List of Publications by Year in descending order

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159 papers	68,599 citations	4388 86 h-index	6996 154 g-index
173 all docs	173 docs citations	173 times ranked	50352 citing authors

#	Article	IF	Citations
1	A technique for radiolabeling DNA restriction endonuclease fragments to high specific activity. Analytical Biochemistry, 1983, 132, 6-13.	2.4	24,572
2	Minfi: a flexible and comprehensive Bioconductor package for the analysis of Infinium DNA methylation microarrays. Bioinformatics, 2014, 30, 1363-1369.	4.1	3,192
3	Hypomethylation distinguishes genes of some human cancers from their normal counterparts. Nature, 1983, 301, 89-92.	27.8	2,175
4	The history of cancer epigenetics. Nature Reviews Cancer, 2004, 4, 143-153.	28.4	2,061
5	The human colon cancer methylome shows similar hypo- and hypermethylation at conserved tissue-specific CpG island shores. Nature Genetics, 2009, 41, 178-186.	21.4	1,977
6	The epigenetic progenitor origin of human cancer. Nature Reviews Genetics, 2006, 7, 21-33.	16.3	1,642
7	Phenotypic plasticity and the epigenetics of human disease. Nature, 2007, 447, 433-440.	27.8	1,475
8	DNMT1 and DNMT3b cooperate to silence genes in human cancer cells. Nature, 2002, 416, 552-556.	27.8	1,126
9	Differential methylation of tissue- and cancer-specific CpG island shores distinguishes human induced pluripotent stem cells, embryonic stem cells and fibroblasts. Nature Genetics, 2009, 41, 1350-1353.	21.4	1,076
10	Increased methylation variation in epigenetic domains across cancer types. Nature Genetics, 2011, 43, 768-775.	21.4	968
11	DNA methylation age of blood predicts all-cause mortality in later life. Genome Biology, 2015, 16, 25.	8.8	928
12	Association of In Vitro Fertilization with Beckwith-Wiedemann Syndrome and Epigenetic Alterations of LIT1 and H19. American Journal of Human Genetics, 2003, 72, 156-160.	6.2	875
13	Epigenome-wide association data implicate DNA methylation as an intermediary of genetic risk in rheumatoid arthritis. Nature Biotechnology, 2013, 31, 142-147.	17.5	874
14	DNA methylation-based measures of biological age: meta-analysis predicting time to death. Aging, 2016, 8, 1844-1865.	3.1	786
15	Relaxation of imprinted genes in human cancer. Nature, 1993, 362, 747-749.	27.8	780
16	Epigenetic silencing of tumour suppressor gene p15 by its antisense RNA. Nature, 2008, 451, 202-206.	27.8	777
17	DNA Methylation in Newborns and Maternal Smoking in Pregnancy: Genome-wide Consortium Meta-analysis. American Journal of Human Genetics, 2016, 98, 680-696.	6.2	717
18	Loss of IGF2 Imprinting: A Potential Marker of Colorectal Cancer Risk. Science, 2003, 299, 1753-1755.	12.6	704

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19	Epigenetic modulators, modifiers and mediators in cancer aetiology and progression. Nature Reviews Genetics, 2016, 17, 284-299.	16.3	679
20	Intra-individual Change Over Time in DNA Methylation With Familial Clustering. JAMA - Journal of the American Medical Association, 2008, 299, 2877.	7.4	602
21	The NASA Twins Study: A multidimensional analysis of a year-long human spaceflight. Science, 2019, 364, .	12.6	576
22	Bump hunting to identify differentially methylated regions in epigenetic epidemiology studies. International Journal of Epidemiology, 2012, 41, 200-209.	1.9	567
23	Comprehensive methylome map of lineage commitment from haematopoietic progenitors. Nature, 2010, 467, 338-342.	27.8	554
24	Donor cell type can influence the epigenome and differentiation potential of human induced pluripotent stem cells. Nature Biotechnology, 2011, 29, 1117-1119.	17.5	547
