

# Benedikt Brors

## List of Publications by Year in descending order

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Version: 2024-02-01

235  
papers

25,185  
citations

10956

71  
h-index

8370

147  
g-index

250  
all docs

250  
docs citations

250  
times ranked

41293  
citing authors

#	ARTICLE	IF	CITATIONS
1	<a href="#">circize</a> implements and enhances circular visualization in R. <i>Bioinformatics</i> , 2014, 30, 2811-2812.	1.8	2,736
2	The landscape of genomic alterations across childhood cancers. <i>Nature</i> , 2018, 555, 321-327.	13.7	1,068
3	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, 827-838.	9.4	795
4	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , 2017, 547, 311-317.	13.7	787
5	Dissecting the genomic complexity underlying medulloblastoma. <i>Nature</i> , 2012, 488, 100-105.	13.7	765
6	Genome Sequencing of Pediatric Medulloblastoma Links Catastrophic DNA Rearrangements with TP53 Mutations. <i>Cell</i> , 2012, 148, 59-71.	13.5	743
7	Recurrent somatic alterations of FGFR1 and NTRK2 in pilocytic astrocytoma. <i>Nature Genetics</i> , 2013, 45, 927-932.	9.4	674
8	Genome Sequencing of SHH Medulloblastoma Predicts Genotype-Related Response to Smoothed Inhibition. <i>Cancer Cell</i> , 2014, 25, 393-405.	7.7	627
9	Enhancer hijacking activates GFI1 family oncogenes in medulloblastoma. <i>Nature</i> , 2014, 511, 428-434.	13.7	520
10	Promiscuous gene expression in thymic epithelial cells is regulated at multiple levels. <i>Journal of Experimental Medicine</i> , 2005, 202, 33-45.	4.2	498
11	Identification of Regulatory Networks in HSCs and Their Immediate Progeny via Integrated Proteome, Transcriptome, and DNA Methyome Analysis. <i>Cell Stem Cell</i> , 2014, 15, 507-522.	5.2	439
12	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. <i>Nature Genetics</i> , 2020, 52, 331-341.	9.4	431
13	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149.	13.5	404
14	Recurrent mutation of the ID3 gene in Burkitt lymphoma identified by integrated genome, exome and transcriptome sequencing. <i>Nature Genetics</i> , 2012, 44, 1316-1320.	9.4	389
15	Decoding the regulatory landscape of medulloblastoma using DNA methylation sequencing. <i>Nature</i> , 2014, 510, 537-541.	13.7	378
16	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. <i>Genome Biology</i> , 2015, 16, 133.	3.8	325
17	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, 155-166.	4.2	317
18	Transient colocalization of X-inactivation centres accompanies the initiation of X inactivation. <i>Nature Cell Biology</i> , 2006, 8, 293-299.	4.6	304

