursor protein family members in the adult cortex. BMC Genomics, 2011, 12, 160.	2.8	39
121	Identification of DNA methylation changes atcis-regulatory elements during early steps of HSC differentiation using tagmentation-based whole genome bisulfite sequencing. Cell Cycle, 2014, 13, 3476-3487.	2.6	39
122	Linking aberrant chromatin features in chronic lymphocytic leukemia to transcription factor networks. Molecular Systems Biology, 2019, 15, e8339.	7.2	39
123	MicroRNA profiling of primary highâ€grade soft tissue sarcomas. Genes Chromosomes and Cancer, 2012, 51, 982-996.	2.8	38
124	Human Resting CD4+ T Cells Are Constitutively Inhibited by TGFÎ² under Steady-State Conditions. Journal of Immunology, 2007, 178, 6931-6940.	0.8	37
125	Succession of transiently active tumorâ€initiating cell clones in human pancreatic cancer xenografts. EMBO Molecular Medicine, 2017, 9, 918-932.	6.9	36
126	From somatic variants towards precision oncology: Evidence-driven reporting of treatment options in molecular tumor boards. Genome Medicine, 2018, 10, 18.	8.2	36

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127	Response to olaparib in a PALB2 germline mutated prostate cancer and genetic events associated with resistance. Journal of Physical Education and Sports Management, 2019, 5, a003657.	1.2	36
128	Homology Modelling and Molecular Docking Studies of Selected Substituted Lyase Receptor. Bioinformatics and Biology Insights, 2019, 13, 117793221986553.	2.0	35
129	Decreased contractility due to energy deprivation in a transgenic rat model of hypertrophic cardiomyopathy. Journal of Molecular Medicine, 2009, 87, 411-422.	3.9	34
130	Chromosome 17/17q gain and unaltered profiles in high resolution arrayâ€CGH are prognostically informative in neuroblastoma. Genes Chromosomes and Cancer, 2014, 53, 639-649.	2.8	34
131	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. Leukemia, 2021, 35, 2002-2016.	7.2	34
132	IGF1R upregulation confers resistance to isoform-specific inhibitors of PI3K in PIK3CA-driven ovarian cancer. Cell Death and Disease, 2018, 9, 944.	6.3	33
133	Revisiting the Road Map of Medullary Thymic Epithelial Cell Differentiation. Journal of Immunology, 2017, 199, 3488-3503.	0.8	32
134	Feasibility of real-time molecular profiling for patients with newly diagnosed glioblastoma without MGMT promoter hypermethylationâ€"the NCT Neuro Master Match (N2M2) pilot study. Neuro-Oncology, 2018, 20, 826-837.	1.2	32
135	Assessment of modelling strategies for drug response prediction in cell lines and xenografts. Scientific Reports, 2020, 10, 2849.	3.3	31
136	Investigation of manic and euthymic episodes identifies state- and trait-specific gene expression and STAB1 as a new candidate gene for bipolar disorder. Translational Psychiatry, 2014, 4, e426-e426.	4.8	30
137	Genetic subclone architecture of tumor clone-initiating cells in colorectal cancer. Journal of Experimental Medicine, 2017, 214, 2073-2088.	8.5	30
138	Mutant KIT as imatinib-sensitive target in metastatic sinonasal carcinoma. Annals of Oncology, 2017, 28, 142-148.	1.2	30
139	Pathways of urothelial cancer progression suggested by Bayesian network analysis of allelotyping data. International Journal of Cancer, 2004, 110, 850-856.	5.1	29
140	Cross-study analysis of gene expression data for intermediate neuroblastoma identifies two biological subtypes. BMC Cancer, 2007, 7, 89.	2.6	29
141	Identification of the Rage-dependent gene regulatory network in a mouse model of skin inflammation. BMC Genomics, 2010, 11, 537.	2.8	29
142	Mining Quasi-Bicliques from HIV-1-Human Protein Interaction Network: A Multiobjective Biclustering Approach. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 423-435.	3.0	29
143	Targeting Fibroblast Growth Factor Receptor 1 for Treatment of Soft-Tissue Sarcoma. Clinical Cancer Research, 2017, 23, 962-973.	7.0	29
144	RSPO2 gene rearrangement: a powerful driver of Î²-catenin activation in liver tumours. Gut, 2019, 68, 1287-1296.	12.1	29