25	Large histone H3 lysine 9 dimethylated chromatin blocks distinguish differentiated from embryonic stem cells. Nature Genetics, 2009, 41, 246-250.	21.4	540
26	Cancer as a dysregulated epigenome allowing cellular growth advantage at the expense of the host. Nature Reviews Cancer, 2013, 13, 497-510.	28.4	490
27	Stochastic epigenetic variation as a driving force of development, evolutionary adaptation, and disease. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 1757-1764.	7.1	477
28	Hypomethylation of ras oncogenes in primary human cancers. Biochemical and Biophysical Research Communications, 1983, 111, 47-54.	2.1	470
29	Fusion of the nucleoporin gene NUP98 to HOXA9 by the chromosome translocation t(7;11)(p15;p15) in human myeloid leukaemia. Nature Genetics, 1996, 12, 154-158.	21.4	459
30	Loss of imprinting of IGF2 is linked to reduced expression and abnormal methylation of H19 in Wilms' tumour. Nature Genetics, 1994, 7, 433-439.	21.4	454
31	Somatic deletion and duplication of genes on chromosome 11 in Wilms' tumours. Nature, 1984, 309, 176-178.	27.8	426
32	A comparison of non-integrating reprogramming methods. Nature Biotechnology, 2015, 33, 58-63.	17.5	424
33	The Key Role of Epigenetics in Human Disease Prevention and Mitigation. New England Journal of Medicine, 2018, 378, 1323-1334.	27.0	419
34	An integrated epigenetic and genetic approach to common human disease. Trends in Genetics, 2004, 20, 350-358.	6.7	408
35	Comprehensive high-throughput arrays for relative methylation (CHARM). Genome Research, 2008, 18, 780-790.	5.5	379
36	Epigenomic reprogramming during pancreatic cancer progression links anabolic glucose metabolism to distant metastasis. Nature Genetics, 2017, 49, 367-376.	21.4	365

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37	Human KVLQT1 gene shows tissue-specific imprinting and encompasses Beckwith-Wiedemann syndrome chromosomal rearrangements. Nature Genetics, 1997, 15, 181-185.	21.4	354
38	Genome-scale epigenetic reprogramming during epithelial-to-mesenchymal transition. Nature Structural and Molecular Biology, 2011, 18, 867-874.	8.2	340
39	Loss of genes on the short arm of chromosome 11 in bladder cancer. Nature, 1985, 318, 377-380.	27.8	334
40	Epigenetics at the Epicenter of Modern Medicine. JAMA - Journal of the American Medical Association, 2008, 299, 1345.	7.4	331
41	An X Chromosome Gene, WTX , Is Commonly Inactivated in Wilms Tumor. Science, 2007, 315, 642-645.	12.6	321
42	BORIS, a novel male germ-line-specific protein associated with epigenetic reprogramming events, shares the same 11-zinc-finger domain with CTCF, the insulator protein involved in reading imprinting marks in the soma. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 6806-6811.	7.1	319
43	Loss of Imprinting of Igf2 Alters Intestinal Maturation and Tumorigenesis in Mice. Science, 2005, 307, 1976-1978.	12.6	312
44	Epigenetics and Assisted Reproductive Technology: A Call for Investigation. American Journal of Human Genetics, 2004, 74, 599-609.	6.2	311
45	Reversible switching between epigenetic states in honeybee behavioral subcastes. Nature Neuroscience, 2012, 15, 1371-1373.	14.8	305
46	Loss of imprinting in colorectal cancer linked to hypomethylation of H19 and IGF2. Cancer Research, 2002, 62, 6442-6.	0.9	305
47	The epigenetics of cancer etiology. Seminars in Cancer Biology, 2004, 14, 427-432.	9.6	300
48	Personalized Epigenomic Signatures That Are Stable Over Time and Covary with Body Mass Index. Science Translational Medicine, 2010, 2, 49ra67.	12.4	292
49	The emerging science of epigenomics. Human Molecular Genetics, 2006, 15, R95-R101.	2.9	283