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19	Integrative Genomic Analyses Reveal an Androgen-Driven Somatic Alteration Landscape in Early-Onset Prostate Cancer. <i>Cancer Cell</i> , 2013, 23, 159-170.	7.7	292
20	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. <i>Nature Communications</i> , 2015, 6, 10001.	5.8	266
21	Next-generation personalised medicine for high-risk paediatric cancer patients – The INFORM pilot study. <i>European Journal of Cancer</i> , 2016, 65, 91-101.	1.3	262
22	DNA methylation dynamics during B cell maturation underlie a continuum of disease phenotypes in chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2016, 48, 253-264.	9.4	254
23	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, 10008-10013.	3.3	246
24	Customized Oligonucleotide Microarray Gene Expression–Based Classification of Neuroblastoma Patients Outperforms Current Clinical Risk Stratification. <i>Journal of Clinical Oncology</i> , 2006, 24, 5070-5078.	0.8	243
25	Sarcoma classification by DNA methylation profiling. <i>Nature Communications</i> , 2021, 12, 498.	5.8	237
26	DNMT and HDAC inhibitors induce cryptic transcription start sites encoded in long terminal repeats. <i>Nature Genetics</i> , 2017, 49, 1052-1060.	9.4	235
27	Intratumor DNA Methylation Heterogeneity Reflects Clonal Evolution in Aggressive Prostate Cancer. <i>Cell Reports</i> , 2014, 8, 798-806.	2.9	219
28	Distinct transcriptional MYCN/c-MYC activities are associated with spontaneous regression or malignant progression in neuroblastomas. <i>Genome Biology</i> , 2008, 9, R150.	13.9	215
29	Accurate and efficient detection of gene fusions from RNA sequencing data. <i>Genome Research</i> , 2021, 31, 448-460.	2.4	215
30	Cell competition is a tumour suppressor mechanism in the thymus. <i>Nature</i> , 2014, 509, 465-470.	13.7	209
31	Thymic B Cells Are Licensed to Present Self Antigens for Central T Cell Tolerance Induction. <i>Immunity</i> , 2015, 42, 1048-1061.	6.6	201
32	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.	1.9	198
33	Integrative genomic and transcriptomic analysis of leiomyosarcoma. <i>Nature Communications</i> , 2018, 9, 144.	5.8	197
34	Genome-wide DNA-methylation landscape defines specialization of regulatory T cells in tissues. <i>Nature Immunology</i> , 2017, 18, 1160-1172.	7.0	193
35	Molecular Evolution of Early-Onset Prostate Cancer Identifies Molecular Risk Markers and Clinical Trajectories. <i>Cancer Cell</i> , 2018, 34, 996-1011.e8.	7.7	190
36	<i>NRG1</i> Fusions in <i>KRAS</i> Wild-Type Pancreatic Cancer. <i>Cancer Discovery</i> , 2018, 8, 1087-1095.	7.7	189

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37	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-e586.	2.7	184
38	Cross-platform analysis of cancer microarray data improves gene expression based classification of phenotypes. <i>BMC Bioinformatics</i> , 2005, 6, 265.	1.2	183
39	Recurrent MET fusion genes represent a drug target in pediatric glioblastoma. <i>Nature Medicine</i> , 2016, 22, 1314-1320.	15.2	183
40	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.	6.6	174
41	Seromic profiling of ovarian and pancreatic cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 5088-5093.	3.3	163
42	Gene Expression Pattern in Biomechanically Stretched Cardiomyocytes. <i>Hypertension</i> , 2008, 51, 309-318.	1.3	161
43	Genome-Wide Association-, Replication-, and Neuroimaging Study Implicates HOMER1 in the Etiology of Major Depression. <i>Biological Psychiatry</i> , 2010, 68, 578-585.	0.7	156
44	Gene Expression Signature Predicting Pathologic Complete Response With Gemcitabine, Epirubicin, and Docetaxel in Primary Breast Cancer. <i>Journal of Clinical Oncology</i> , 2006, 24, 1839-1845.	0.8	146
45	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, 955-960.	3.3	145
46	BAZ2A (TIP5) is involved in epigenetic alterations in prostate cancer and its overexpression predicts disease recurrence. <i>Nature Genetics</i> , 2015, 47, 22-30.	9.4	141
47	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.	6.6	140
48	CD95-Ligand on Peripheral Myeloid Cells Activates Syk Kinase to Trigger Their Recruitment to the Inflammatory Site. <i>Immunity</i> , 2010, 32, 240-252.	6.6	134
49	Temporal transcriptomic analysis of the <i>Listeria monocytogenes</i> EGD-e $\beta$ regulon. <i>BMC Microbiology</i> , 2008, 8, 20.	1.3	133
50	MicroRNA miR-885-5p targets CDK2 and MCM5, activates p53 and inhibits proliferation and survival. <i>Cell Death and Differentiation</i> , 2011, 18, 974-984.	5.0	133
51	Precision oncology based on omics data: The NCT Heidelberg experience. <i>International Journal of Cancer</i> , 2017, 141, 877-886.	2.3	133
52	Group testing for pathway analysis improves comparability of different microarray datasets. <i>Bioinformatics</i> , 2006, 22, 2500-2506.	1.8	129
53	Prognostic Impact of Gene Expression-Based Classification for Neuroblastoma. <i>Journal of Clinical Oncology</i> , 2010, 28, 3506-3515.	0.8	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. <i>American Journal of Gastroenterology</i> , 2010, 105, 2060-2071.	0.2	126