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145	Clinical Impact of Molecular Subtyping of Pancreatic Cancer. Frontiers in Cell and Developmental Biology, 2021, 9, 743908.	3.7	29
146	Translating Expression Profiling into a Clinically Feasible Test to Predict Neuroblastoma Outcome. Clinical Cancer Research, 2007, 13, 1459-1465.	7.0	28
147	Between-species differences in gene copy number are enriched among functions critical for adaptive evolution in Arabidopsis halleri. BMC Genomics, 2016, 17, 1034.	2.8	28
148	Macrophages/Microglia Represent the Major Source of Indolamine 2,3-Dioxygenase Expression in Melanoma Metastases of the Brain. Frontiers in Immunology, 2020, 11, 120.	4.8	28
149	Selective elimination of immunosuppressive T cells in patients with multiple myeloma. Leukemia, 2021, 35, 2602-2615.	7.2	27
150	Patient-derived xenografts of gastrointestinal cancers are susceptible to rapid and delayed B-lymphoproliferation. International Journal of Cancer, 2017, 140, 1356-1363.	5.1	26
151	Molecular Classification Substitutes for the Prognostic Variables Stage, Age, and MYCN Status in Neuroblastoma Risk Assessment. Neoplasia, 2017, 19, 982-990.	5.3	26
152	Autotaxin is expressed in FLT3-ITD positive acute myeloid leukemia and hematopoietic stem cells and promotes cell migration and proliferation. Experimental Hematology, 2013, 41, 444-461.e4.	0.4	25
153	Subclassification and Individual Survival Time Prediction from Gene Expression Data of Neuroblastoma Patients by Using CASPAR. Clinical Cancer Research, 2008, 14, 6590-6601.	7.0	23
154	Targetable ERBB2 mutations identified in neurofibroma/schwannoma hybrid nerve sheath tumors. Journal of Clinical Investigation, 2020, 130, 2488-2495.	8.2	23
155	FGFR2 is overexpressed in myxoid liposarcoma and inhibition of FGFR signaling impairs tumor growth in vitro. Oncotarget, 2015, 6, 20215-20230.	1.8	23
156	Classification of neuroblastoma patients by published gene-expression markers reveals a low sensitivity for unfavorable courses of MYCN non-amplified disease. Cancer Letters, 2007, 250, 250-267.	7.2	22
157	Drug-based perturbation screen uncovers synergistic drug combinations in Burkitt lymphoma. Scientific Reports, 2018, 8, 12046.	3.3	22
158	KIT-Dependent and KIT-Independent Genomic Heterogeneity of Resistance in Gastrointestinal Stromal Tumors â€" TORC1/2 Inhibition as Salvage Strategy. Molecular Cancer Therapeutics, 2019, 18, 1985-1996.	4.1	22
159	Community-driven development of a modified progression-free survival ratio for precision oncology. ESMO Open, 2019, 4, e000583.	4.5	22
160	Validating Comprehensive Next-Generation Sequencing Results for Precision Oncology: The NCT/DKTK Molecularly Aided Stratification for Tumor Eradication Research Experience. JCO Precision Oncology, 2018, 2, 1-13.	3.0	20
161	CATCH: A Prospective Precision Oncology Trial in Metastatic Breast Cancer. JCO Precision Oncology, 2021, 5, 676-686.	3.0	20
162	Evolutionary conserved gene co-expression drives generation ofÂself-antigen diversity in medullary thymic epithelial cells. Journal of Autoimmunity, 2016, 67, 65-75.	6.5	19

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163	MDM4 Is Targeted by 1q Gain and Drives Disease in Burkitt Lymphoma. Cancer Research, 2019, 79, 3125-3138.	0.9	19
164	Distributed Ledger Technology in genomics: a call for Europe. European Journal of Human Genetics, 2020, 28, 139-140.	2.8	19
165	Identification and characterization of a BRAF fusion oncoprotein with retained autoinhibitory domains. Oncogene, 2020, 39, 814-832.	5.9	19
166	Search for novel redox groups in mitochondrial NADH:ubiquinone oxidoreductase (complex I) by diode array UV/VIS spectroscopy. BioFactors, 1998, 8, 177-186.	5.4	18
167	Iroquois homeobox 2 suppresses cellular motility and chemokine expression in breast cancer cells. BMC Cancer, 2015, 15, 896.	2.6	18
168	Discovery of transcriptional programs in cerebral ischemia by in silico promoter analysis. Brain Research, 2009, 1272, 3-13.	2.2	17
169	Whole-genome analysis of gene expression associates the ubiquitin-proteasome system with the cardiomyopathy phenotype in disease-sensitized congenic mouse strains. Cardiovascular Research, 2012, 94, 87-95.	3.8	17
170	Identification of BCL-XL as highly active survival factor and promising therapeutic target in colorectal cancer. Cell Death and Disease, 2020, 11, 875.	6.3	17
171	Computational identification of signalling pathways in Plasmodium falciparum. Infection, Genetics and Evolution, 2011, 11, 755-764.	2.3	15
172	Integrating proteomics into precision oncology. International Journal of Cancer, 2021, 148, 1438-1451.	5.1	15
173	Characteristics and outcome of patients with acute myeloid leukaemia and t(8;16)(p11;p13): results from an International Collaborative Study*. British Journal of Haematology, 2021, 192, 832-842.	2.5	15
174	A cut-off based approach for gene expression analysis of formalin-fixed and paraffin-embedded tissue samples. Genomics, 2008, 91, 522-529.	2.9	14
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