

Benedikt Brors

List of Publications by Year in Descending Order

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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	The genomic and transcriptional landscape of primary central nervous system lymphoma.. <i>Nature Communications</i> , 2022 , 13, 2558	17.4	4
218	Clinical Impact of Molecular Subtyping of Pancreatic Cancer. <i>Frontiers in Cell and Developmental Biology</i> , 2021 , 9, 743908	5.7	4
217	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
216	CATCH: A Prospective Precision Oncology Trial in Metastatic Breast Cancer. <i>JCO Precision Oncology</i> , 2021 , 5,	3.6	5
215	Deconvolution of sarcoma methylomes reveals varying degrees of immune cell infiltrates with association to genomic aberrations. <i>Journal of Translational Medicine</i> , 2021 , 19, 204	8.5	1
214	Whole-exome sequencing in eccrine porocarcinoma indicates promising therapeutic strategies. <i>Cancer Gene Therapy</i> , 2021 ,	5.4	3
213	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. <i>Leukemia</i> , 2021 , 35, 2002-2016	10.7	3
212	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
211	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
210	Integrating proteomics into precision oncology. <i>International Journal of Cancer</i> , 2021 , 148, 1438-1451	7.5	5
209	Accurate and efficient detection of gene fusions from RNA sequencing data. <i>Genome Research</i> , 2021 , 31, 448-460	9.7	45
208	Characteristics and outcome of patients with acute myeloid leukaemia and t(8;16)(p11;p13): results from an International Collaborative Study. <i>British Journal of Haematology</i> , 2021 , 192, 832-842	4.5	4
207	Alternative lengthening of telomeres in childhood neuroblastoma from genome to proteome. <i>Nature Communications</i> , 2021 , 12, 1269	17.4	12
206	Selective elimination of immunosuppressive T cells in patients with multiple myeloma. <i>Leukemia</i> , 2021 , 35, 2602-2615	10.7	5
205	RosettaSX: Reliable gene expression signature scoring of cancer models and patients. <i>Neoplasia</i> , 2021 , 23, 1069-1077	6.4	0
204	Sarcoma classification by DNA methylation profiling. <i>Nature Communications</i> , 2021 , 12, 498	17.4	74
203	The landscape of chromothripsis across adult cancer types. <i>Nature Communications</i> , 2020 , 11, 2320	17.4	32

202	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
201	Germline SDHB-inactivating mutation in gastric spindle cell sarcoma. <i>Genes Chromosomes and Cancer</i> , 2020 , 59, 601-608	5	2
200	Comprehensive genomic characterization of gene therapy-induced T-cell acute lymphoblastic leukemia. <i>Leukemia</i> , 2020 , 34, 2785-2789	10.7	1
199	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
198	Assessment of modelling strategies for drug response prediction in cell lines and xenografts. <i>Scientific Reports</i> , 2020 , 10, 2849	4.9	8
197	Genomic footprints of activated telomere maintenance mechanisms in cancer. <i>Nature Communications</i> , 2020 , 11, 733	17.4	40
196	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. <i>Nature Genetics</i> , 2020 , 52, 331-341	36.3	168
195	Whole-genome fingerprint of the DNA methylome during chemically induced differentiation of the human AML cell line HL-60/S4. <i>Biology Open</i> , 2020 , 9,	2.2	1
194	Targetable ERBB2 mutations identified in neurofibroma/schwannoma hybrid nerve sheath tumors. <i>Journal of Clinical Investigation</i> , 2020 , 130, 2488-2495	15.9	8
193	Genome-Wide DNA Methylation Profiling in Early Stage I Lung Adenocarcinoma Reveals Predictive Aberrant Methylation in the Promoter Region of the Long Noncoding RNA PLUT: An Exploratory Study. <i>Journal of Thoracic Oncology</i> , 2020 , 15, 1338-1350	8.9	4
192	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
191	Identification of BCL-XL as highly active survival factor and promising therapeutic target in colorectal cancer. <i>Cell Death and Disease</i> , 2020 , 11, 875	9.8	9
190	Successful BRAF/MEK inhibition in a patient with -mutated extrapancreatic acinar cell carcinoma. <i>Journal of Physical Education and Sports Management</i> , 2020 , 6,	2.8	4
189	Distributed Ledger Technology in genomics: a call for Europe. <i>European Journal of Human Genetics</i> , 2020 , 28, 139-140	5.3	10
188	Identification and characterization of a BRAF fusion oncoprotein with retained autoinhibitory domains. <i>Oncogene</i> , 2020 , 39, 814-832	9.2	10
187	TelomereHunter - in silico estimation of telomere content and composition from cancer genomes. <i>BMC Bioinformatics</i> , 2019 , 20, 272	3.6	24
186	Linking aberrant chromatin features in chronic lymphocytic leukemia to transcription factor networks. <i>Molecular Systems Biology</i> , 2019 , 15, e8339	12.2	20
185	Impact of post-surgical freezing delay on brain tumor metabolomics. <i>Metabolomics</i> , 2019 , 15, 78	4.7	3

