

Benedikt Brors

List of Publications by Year in descending order

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Version: 2024-02-01

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	Whole-exome sequencing in eccrine porocarcinoma indicates promising therapeutic strategies. <i>Cancer Gene Therapy</i> , 2022, 29, 697-708.	4.6	10
2	A scoping review of distributed ledger technology in genomics: thematic analysis and directions for future research. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2022, 29, 1433-1444.	4.4	6
3	The genomic and transcriptional landscape of primary central nervous system lymphoma. <i>Nature Communications</i> , 2022, 13, 2558.	12.8	52
4	Rare Germline Variants Are Associated with Rapid Biochemical Recurrence After Radical Prostate Cancer Treatment: A Pan Prostate Cancer Group Study. <i>European Urology</i> , 2022, 82, 201-211.	1.9	2
5	Gene expression-based prediction of pazopanib efficacy in sarcoma. <i>European Journal of Cancer</i> , 2022, 172, 107-118.	2.8	0
6	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.	9.4	65
7	Integrating proteomics into precision oncology. <i>International Journal of Cancer</i> , 2021, 148, 1438-1451.	5.1	15
8	Accurate and efficient detection of gene fusions from RNA sequencing data. <i>Genome Research</i> , 2021, 31, 448-460.	5.5	215
9	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.	2.5	15
10	Alternative lengthening of telomeres in childhood neuroblastoma from genome to proteome. <i>Nature Communications</i> , 2021, 12, 1269.	12.8	46
11	Selective elimination of immunosuppressive T cells in patients with multiple myeloma. <i>Leukemia</i> , 2021, 35, 2602-2615.	7.2	27
12	Single-cell chromatin accessibility landscape identifies tissue repair program in human regulatory TÀcells. <i>Immunity</i> , 2021, 54, 702-720.e17.	14.3	78
13	CATCH: A Prospective Precision Oncology Trial in Metastatic Breast Cancer. <i>JCO Precision Oncology</i> , 2021, 5, 676-686.	3.0	20
14	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.	4.4	5
15	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. <i>Leukemia</i> , 2021, 35, 2002-2016.	7.2	34
16	Comprehensive Genomic and Transcriptomic Analysis for Guiding Therapeutic Decisions in Patients with Rare Cancers. <i>Cancer Discovery</i> , 2021, 11, 2780-2795.	9.4	125
17	RosettaSX: Reliable gene expression signature scoring of cancer models and patients. <i>Neoplasia</i> , 2021, 23, 1069-1077.	5.3	3
18	Sarcoma classification by DNA methylation profiling. <i>Nature Communications</i> , 2021, 12, 498.	12.8	237

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19	Clinical Impact of Molecular Subtyping of Pancreatic Cancer. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 743908.	3.7	29
20	Distributed Ledger Technology in genomics: a call for Europe. <i>European Journal of Human Genetics</i> , 2020, 28, 139-140.	2.8	19
21	Identification and characterization of a BRAF fusion oncoprotein with retained autoinhibitory domains. <i>Oncogene</i> , 2020, 39, 814-832.	5.9	19
22	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.	14.3	140
23	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.	6.3	17
24	Successful BRAF/MEK inhibition in a patient with <i>BRAF</i> ^{V600E} -mutated extrapancreatic acinar cell carcinoma. <i>Journal of Physical Education and Sports Management</i> , 2020, 6, a005553.	1.2	13
25	The landscape of chromothripsis across adult cancer types. <i>Nature Communications</i> , 2020, 11, 2320.	12.8	75
26	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.	10.3	93
27	Germline <i>SDHB</i> inactivating mutation in gastric spindle cell sarcoma. <i>Genes Chromosomes and Cancer</i> , 2020, 59, 601-608.	2.8	4
28	Comprehensive genomic characterization of gene therapy-induced T-cell acute lymphoblastic leukemia. <i>Leukemia</i> , 2020, 34, 2785-2789.	7.2	4
29	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.	4.8	28
30	Assessment of modelling strategies for drug response prediction in cell lines and xenografts. <i>Scientific Reports</i> , 2020, 10, 2849.	3.3	31
31	Genomic footprints of activated telomere maintenance mechanisms in cancer. <i>Nature Communications</i> , 2020, 11, 733.	12.8	87
32	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. <i>Nature Genetics</i> , 2020, 52, 331-341.	21.4	431
33	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, .	1.2	3
34	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.	1.1	8
35	Targetable ERBB2 mutations identified in neurofibroma/schwannoma hybrid nerve sheath tumors. <i>Journal of Clinical Investigation</i> , 2020, 130, 2488-2495.	8.2	23
36	Abstract 821: Comprehensive genomic analysis of rare cancers: Results of the MASTER precision oncology trial of the German Cancer Consortium. , 2020, , .		0