50	Loss of imprinting in normal tissue of colorectal cancer patients with microsatellite instability. Nature Medicine, 1998, 4, 1276-1280.	30.7	279
51	Targeted disruption of the Kvlqt1 gene causes deafness and gastric hyperplasia in mice. Journal of Clinical Investigation, 2000, 106, 1447-1455.	8.2	269
52	Epigenetic Alterations of H19 and LIT1 Distinguish Patients with Beckwith-Wiedemann Syndrome with Cancer and Birth Defects. American Journal of Human Genetics, 2002, 70, 604-611.	6.2	267
53	DNA Methylation Signatures within the Human Brain. American Journal of Human Genetics, 2007, 81, 1304-1315.	6.2	256
54	DNA methylation of cord blood cell types: Applications for mixed cell birth studies. Epigenetics, 2016, 11, 354-362.	2.7	256

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55	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. Genome Biology, 2016, 17, 255.	8.8	251
56	Regulated Noise in the Epigenetic Landscape of Development and Disease. Cell, 2012, 148, 1123-1131.	28.9	220
57	Association between Beckwith-Wiedemann syndrome and assisted reproductive technology: A case series of 19 patients. Fertility and Sterility, 2005, 83, 349-354.	1.0	214
58	Microallelotyping defines the sequence and tempo of alleiic losses at tumour suppressor gene loci during colorectal cancer progression. Nature Medicine, 1995, 1, 902-909.	30.7	201
59	DNA methylation and genomic imprinting: insights from cancer into epigenetic mechanisms. Seminars in Cancer Biology, 2002, 12, 389-398.	9.6	196
60	Genomic imprinting and gene activation in cancer. Nature Genetics, 1993, 4, 110-113.	21.4	182
61	Distinct effects on gene expression of chemical and genetic manipulation of the cancer epigenome revealed by a multimodality approach. Cancer Cell, 2004, 6, 361-371.	16.8	172
62	Large hypomethylated blocks as a universal defining epigenetic alteration in human solid tumors. Genome Medicine, 2014, 6, 61.	8.2	170
63	A Genome-Wide Screen for Normally Methylated Human CpG Islands That Can Identify Novel Imprinted Genes. Genome Research, 2002, 12, 543-554.	5.5	158
64	Redefining CpG islands using hidden Markov models. Biostatistics, 2010, 11, 499-514.	1.5	151
65	Association of DNA Methylation Differences With Schizophrenia in an Epigenome-Wide Association Study. JAMA Psychiatry, 2016, 73, 506.	11.0	151
66	Blood Leukocyte DNA Methylation Predicts Risk of Future Myocardial Infarction and Coronary Heart Disease. Circulation, 2019, 140, 645-657.	1.6	151
67	Low Frequency of p57KIP2 Mutation in Beckwith-Wiedemann Syndrome. American Journal of Human Genetics, 1997, 61, 304-309.	6.2	148
68	DNA methylation as a mediator of HLA-DRB1*15:01 and a protective variant in multiple sclerosis. Nature Communications, 2018, 9, 2397.	12.8	147
69	Tumor-associated zinc finger mutations in the CTCF transcription factor selectively alter tts DNA-binding specificity. Cancer Research, 2002, 62, 48-52.	0.9	141
70	Meta-analysis of epigenome-wide association studies in neonates reveals widespread differential DNA methylation associated with birthweight. Nature Communications, 2019, 10, 1893.	12.8	140
71	Large-scale hypomethylated blocks associated with Epstein-Barr virusâ€“induced B-cell immortalization. Genome Research, 2014, 24, 177-184.	5.5	130
72	Microdeletion of LIT1 in Familial Beckwith-Wiedemann Syndrome. American Journal of Human Genetics, 2004, 75, 844-849.	6.2	126

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73	Paternal sperm DNA methylation associated with early signs of autism risk in an autism-enriched cohort. International Journal of Epidemiology, 2015, 44, 1199-1210.	1.9	121