184	Variant classification in precision oncology. <i>International Journal of Cancer</i> , 2019 , 145, 2996-3010	7.5	28
183	MDM4 Is Targeted by 1q Gain and Drives Disease in Burkitt Lymphoma. <i>Cancer Research</i> , 2019 , 79, 3125-3138	3.8	8
182	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
181	Defective homologous recombination DNA repair as therapeutic target in advanced chordoma. <i>Nature Communications</i> , 2019 , 10, 1635	17.4	33
180	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. <i>Nature Communications</i> , 2019 , 10, 1459	17.4	49
179	Generation of Whole Genome Bisulfite Sequencing Libraries from Very Low DNA Input. <i>Methods in Molecular Biology</i> , 2019 , 1956, 229-248	1.4	0
178	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
177	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
176	gene rearrangement: a powerful driver of β -catenin activation in liver tumours. <i>Gut</i> , 2019 , 68, 1287-1296	19.2	15
175	Abstract 919: Clinical relevance of comprehensive genomic analysis in patients with advanced-stage neuroendocrine neoplasms: Results from the MASTER trial of the German Cancer Consortium 2019 ,		2
174	Glioblastoma evolution pattern under surgery and radio(chemo)therapy (RCHT) to identify novel methylome based glioma subtypes.. <i>Journal of Clinical Oncology</i> , 2019 , 37, 2012-2012	2.2	2
173	A Comprehensive Analysis of Single-Cell Chromatin Accessibility and Gene Expression Identifies Intra-Tumor Heterogeneity and Molecular Treatment Responses in Relapsed/Refractory Multiple Myeloma. <i>Blood</i> , 2019 , 134, 575-575	2.2	
172	No Evidence for Hematopoietic Stem Cell Self-Renewal in-Vivo Following Inflammatory Challenge. <i>Blood</i> , 2019 , 134, 456-456	2.2	
171	Dissecting Heterogeneity of Tumor Cells and Their Microenvironment in Refractory Multiple Myeloma. <i>Blood</i> , 2019 , 134, 571-571	2.2	
170	Biallelic Inactivation of Multiple Tumor Suppressors Is Associated with Early Relapse after Stem Cell Transplant in Newly Diagnosed Myeloma. <i>Blood</i> , 2019 , 134, 1783-1783	2.2	
169	Deconvolution of Hematopoietic Commitment Decisions By Genome-Wide Analysis of Progressive DNA Methylation Changes. <i>Blood</i> , 2019 , 134, 1179-1179	2.2	
168	Community-driven development of a modified progression-free survival ratio for precision oncology. <i>ESMO Open</i> , 2019 , 4, e000583	6	9
167	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

166	The landscape of genomic alterations across childhood cancers. <i>Nature</i> , 2018 , 555, 321-327	50.4	603
165	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
164	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
163	Integrative genomic and transcriptomic analysis of leiomyosarcoma. <i>Nature Communications</i> , 2018 , 9, 144	17.4	115
162	MetaboDiff: an R package for differential metabolomic analysis. <i>Bioinformatics</i> , 2018 , 34, 3417-3418	7.2	22
161	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
160	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
159	Drug-based perturbation screen uncovers synergistic drug combinations in Burkitt lymphoma. <i>Scientific Reports</i> , 2018 , 8, 12046	4.9	15
158	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
157	Towards a molecular algorithm predicting glioma treatment response and resistance: A biomarker analysis and path to real time profiling in N2M2.. <i>Journal of Clinical Oncology</i> , 2018 , 36, 12090-12090	2.2	
156	Recurrent Mutations in EGR2 Direct Specific Epigenetic Reconfiguration in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2018 , 132, 650-650	2.2	
155	Cooperative Effects of a Dnmt Inhibitor and All-Trans Retinoic Acid in an AML Cell Line Model Lacking PML-Rara. <i>Blood</i> , 2018 , 132, 1359-1359	2.2	
154	Validating Comprehensive Next-Generation Sequencing Results for Precision Oncology: The NCT/DKTK Molecularly Aided Stratification for Tumor Eradication Research Experience.. <i>JCO Precision Oncology</i> , 2018 , 2, 1-13	3.6	4
153	Integrative analysis of single-cell expression data reveals distinct regulatory states in bidirectional promoters. <i>Epigenetics and Chromatin</i> , 2018 , 11, 66	5.8	4
152	Whole genome sequencing puts forward hypotheses on metastasis evolution and therapy in colorectal cancer. <i>Nature Communications</i> , 2018 , 9, 4782	17.4	51
151	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
150	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
149	Fusions in Wild-Type Pancreatic Cancer. <i>Cancer Discovery</i> , 2018 , 8, 1087-1095	24.4	99