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37	Abstract 820: Genomics based personalized oncology of cancer of unknown primary. , 2020, , .		0
38	Homology Modelling and Molecular Docking Studies of Selected Substituted Lyase Receptor. <i>Bioinformatics and Biology Insights</i> , 2019, 13, 117793221986553.	2.0	35
39	KIT-Dependent and KIT-Independent Genomic Heterogeneity of Resistance in Gastrointestinal Stromal Tumors â€” TORC1/2 Inhibition as Salvage Strategy. <i>Molecular Cancer Therapeutics</i> , 2019, 18, 1985-1996.	4.1	22
40	TelomereHunter â€” in silico estimation of telomere content and composition from cancer genomes. <i>BMC Bioinformatics</i> , 2019, 20, 272.	2.6	56
41	Linking aberrant chromatin features in chronic lymphocytic leukemia to transcription factor networks. <i>Molecular Systems Biology</i> , 2019, 15, e8339.	7.2	39
42	Impact of post-surgical freezing delay on brain tumor metabolomics. <i>Metabolomics</i> , 2019, 15, 78.	3.0	9
43	Variant classification in precision oncology. <i>International Journal of Cancer</i> , 2019, 145, 2996-3010.	5.1	76
44	MDM4 Is Targeted by 1q Gain and Drives Disease in Burkitt Lymphoma. <i>Cancer Research</i> , 2019, 79, 3125-3138.	0.9	19
45	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.	1.2	36
46	Defective homologous recombination DNA repair as therapeutic target in advanced chordoma. <i>Nature Communications</i> , 2019, 10, 1635.	12.8	64
47	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. <i>Nature Communications</i> , 2019, 10, 1459.	12.8	99
48	Generation of Whole Genome Bisulfite Sequencing Libraries from Very Low DNA Input. <i>Methods in Molecular Biology</i> , 2019, 1956, 229-248.	0.9	1
49	Community-driven development of a modified progression-free survival ratio for precision oncology. <i>ESMO Open</i> , 2019, 4, e000583.	4.5	22
50	The mutational landscape underlying carfilzomib and pomalidomide resistance in relapsed /refractory multiple myeloma. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2019, 19, e83-e84.	0.4	0
51	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.	1.2	100
52	<i>RSPO2</i> gene rearrangement: a powerful driver of β -catenin activation in liver tumours. <i>Gut</i> , 2019, 68, 1287-1296.	12.1	29
53	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. <i>Cancer Research</i> , 2019, 79, 919-919.	0.9	2
54	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.	1.6	3

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55	Abstract 1686: Comprehensive genomic and transcriptomic profiling of gastrointestinal stromal tumors. , 2019, , .		0
56	Abstract 468: Clinical relevance of comprehensive genomic analysis in advanced-stage cancers and rare malignancies: Results from the MASTER trial of the German Cancer Consortium. , 2019, , .		0
57	Abstract 2723: Defective homologous recombination DNA repair as therapeutic target in advanced chordoma. , 2019, , .		0
58	A Comprehensive Analysis of Single-Cell Chromatin Accessibility and Gene Expression Identifies Intra-Tumor Heterogeneity and Molecular Treatment Responses in Relapsed/Refractory Multiple Myeloma. Blood, 2019, 134, 575-575.	1.4	0
59	No Evidence for Hematopoietic Stem Cell Self-Renewal in-Vivo Following Inflammatory Challenge. Blood, 2019, 134, 456-456.	1.4	1
60	Dissecting Heterogeneity of Tumor Cells and Their Microenvironment in Refractory Multiple Myeloma. Blood, 2019, 134, 571-571.	1.4	0
61	Biallelic Inactivation of Multiple Tumor Suppressors Is Associated with Early Relapse after Stem Cell Transplant in Newly Diagnosed Myeloma. Blood, 2019, 134, 1783-1783.	1.4	3
62	Deconvolution of Hematopoietic Commitment Decisions By Genome-Wide Analysis of Progressive DNA Methylation Changes. Blood, 2019, 134, 1179-1179.	1.4	0
63	Abstract LB-B08: Identification and characterization of an unusual BRAF fusion oncoprotein with retained autoinhibitory domains. , 2019, , .		0
64	The landscape of genomic alterations across childhood cancers. Nature, 2018, 555, 321-327.	27.8	1,068
65	Methylation profiling identifies two subclasses of squamous cell carcinoma related to distinct cells of origin. Nature Communications, 2018, 9, 577.	12.8	64
66	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
67	Integrative genomic and transcriptomic analysis of leiomyosarcoma. Nature Communications, 2018, 9, 144.	12.8	197
68	MetaboDiff: an R package for differential metabolomic analysis. Bioinformatics, 2018, 34, 3417-3418.	4.1	41
69	From somatic variants towards precision oncology: Evidence-driven reporting of treatment options in molecular tumor boards. Genome Medicine, 2018, 10, 18.	8.2	36
70	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
71	Integrative analysis of single-cell expression data reveals distinct regulatory states in bidirectional promoters. Epigenetics and Chromatin, 2018, 11, 66.	3.9	6
72	Whole genome sequencing puts forward hypotheses on metastasis evolution and therapy in colorectal cancer. Nature Communications, 2018, 9, 4782.	12.8	103