74	An LSC epigenetic signature is largely mutation independent and implicates the HOXA cluster in AML pathogenesis. Nature Communications, 2015, 6, 8489.	12.8	121
75	Neuronal brain-region-specific DNA methylation and chromatin accessibility are associated with neuropsychiatric trait heritability. Nature Neuroscience, 2019, 22, 307-316.	14.8	120
76	Genome-Wide DNA Methylation Scan in Major Depressive Disorder. PLoS ONE, 2012, 7, e34451.	2.5	120
77	Loss of imprinting of insulin growth factor II gene: a potential heritable biomarker for colon neoplasia predispositionâ˜†. Gastroenterology, 2004, 126, 964-970.	1.3	119
78	Loss of Imprinting of IGF2: A Common Epigenetic Modifier of Intestinal Tumor Risk. Cancer Research, 2005, 65, 11236-11240.	0.9	119
79	Genome-scale approaches to the epigenetics of common human disease. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2010, 456, 13-21.	2.8	116
80	Potential energy landscapes identify the information-theoretic nature of the epigenome. Nature Genetics, 2017, 49, 719-729.	21.4	114
81	Age and sun exposure-related widespread genomic blocks of hypomethylation in nonmalignant skin. Genome Biology, 2015, 16, 80.	8.8	111
82	Hot-stop PCR: a simple and general assay for linear quantitation of allele ratios. Nature Genetics, 2000, 25, 375-376.	21.4	106
83	Epigenomics reveals a functional genome anatomy and a new approach to common disease. Nature Biotechnology, 2010, 28, 1049-1052.	17.5	99
84	Mouse-Human Experimental Epigenetic Analysis Unmasks Dietary Targets and Genetic Liability for Diabetic Phenotypes. Cell Metabolism, 2015, 21, 138-149.	16.2	98
85	Enhanced sensitivity to IGF-II signaling links loss of imprinting ofIGF2to increased cell proliferation and tumor risk. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 20926-20931.	7.1	97
86	Epigenetic Specificity of Loss of Imprinting of the IGF2 Gene in Wilms Tumors. Journal of the National Cancer Institute, 2007, 99, 1270-1273.	6.3	97
87	Presence of an epigenetic signature of prenatal cigarette smoke exposure in childhood. Environmental Research, 2016, 144, 139-148.	7.5	96
88	GeMes, Clusters of DNA Methylation under Genetic Control, Can Inform Genetic and Epigenetic Analysis of Disease. American Journal of Human Genetics, 2014, 94, 485-495.	6.2	93
89	Significance analysis and statistical dissection of variably methylated regions. Biostatistics, 2012, 13, 166-178.	1.5	92
90	Measuring cell-type specific differential methylation in human brain tissue. Genome Biology, 2013, 14, R94.	9.6	92

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91	Genomic Imprinting and Cancer. , 2001, , 358-362.		87
92	A nucleolar protein, H19 opposite tumor suppressor (HOTS), is a tumor growth inhibitor encoded by a human imprinted H19 antisense transcript. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 16759-16764.	7.1	86
93	A 2.5-Mb Transcript Map of a Tumor-Suppressing Subchromosomal Transferable Fragment from 11p15.5, and Isolation and Sequence Analysis of Three Novel Genes. Genomics, 1997, 46, 9-17.	2.9	84
94	BAT3 and SET1A Form a Complex with CTCFL/BORIS To Modulate H3K4 Histone Dimethylation and Gene Expression. Molecular and Cellular Biology, 2008, 28, 6720-6729.	2.3	84
95	Higher order chromatin organization in cancer. Seminars in Cancer Biology, 2013, 23, 109-115.	9.6	83
96	Methylation meets genomics. Nature Genetics, 2001, 27, 9-10.	21.4	78
97	Epigenetics at the Crossroads of Genes and the Environment. JAMA - Journal of the American Medical Association, 2015, 314, 1129.	7.4	77