148	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>OncImmunity</i> , 2017 , 6, e1279777 ²	7.7	40
147	Genetic and epigenetic profiling of a solitary Peutz-Jeghers colon polyp. <i>Journal of Physical Education and Sports Management</i> , 2017 , 3, a001610	2.8	7
146	Precision oncology based on omics data: The NCT Heidelberg experience. <i>International Journal of Cancer</i> , 2017 , 141, 877-886	7.5	82
145	Succession of transiently active tumor-initiating cell clones in human pancreatic cancer xenografts. <i>EMBO Molecular Medicine</i> , 2017 , 9, 918-932	12	26
144	Genetic subclone architecture of tumor clone-initiating cells in colorectal cancer. <i>Journal of Experimental Medicine</i> , 2017 , 214, 2073-2088	16.6	23
143	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
142	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
141	Revisiting the Road Map of Medullary Thymic Epithelial Cell Differentiation. <i>Journal of Immunology</i> , 2017 , 199, 3488-3503	5.3	17
140	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , 2017 , 547, 311-317	50.4	472
139	Genome-wide DNA-methylation landscape defines specialization of regulatory T cells in tissues. <i>Nature Immunology</i> , 2017 , 18, 1160-1172	19.1	125
138	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
137	Targeting Fibroblast Growth Factor Receptor 1 for Treatment of Soft-Tissue Sarcoma. <i>Clinical Cancer Research</i> , 2017 , 23, 962-973	12.9	17
136	Mutant KIT as imatinib-sensitive target in metastatic sinonasal carcinoma. <i>Annals of Oncology</i> , 2017 , 28, 142-148	10.3	16
135	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
134	Genetic Contribution to Alcohol Dependence: Investigation of a Heterogeneous German Sample of Individuals with Alcohol Dependence, Chronic Alcoholic Pancreatitis, and Alcohol-Related Cirrhosis. <i>Genes</i> , 2017 , 8,	4.2	8
133	Epigenetic dynamics of monocyte-to-macrophage differentiation. <i>Epigenetics and Chromatin</i> , 2016 , 9, 33	5.8	54
132	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
131	Recurrent MET fusion genes represent a drug target in pediatric glioblastoma. <i>Nature Medicine</i> , 2016 , 22, 1314-1320	50.5	137

130	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016 , 167, 1145-1149	56.2	232
129	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
128	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
127	Genome-wide association study of pathological gambling. <i>European Psychiatry</i> , 2016 , 36, 38-46	6	68
126	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
125	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
124	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
123	Umbrella protocol for phase I/IIa trials of molecularly matched targeted therapies plus radiotherapy in patients with newly diagnosed glioblastoma without MGMT promoter methylation Neuro Master Match (NMM).. <i>Journal of Clinical Oncology</i> , 2016 , 34, TPS2084-TPS2084	2.2	4
122	Hematopoietic Stem Cells Fail to Regenerate In Vivo Following Inflammatory Stress. <i>Blood</i> , 2016 , 128, 1472-1472	2.2	
121	Epigenetic Drug Treatment Globally Induces Cryptic Transcription Start Sites Encoded in Long Terminal Repeats. <i>Blood</i> , 2016 , 128, 3931-3931	2.2	
120	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
119	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
118	Braf Mutations Initiate the Development of Rat Gliomas Induced by Postnatal Exposure to N-Ethyl-N-Nitrosourea. <i>American Journal of Pathology</i> , 2016 , 186, 2569-76	5.8	6
117	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
116	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
115	Recurrent CDKN1B (p27) mutations in hairy cell leukemia. <i>Blood</i> , 2015 , 126, 1005-8	2.2	66
114	XRCC5 as a risk gene for alcohol dependence: evidence from a genome-wide gene-set-based analysis and follow-up studies in <i>Drosophila</i> and humans. <i>Neuropsychopharmacology</i> , 2015 , 40, 361-71	8.7	12
113	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