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73	Molecular Evolution of Early-Onset Prostate Cancer Identifies Molecular Risk Markers and Clinical Trajectories. <i>Cancer Cell</i> , 2018, 34, 996-1011.e8.	16.8	190
74	IGF1R upregulation confers resistance to isoform-specific inhibitors of PI3K in PIK3CA-driven ovarian cancer. <i>Cell Death and Disease</i> , 2018, 9, 944.	6.3	33
75	<i>NRG1</i> Fusions in <i>KRAS</i> Wild-Type Pancreatic Cancer. <i>Cancer Discovery</i> , 2018, 8, 1087-1095.	9.4	189
76	HiGHmed – An Open Platform Approach to Enhance Care and Research across Institutional Boundaries. <i>Methods of Information in Medicine</i> , 2018, 57, e66-e81.	1.2	64
77	Drug-based perturbation screen uncovers synergistic drug combinations in Burkitt lymphoma. <i>Scientific Reports</i> , 2018, 8, 12046.	3.3	22
78	Distinct human circulating NKp30 ⁺ FcγRII ³ 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.	7.1	43
79	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.	1.6	0
80	Recurrent Mutations in <i>EGR2</i> Direct Specific Epigenetic Reconfiguration in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2018, 132, 650-650.	1.4	0
81	Cooperative Effects of a <i>Dnmt</i> Inhibitor and All-Trans Retinoic Acid in an AML Cell Line Model Lacking <i>PML-Rara</i> . <i>Blood</i> , 2018, 132, 1359-1359.	1.4	0
82	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.	4.6	50
83	Genetic and epigenetic profiling of a solitary Peutz-Jeghers colon polyp. <i>Journal of Physical Education and Sports Management</i> , 2017, 3, a001610.	1.2	10
84	Precision oncology based on omics data: The NCT Heidelberg experience. <i>International Journal of Cancer</i> , 2017, 141, 877-886.	5.1	133
85	Succession of transiently active tumor-initiating cell clones in human pancreatic cancer xenografts. <i>EMBO Molecular Medicine</i> , 2017, 9, 918-932.	6.9	36
86	Genetic subclone architecture of tumor clone-initiating cells in colorectal cancer. <i>Journal of Experimental Medicine</i> , 2017, 214, 2073-2088.	8.5	30
87	DNMT and HDAC inhibitors induce cryptic transcription start sites encoded in long terminal repeats. <i>Nature Genetics</i> , 2017, 49, 1052-1060.	21.4	235
88	Patient-derived xenografts of gastrointestinal cancers are susceptible to rapid and delayed B-lymphoproliferation. <i>International Journal of Cancer</i> , 2017, 140, 1356-1363.	5.1	26
89	Revisiting the Road Map of Medullary Thymic Epithelial Cell Differentiation. <i>Journal of Immunology</i> , 2017, 199, 3488-3503.	0.8	32
90	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , 2017, 547, 311-317.	27.8	787