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55	Comprehensive Genomic and Transcriptomic Analysis for Guiding Therapeutic Decisions in Patients with Rare Cancers. <i>Cancer Discovery</i> , 2021, 11, 2780-2795.	7.7	125
56	Prediction of clinical outcome and biological characterization of neuroblastoma by expression profiling. <i>Oncogene</i> , 2005, 24, 7902-7912.	2.6	113
57	Combining transcription factor binding affinities with open-chromatin data for accurate gene expression prediction. <i>Nucleic Acids Research</i> , 2017, 45, 54-66.	6.5	112
58	Microarray-based approach identifies microRNAs and their target functional patterns in polycystic kidney disease. <i>BMC Genomics</i> , 2008, 9, 624.	1.2	107
59	MYC/MIZ1-dependent gene repression inversely coordinates the circadian clock with cell cycle and proliferation. <i>Nature Communications</i> , 2016, 7, 11807.	5.8	103
60	Whole genome sequencing puts forward hypotheses on metastasis evolution and therapy in colorectal cancer. <i>Nature Communications</i> , 2018, 9, 4782.	5.8	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. <i>Neuro-Oncology</i> , 2019, 21, 95-105.	0.6	100
62	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. <i>Nature Communications</i> , 2019, 10, 1459.	5.8	99
63	High <i>ALK</i> Receptor Tyrosine Kinase Expression Supersedes <i>ALK</i> Mutation as a Determining Factor of an Unfavorable Phenotype in Primary Neuroblastoma. <i>Clinical Cancer Research</i> , 2011, 17, 5082-5092.	3.2	95
64	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.	4.6	93
65	Recurrent CDKN1B (p27) mutations in hairy cell leukemia. <i>Blood</i> , 2015, 126, 1005-1008.	0.6	88
66	Genomic footprints of activated telomere maintenance mechanisms in cancer. <i>Nature Communications</i> , 2020, 11, 733.	5.8	87
67	Accurate Outcome Prediction in Neuroblastoma across Independent Data Sets Using a Multigene Signature. <i>Clinical Cancer Research</i> , 2010, 16, 1532-1541.	3.2	86
68	Genome-wide association study of pathological gambling. <i>European Psychiatry</i> , 2016, 36, 38-46.	0.1	82
69	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, 1904-1915.	3.2	80
70	Integrative DNA methylation and gene expression analysis in high-grade soft tissue sarcomas. <i>Genome Biology</i> , 2013, 14, r137.	13.9	78
71	Single-cell chromatin accessibility landscape identifies tissue repair program in human regulatory T cells. <i>Immunity</i> , 2021, 54, 702-720.e17.	6.6	78
72	Variant classification in precision oncology. <i>International Journal of Cancer</i> , 2019, 145, 2996-3010.	2.3	76