98	Loss of Imprinting in Disease Progression in Chronic Myelogenous Leukemia. Blood, 1998, 91, 3144-3147.	1.4	76
99	Case-control meta-analysis of blood DNA methylation and autism spectrum disorder. Molecular Autism, 2018, 9, 40.	4.9	74
100	DNA methylation shows genome-wide association ofNFIX,RAPGEF2andMSRB3with gestational age at birth. International Journal of Epidemiology, 2012, 41, 188-199.	1.9	71
101	Monoallelic expression and methylation of imprinted genes in human and mouse embryonic germ cell lineages. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 10599-10604.	7.1	69
102	Genetics and Epigenetics â€" Nature's Pen-and-Pencil Set. New England Journal of Medicine, 2007, 356, 731-733.	27.0	69
103	Accurate genome-scale percentage DNA methylation estimates from microarray data. Biostatistics, 2011, 12, 197-210.	1.5	67
104	Cross-tissue integration of genetic and epigenetic data offers insight into autism spectrum disorder. Nature Communications, 2017, 8, 1011.	12.8	66
105	Statistical mechanics meets single-cell biology. Nature Reviews Genetics, 2021, 22, 459-476.	16.3	65
106	â€œGap huntingâ€•to characterize clustered probe signals in Illumina methylation array data. Epigenetics and Chromatin, 2016, 9, 56.	3.9	61
107	SNP-specific array-based allele-specific expression analysis. Genome Research, 2008, 18, 771-779.	5.5	60
108	Prenatal mercury concentration is associated with changes in DNA methylation atTCEANC2in newborns. International Journal of Epidemiology, 2015, 44, 1249-1262.	1.9	60

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109	The commonality of plasticity underlying multipotent tumor cells and embryonic stem cells. Journal of Cellular Biochemistry, 2007, 101, 908-917.	2.6	59
110	Epigenetic marks of prenatal air pollution exposure found in multiple tissues relevant for child health. Environment International, 2019, 126, 363-376.	10.0	58
111	A species-generalized probabilistic model-based definition of CpG islands. Mammalian Genome, 2009, 20, 674-80.	2.2	52
112	Alterations in DNA methylation in human colon neoplasia. Journal of Surgical Oncology, 1987, 3, 149-151.	1.4	48
113	Detailed DNA methylation profiles of the E-cadherin promoter in the NCI-60 cancer cells. Molecular Cancer Therapeutics, 2007, 6, 391-403.	4.1	48
114	DNA methylation mediates genotype and smoking interaction in the development of anti-citrullinated peptide antibody-positive rheumatoid arthritis. Arthritis Research and Therapy, 2017, 19, 71.	3.5	48
115	Cancer epigenetics is no Mickey Mouse. Cancer Cell, 2005, 8, 267-268.	16.8	46
116	Epigenetic effects in eukaryotic gene expression. Genesis, 1994, 15, 458-462.	2.1	45
117	An Epigenetic Approach to Cancer Etiology. Cancer Journal (Sudbury, Mass), 2007, 13, 70-74.	2.0	45
118	Factors associated with preterm delivery in mothers of children with Beckwith-Wiedemann syndrome: A case cohort study from the BWS registry. American Journal of Medical Genetics, Part A, 2005, 134A, 187-191.	1.2	44
119	DNA methylation is stable during replication and cell cycle arrest. Scientific Reports, 2016, 5, 17911.	3.3	44
120	DNA Methyltransferase 1 and 3B Activate BAG-1 Expression via Recruitment of CTCFL/BORIS and Modulation of Promoter Histone Methylation. Cancer Research, 2008, 68, 2726-2735.	0.9	43
121	Association of chromosome arm 16q loss with loss of imprinting of insulin-like growth factor-II in Wilms tumor. Genes Chromosomes and Cancer, 2005, 43, 155-161.	2.8	40
122	CTCFL/BORIS Is a Methylation-Independent DNA-Binding Protein That Preferentially Binds to the Paternal H19 Differentially Methylated Region. Cancer Research, 2008, 68, 5546-5551.	0.9	40