112	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
111	Iroquois homeobox 2 suppresses cellular motility and chemokine expression in breast cancer cells. <i>BMC Cancer</i> , 2015 , 15, 896	4.8	8
110	In Silico Gene Regulatory Network of the Maurer's Cleft Pathway in Plasmodium falciparum. <i>Evolutionary Bioinformatics</i> , 2015 , 11, 231-8	1.9	2
109	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
108	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
107	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. <i>Nature Communications</i> , 2015 , 6, 10001	17.4	199
106	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. <i>Genome Biology</i> , 2015 , 16, 133	18.3	212
105	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
104	Progressive Epigenetic Programming during B Cell Maturation Is Reflected in a Continuum of Epigenetic Disease Phenotypes in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2015 , 126, 2436-2436	2.2	1
103	MYCN amplification confers enhanced folate dependence and methotrexate sensitivity in neuroblastoma. <i>Oncotarget</i> , 2015 , 6, 15510-23	3.3	11
102	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
101	Cooperative Activity of BRAF F595L and Mutant HRAS in Histiocytic Sarcoma Provides New Insights into Oncogenic BRAF Signaling. <i>Blood</i> , 2015 , 126, 1631-1631	2.2	
100	Genome sequencing of SHH medulloblastoma predicts genotype-related response to smoothed inhibition. <i>Cancer Cell</i> , 2014 , 25, 393-405	24.3	469
99	Cell competition is a tumour suppressor mechanism in the thymus. <i>Nature</i> , 2014 , 509, 465-70	50.4	156
98	Decoding the regulatory landscape of medulloblastoma using DNA methylation sequencing. <i>Nature</i> , 2014 , 510, 537-41	50.4	296
97	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	4.7	31
96	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
95	Intratumor DNA methylation heterogeneity reflects clonal evolution in aggressive prostate cancer. <i>Cell Reports</i> , 2014 , 8, 798-806	10.6	177

94	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
93	circlize Implements and enhances circular visualization in R. <i>Bioinformatics</i> , 2014 , 30, 2811-2	7.2	1242
92	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
91	Enhancer hijacking activates GF11 family oncogenes in medulloblastoma. <i>Nature</i> , 2014 , 511, 428-34	50.4	377
90	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
89	BRAF inhibitor-associated ERK activation drives development of chronic lymphocytic leukemia. <i>Journal of Clinical Investigation</i> , 2014 , 124, 5074-84	15.9	46
88	Initiation of an inflammatory response in resident intestinal lamina propria cells -use of a human organ culture model. <i>PLoS ONE</i> , 2014 , 9, e97780	3.7	6
87	Integrated pathway-based approach identifies association between genomic regions at CTCF and CACNB2 and schizophrenia. <i>PLoS Genetics</i> , 2014 , 10, e1004345	6	35
86	Genetic variants in apoptosis-related genes associated with colorectal hyperplasia. <i>Genes Chromosomes and Cancer</i> , 2014 , 53, 769-78	5	1
85	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
84	Recurrent somatic alterations of FGFR1 and NTRK2 in pilocytic astrocytoma. <i>Nature Genetics</i> , 2013 , 45, 927-32	36.3	550
83	Hypermutation of the inactive X chromosome is a frequent event in cancer. <i>Cell</i> , 2013 , 155, 567-81	56.2	50
82	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
81	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
80	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
79	Mining quasi-biclques 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
78	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
77	Integrative DNA methylation and gene expression analysis in high-grade soft tissue sarcomas. <i>Genome Biology</i> , 2013 , 14, r137	18.3	58

76	Decision-tree based model analysis for efficient identification of parameter relations leading to different signaling states. <i>PLoS ONE</i> , 2013 , 8, e82593	3.7	9
75	Coverage bias and sensitivity of variant calling for four whole-genome sequencing technologies. <i>PLoS ONE</i> , 2013 , 8, e66621	3.7	58
74	Automated universal BRAF state detection within the activation segment in skin metastases by pyrosequencing-based assay U-BRAF(V600). <i>PLoS ONE</i> , 2013 , 8, e59221	3.7	8
73	Multi-parametric analysis and modeling of relationships between mitochondrial morphology and apoptosis. <i>PLoS ONE</i> , 2012 , 7, e28694	3.7	39
72	Genome sequencing of pediatric medulloblastoma links catastrophic DNA rearrangements with TP53 mutations. <i>Cell</i> , 2012 , 148, 59-71	56.2	600
71	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
70	ICGC PedBrain - dissecting the genomic complexity underlying medulloblastoma using whole-genome sequencing. <i>BMC Proceedings</i> , 2012 , 6,	2.3	1
69	Dissecting the genomic complexity underlying medulloblastoma. <i>Nature</i> , 2012 , 488, 100-5	50.4	623
68	MicroRNA profiling of primary high-grade soft tissue sarcomas. <i>Genes Chromosomes and Cancer</i> , 2012 , 51, 982-96	5	30
67	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
66	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
65	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
64	Proteomic bronchiolitis obliterans syndrome risk monitoring in lung transplant recipients. <i>Transplantation</i> , 2011 , 92, 477-85	1.8	11
63	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
62	Comparative transcriptome profiling of amyloid precursor protein family members in the adult cortex. <i>BMC Genomics</i> , 2011 , 12, 160	4.5	33
61	Computational identification of signalling pathways in Plasmodium falciparum. <i>Infection, Genetics and Evolution</i> , 2011 , 11, 755-64	4.5	13
60	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
59	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

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