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73	The landscape of chromothripsis across adult cancer types. <i>Nature Communications</i> , 2020, 11, 2320.	5.8	75
74	Two genes of the putative mitochondrial fatty acid synthase in the genome of <i>Saccharomyces cerevisiae</i> . <i>Current Genetics</i> , 1997, 32, 384-388.	0.8	74
75	Coverage Bias and Sensitivity of Variant Calling for Four Whole-genome Sequencing Technologies. <i>PLoS ONE</i> , 2013, 8, e66621.	1.1	74
76	Molecular profiling of long-term survivors identifies a subgroup of glioblastoma characterized by chromosome 19/20 co-gain. <i>Acta Neuropathologica</i> , 2015, 130, 419-434.	3.9	74
77	Epigenetic dynamics of monocyte-to-macrophage differentiation. <i>Epigenetics and Chromatin</i> , 2016, 9, 33.	1.8	73
78	Identification of Two Tetranuclear FeS Clusters on the Ferredoxin-Type Subunit of NADH:Ubiquinone Oxidoreductase (Complex I). <i>Biochemistry</i> , 2001, 40, 6124-6131.	1.2	72
79	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, 1130-1142.	1.5	72
80	Argonaute—a database for gene regulation by mammalian microRNAs. <i>Nucleic Acids Research</i> , 2006, 34, D115-D118.	6.5	72
81	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.	3.3	70
82	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, 653-664.	1.3	68
83	Comparison of normalization methods for Illumina BeadChip HumanHT-12 v3. <i>BMC Genomics</i> , 2010, 11, 349.	1.2	68
84	Reduced Expression of CAMTA1 Correlates with Adverse Outcome in Neuroblastoma Patients. <i>Clinical Cancer Research</i> , 2006, 12, 131-138.	3.2	67
85	Hypermutation of the Inactive X Chromosome Is a Frequent Event in Cancer. <i>Cell</i> , 2013, 155, 567-581.	13.5	67
86	Distinct gene expression patterns associated with FLT3- and NRAS-activating mutations in acute myeloid leukemia with normal karyotype. <i>Oncogene</i> , 2005, 24, 1580-1588.	2.6	65
87	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.	7.7	65
88	Methylation profiling identifies two subclasses of squamous cell carcinoma related to distinct cells of origin. <i>Nature Communications</i> , 2018, 9, 577.	5.8	64
89	HiGHmed — An Open Platform Approach to Enhance Care and Research across Institutional Boundaries. <i>Methods of Information in Medicine</i> , 2018, 57, e66-e81.	0.7	64
90	Defective homologous recombination DNA repair as therapeutic target in advanced chordoma. <i>Nature Communications</i> , 2019, 10, 1635.	5.8	64

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91	Mitochondrial fatty acid synthesis: a relic of endosymbiotic origin and a specialized means for respiration. <i>FEBS Letters</i> , 1997, 407, 249-252.	1.3	62
92	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, 258-266.	0.9	62
93	Differential Expression of Neuronal Genes Defines Subtypes of Disseminated Neuroblastoma with Favorable and Unfavorable Outcome. <i>Clinical Cancer Research</i> , 2006, 12, 5118-5128.	3.2	60
94	Microarray data warehouse allowing for inclusion of experiment annotations in statistical analysis. <i>Bioinformatics</i> , 2002, 18, 423-433.	1.8	59
95	CCM2 Mediates Death Signaling by the TrkA Receptor Tyrosine Kinase. <i>Neuron</i> , 2009, 63, 585-591.	3.8	58
96	An integrated genome research network for studying the genetics of alcohol addiction. <i>Addiction Biology</i> , 2010, 15, 369-379.	1.4	57
97	Integration of genomics and histology revises diagnosis and enables effective therapy of refractory cancer of unknown primary with <i>PDL1</i> amplification. <i>Journal of Physical Education and Sports Management</i> , 2016, 2, a001180.	0.5	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. <i>Journal of Molecular Biology</i> , 1999, 292, 569-580.	2.0	56
99	BRAF inhibitor-associated ERK activation drives development of chronic lymphocytic leukemia. <i>Journal of Clinical Investigation</i> , 2014, 124, 5074-5084.	3.9	56
100	TelomereHunter – in silico estimation of telomere content and composition from cancer genomes. <i>BMC Bioinformatics</i> , 2019, 20, 272.	1.2	56
101	Intratumoral Cytokines and Tumor Cell Biology Determine Spontaneous Breast Cancer-Specific Immune Responses and Their Correlation to Prognosis. <i>Cancer Research</i> , 2009, 69, 8420-8428.	0.4	55
102	TMPRSS2-ERG Fusions Are Strongly Linked to Young Patient Age in Low-grade Prostate Cancer. <i>European Urology</i> , 2014, 66, 978-981.	0.9	54
103	Cooperation of BRAFF595L and mutant HRAS in histiocytic sarcoma provides new insights into oncogenic BRAF signaling. <i>Leukemia</i> , 2016, 30, 937-946.	3.3	52
104	The genomic and transcriptional landscape of primary central nervous system lymphoma. <i>Nature Communications</i> , 2022, 13, 2558.	5.8	52
105	High <i>Skp2</i> Expression Characterizes High-Risk Neuroblastomas Independent of <i>MYCN</i> Status. <i>Clinical Cancer Research</i> , 2007, 13, 4695-4703.	3.2	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. <i>Oncolmmunology</i> , 2017, 6, e1279777.	2.1	50
107	Recurrent Mutations within the Amino-Terminal Region of $\beta$ -Catenin Are Probable Key Molecular Driver Events in Sinonasal Hemangiopericytoma. <i>American Journal of Pathology</i> , 2015, 185, 563-571.	1.9	49
108	A Systems Biology Approach To Identify the Combination Effects of Human Herpesvirus 8 Genes on NF- $\kappa$ B Activation. <i>Journal of Virology</i> , 2009, 83, 2563-2574.	1.5	47