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91	Genome-wide DNA-methylation landscape defines specialization of regulatory T cells in tissues. <i>Nature Immunology</i> , 2017, 18, 1160-1172.	14.5	193
92	Molecular Classification Substitutes for the Prognostic Variables Stage, Age, and MYCN Status in Neuroblastoma Risk Assessment. <i>Neoplasia</i> , 2017, 19, 982-990.	5.3	26
93	Targeting Fibroblast Growth Factor Receptor 1 for Treatment of Soft-Tissue Sarcoma. <i>Clinical Cancer Research</i> , 2017, 23, 962-973.	7.0	29
94	Mutant KIT as imatinib-sensitive target in metastatic sinonasal carcinoma. <i>Annals of Oncology</i> , 2017, 28, 142-148.	1.2	30
95	Combining transcription factor binding affinities with open-chromatin data for accurate gene expression prediction. <i>Nucleic Acids Research</i> , 2017, 45, 54-66.	14.5	112
96	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, 183.	2.4	11
97	Abstract 4807: Braf mutations initiate the development of rat gliomas induced by postnatal exposure to N-ethyl-N-nitrosourea (ENU). , 2017, , .		0
98	Abstract LB-287: Identification of patients at risk for tumor predisposition syndromes based on the evaluation of sporadic cancer exome sequencing data: experiences from the NCT/DKTK MASTER program. , 2017, , .		0
99	Abstract 1023: Activation of proto-oncogenes by enhancer-hijacking in high-risk neuroblastoma. , 2017, , .		0
100	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.	3.5	43
101	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.	2.8	28
102	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, 2569-2576.	3.8	7
103	Next-generation personalised medicine for high-risk paediatric cancer patients – The INFORM pilot study. <i>European Journal of Cancer</i> , 2016, 65, 91-101.	2.8	262
104	Epigenetic dynamics of monocyte-to-macrophage differentiation. <i>Epigenetics and Chromatin</i> , 2016, 9, 33.	3.9	73
105	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.	14.3	174
106	Recurrent MET fusion genes represent a drug target in pediatric glioblastoma. <i>Nature Medicine</i> , 2016, 22, 1314-1320.	30.7	183
107	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149.	28.9	404
108	MYC/MIZ1-dependent gene repression inversely coordinates the circadian clock with cell cycle and proliferation. <i>Nature Communications</i> , 2016, 7, 11807.	12.8	103

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109	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.	1.2	57
110	Genome-wide association study of pathological gambling. <i>European Psychiatry</i> , 2016, 36, 38-46.	0.2	82
111	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.	21.4	254
112	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.	6.5	19
113	Cooperation of BRAFF595L and mutant HRAS in histiocytic sarcoma provides new insights into oncogenic BRAF signaling. <i>Leukemia</i> , 2016, 30, 937-946.	7.2	52
114	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 (N ² M ²).. <i>Journal of Clinical Oncology</i> , 2016, 34, TPS2084-TPS2084.	1.6	4
115	Abstract LB-287: Combining immunomics and genomics for immunotherapy of refractory and rare cancers. , 2016, , .		0
116	Abstract 910: Genetic subclone heterogeneity of the human colon cancer initiating cell compartment. , 2016, , .		0
117	Hematopoietic Stem Cells Fail to Regenerate In Vivo Following Inflammatory Stress. <i>Blood</i> , 2016, 128, 1472-1472.	1.4	0
118	Epigenetic Drug Treatment Globally Induces Cryptic Transcription Start Sites Encoded in Long Terminal Repeats. <i>Blood</i> , 2016, 128, 3931-3931.	1.4	0
119	Iroquois homeobox 2 suppresses cellular motility and chemokine expression in breast cancer cells. <i>BMC Cancer</i> , 2015, 15, 896.	2.6	18
120	In Silico Gene Regulatory Network of the Maurer's Cleft Pathway in Plasmodium falciparum. <i>Evolutionary Bioinformatics</i> , 2015, 11, EBO.S25585.	1.2	2
121	Thymic B Cells Are Licensed to Present Self Antigens for Central T Cell Tolerance Induction. <i>Immunity</i> , 2015, 42, 1048-1061.	14.3	201
122	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.	7.7	74
123	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. <i>Nature Communications</i> , 2015, 6, 10001.	12.8	266
124	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. <i>Genome Biology</i> , 2015, 16, 133.	8.8	325
125	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, 563-571.	3.8	49
126	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.	9.4	45