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109	Distinct molecular phenotype of malignant CD34+ hematopoietic stem and progenitor cells in chronic myelogenous leukemia. <i>Oncogene</i> , 2005, 24, 5313-5324.	2.6	46
110	Alternative lengthening of telomeres in childhood neuroblastoma from genome to proteome. <i>Nature Communications</i> , 2021, 12, 1269.	5.8	46
111	Suppression of Early Hematogenous Dissemination of Human Breast Cancer Cells to Bone Marrow by Retinoic Acid-Induced 2. <i>Cancer Discovery</i> , 2015, 5, 506-519.	7.7	45
112	Multi-Parametric Analysis and Modeling of Relationships between Mitochondrial Morphology and Apoptosis. <i>PLoS ONE</i> , 2012, 7, e28694.	1.1	44
113	Integrated Pathway-Based Approach Identifies Association between Genomic Regions at CTCF and CACNB2 and Schizophrenia. <i>PLoS Genetics</i> , 2014, 10, e1004345.	1.5	44
114	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.	1.1	44
115	Characterization of two novel redox groups in the respiratory NADH:ubiquinone oxidoreductase (complex I). <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2000, 1459, 305-309.	0.5	43
116	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.	1.7	43
117	Distinct human circulating NKp30 <sup>+</sup> FcγRII <sup>3</sup> CD8 <sup>+</sup> 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.	3.3	43
118	Redox components and structure of the respiratory NADH:ubiquinone oxidoreductase (complex I). <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 1998, 1365, 215-219.	0.5	41
119	MetaboDiff: an R package for differential metabolomic analysis. <i>Bioinformatics</i> , 2018, 34, 3417-3418.	1.8	41
120	Comparative transcriptome profiling of amyloid precursor protein family members in the adult cortex. <i>BMC Genomics</i> , 2011, 12, 160.	1.2	39
121	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, 3476-3487.	1.3	39
122	Linking aberrant chromatin features in chronic lymphocytic leukemia to transcription factor networks. <i>Molecular Systems Biology</i> , 2019, 15, e8339.	3.2	39
123	MicroRNA profiling of primary high-grade soft tissue sarcomas. <i>Genes Chromosomes and Cancer</i> , 2012, 51, 982-996.	1.5	38
124	Human Resting CD4+ T Cells Are Constitutively Inhibited by TGFβ <sup>2</sup> under Steady-State Conditions. <i>Journal of Immunology</i> , 2007, 178, 6931-6940.	0.4	37
125	Succession of transiently active tumor-initiating cell clones in human pancreatic cancer xenografts. <i>EMBO Molecular Medicine</i> , 2017, 9, 918-932.	3.3	36
126	From somatic variants towards precision oncology: Evidence-driven reporting of treatment options in molecular tumor boards. <i>Genome Medicine</i> , 2018, 10, 18.	3.6	36



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127	Response to olaparib in a <i>PALB2</i> germline mutated prostate cancer and genetic events associated with resistance. <i>Journal of Physical Education and Sports Management</i> , 2019, 5, a003657.	0.5	36
128	Homology Modelling and Molecular Docking Studies of Selected Substituted Lyase Receptor. <i>Bioinformatics and Biology Insights</i> , 2019, 13, 117793221986553.	1.0	35
129	Decreased contractility due to energy deprivation in a transgenic rat model of hypertrophic cardiomyopathy. <i>Journal of Molecular Medicine</i> , 2009, 87, 411-422.	1.7	34
130	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, 639-649.	1.5	34
131	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. <i>Leukemia</i> , 2021, 35, 2002-2016.	3.3	34
132	IGF1R upregulation confers resistance to isoform-specific inhibitors of PI3K in PIK3CA-driven ovarian cancer. <i>Cell Death and Disease</i> , 2018, 9, 944.	2.7	33
133	Revisiting the Road Map of Medullary Thymic Epithelial Cell Differentiation. <i>Journal of Immunology</i> , 2017, 199, 3488-3503.	0.4	32
134	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.	0.6	32
135	Assessment of modelling strategies for drug response prediction in cell lines and xenografts. <i>Scientific Reports</i> , 2020, 10, 2849.	1.6	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. <i>Translational Psychiatry</i> , 2014, 4, e426-e426.	2.4	30
137	Genetic subclone architecture of tumor clone-initiating cells in colorectal cancer. <i>Journal of Experimental Medicine</i> , 2017, 214, 2073-2088.	4.2	30
138	Mutant KIT as imatinib-sensitive target in metastatic sinonasal carcinoma. <i>Annals of Oncology</i> , 2017, 28, 142-148.	0.6	30
139	Pathways of urothelial cancer progression suggested by Bayesian network analysis of allelotyping data. <i>International Journal of Cancer</i> , 2004, 110, 850-856.	2.3	29
140	Cross-study analysis of gene expression data for intermediate neuroblastoma identifies two biological subtypes. <i>BMC Cancer</i> , 2007, 7, 89.	1.1	29
141	Identification of the Rage-dependent gene regulatory network in a mouse model of skin inflammation. <i>BMC Genomics</i> , 2010, 11, 537.	1.2	29
142	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, 423-435.	1.9	29
143	Targeting Fibroblast Growth Factor Receptor 1 for Treatment of Soft-Tissue Sarcoma. <i>Clinical Cancer Research</i> , 2017, 23, 962-973.	3.2	29
144	<i>RSPO2</i> gene rearrangement: a powerful driver of $\beta$ -catenin activation in liver tumours. <i>Gut</i> , 2019, 68, 1287-1296.	6.1	29

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145	Clinical Impact of Molecular Subtyping of Pancreatic Cancer. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 743908.	1.8	29
146	Translating Expression Profiling into a Clinically Feasible Test to Predict Neuroblastoma Outcome. <i>Clinical Cancer Research</i> , 2007, 13, 1459-1465.	3.2	28
147	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.	1.2	28
148	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.	2.2	28
149	Selective elimination of immunosuppressive T cells in patients with multiple myeloma. <i>Leukemia</i> , 2021, 35, 2602-2615.	3.3	27
150	Patient-derived xenografts of gastrointestinal cancers are susceptible to rapid and delayed B-lymphoproliferation. <i>International Journal of Cancer</i> , 2017, 140, 1356-1363.	2.3	26
151	Molecular Classification Substitutes for the Prognostic Variables Stage, Age, and MYCN Status in Neuroblastoma Risk Assessment. <i>Neoplasia</i> , 2017, 19, 982-990.	2.3	26
152	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.	0.2	25
153	Subclassification and Individual Survival Time Prediction from Gene Expression Data of Neuroblastoma Patients by Using CASPAR. <i>Clinical Cancer Research</i> , 2008, 14, 6590-6601.	3.2	23
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