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127	Recurrent CDKN1B (p27) mutations in hairy cell leukemia. <i>Blood</i> , 2015, 126, 1005-1008.	1.4	88
128	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, 361-371.	5.4	12
129	BAZ2A (TIP5) is involved in epigenetic alterations in prostate cancer and its overexpression predicts disease recurrence. <i>Nature Genetics</i> , 2015, 47, 22-30.	21.4	141
130	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.	7.0	80
131	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.	1.4	1
132	<i>MYCN</i> amplification confers enhanced folate dependence and methotrexate sensitivity in neuroblastoma. <i>Oncotarget</i> , 2015, 6, 15510-15523.	1.8	13
133	FGFR2 is overexpressed in myxoid liposarcoma and inhibition of FGFR signaling impairs tumor growth <i>in vitro</i> . <i>Oncotarget</i> , 2015, 6, 20215-20230.	1.8	23
134	Abstract 1417: Clonal succession in pancreatic cancer progression is not driven by genetic instability. , 2015, , .		0
135	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.	1.4	2
136	BRAF inhibitor-associated ERK activation drives development of chronic lymphocytic leukemia. <i>Journal of Clinical Investigation</i> , 2014, 124, 5074-5084.	8.2	56
137	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.	2.5	9
138	Integrated Pathway-Based Approach Identifies Association between Genomic Regions at CTCF and CACNB2 and Schizophrenia. <i>PLoS Genetics</i> , 2014, 10, e1004345.	3.5	44
139	Genetic variants in apoptosis-related genes associated with colorectal hyperplasia. <i>Genes Chromosomes and Cancer</i> , 2014, 53, 769-778.	2.8	2
140	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.	2.8	34
141	Genome Sequencing of SHH Medulloblastoma Predicts Genotype-Related Response to Smoothed Inhibition. <i>Cancer Cell</i> , 2014, 25, 393-405.	16.8	627
142	Cell competition is a tumour suppressor mechanism in the thymus. <i>Nature</i> , 2014, 509, 465-470.	27.8	209
143	Decoding the regulatory landscape of medulloblastoma using DNA methylation sequencing. <i>Nature</i> , 2014, 510, 537-541.	27.8	378
144	Identification of DNA methylation changes at <i>cis</i> -regulatory elements during early steps of HSC differentiation using tagmentation-based whole genome bisulfite sequencing. <i>Cell Cycle</i> , 2014, 13, 3476-3487.	2.6	39

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145	TMPRSS2-ERG Fusions Are Strongly Linked to Young Patient Age in Low-grade Prostate Cancer. <i>European Urology</i> , 2014, 66, 978-981.	1.9	54
146	Whole-genome bisulfite sequencing of HSCs and their immediate progeny identifies novel regulatory elements involved in self-renewal and early hematopoietic commitment. <i>Experimental Hematology</i> , 2014, 42, S20.	0.4	0
147	Intratumor DNA Methylation Heterogeneity Reflects Clonal Evolution in Aggressive Prostate Cancer. <i>Cell Reports</i> , 2014, 8, 798-806.	6.4	219
148	Identification of Regulatory Networks in HSCs and Their Immediate Progeny via Integrated Proteome, Transcriptome, and DNA Methylation Analysis. <i>Cell Stem Cell</i> , 2014, 15, 507-522.	11.1	439
149	<i>circize</i> implements and enhances circular visualization in R. <i>Bioinformatics</i> , 2014, 30, 2811-2812.	4.1	2,736
150	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.	4.8	30
151	Enhancer hijacking activates GF1 family oncogenes in medulloblastoma. <i>Nature</i> , 2014, 511, 428-434.	27.8	520
152	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.	3.8	198
153	Recurrent somatic alterations of FGFR1 and NTRK2 in pilocytic astrocytoma. <i>Nature Genetics</i> , 2013, 45, 927-932.	21.4	674
154	Hypermutation of the Inactive X Chromosome Is a Frequent Event in Cancer. <i>Cell</i> , 2013, 155, 567-581.	28.9	67
155	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.	0.4	25
156	Integrative Genomic Analyses Reveal an Androgen-Driven Somatic Alteration Landscape in Early-Onset Prostate Cancer. <i>Cancer Cell</i> , 2013, 23, 159-170.	16.8	292
157	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.	6.3	184
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