123	Euchromatin islands in large heterochromatin domains are enriched for CTCF binding and differentially DNA-methylated regions. BMC Genomics, 2012, 13, 566.	2.8	40
124	Strain-Dependent Developmental Relaxation of Imprinting of an Endogenous Mouse Gene, Kvlqt1. Genomics, 1998, 53, 395-399.	2.9	35
125	Children with Idiopathic Hemihypertrophy and Beckwith-Wiedemann Syndrome Have Different Constitutional Epigenotypes Associated with Wilms Tumor. American Journal of Human Genetics, 2005, 77, 887-891.	6.2	34
126	A new link between epigenetic progenitor lesions in cancer and the dynamics of signal transduction. Cell Cycle, 2009, 8, 383-390.	2.6	33

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127	Reply to â€œReassessing the abundance of H3K9me2 chromatin domains in embryonic stem cellsâ€. Nature Genetics, 2010, 42, 5-6.	21.4	32
128	Epigenetic variability and the evolution of human cancer. Advances in Cancer Research, 2003, 88, 145-168.	5.0	31
129	Overlapping euchromatin/heterochromatin- associated marks are enriched in imprinted gene regions and predict allele-specific modification. Genome Research, 2008, 18, 1806-1813.	5.5	29
130	High-specificity bioinformatics framework for epigenomic profiling of discordant twins reveals specific and shared markers for ACPA and ACPA-positive rheumatoid arthritis. Genome Medicine, 2016, 8, 124.	8.2	27
131	The two-domain hypothesis in Beckwith-Wiedemann syndrome. Journal of Clinical Investigation, 2000, 106, 739-740.	8.2	26
132	Temporal stability and age-related prevalence of loss of imprinting of the insulin-like growth factor-2 gene. Epigenetics, 2009, 4, 114-118.	2.7	23
133	Comprehensive Highâ€Throughput Arrays for Relative Methylation (CHARM). Current Protocols in Human Genetics, 2010, 65, Unit 20.1.1-19.	3.5	23
134	An information-theoretic approach to the modeling and analysis of whole-genome bisulfite sequencing data. BMC Bioinformatics, 2018, 19, 87.	2.6	23
135	Analyzing whole genome bisulfite sequencing data from highly divergent genotypes. Nucleic Acids Research, 2019, 47, e117-e117.	14.5	22
136	Human brain region-specific variably methylated regions are enriched for heritability of distinct neuropsychiatric traits. Genome Biology, 2021, 22, 116.	8.8	22
137	Loss of Imprinting in Disease Progression in Chronic Myelogenous Leukemia. Blood, 1998, 91, 3144-3147.	1.4	21
138	Multiple genetic abnormalities of 11p15 in Wilms' tumor. , 1996, 27, 484-489.		20
139	A developmental context for multiple genetic alterations in Wilmsâ€™ tumor. Journal of Cell Science, 1994, 1994, 7-12.	2.0	17
140	Adaptation of the CHARM DNA methylation platform for the rat genome reveals novel brain region-specific differences. Epigenetics, 2011, 6, 1378-1390.	2.7	17
141	Autism-Associated DNA Methylation at Birth From Multiple Tissues Is Enriched for Autism Genes in the Early Autism Risk Longitudinal Investigation. Frontiers in Molecular Neuroscience, 2021, 14, 775390.	2.9	17
142	Independent Methylome-Wide Association Studies of Schizophrenia Detect Consistent Caseâ€“Control Differences. Schizophrenia Bulletin, 2020, 46, 319-327.	4.3	15
143	The epigenetic basis of common human disease. Transactions of the American Clinical and Climatological Association, 2013, 124, 84-93.	0.5	12
144	Ranking genomic features using an information-theoretic measure of epigenetic discordance. BMC Bioinformatics, 2019, 20, 175.	2.6	11

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145	A Dysregulated DNA Methylation Landscape Linked to Gene Expression in MLL-Rearranged AML. Epigenetics, 2020, 15, 841-858.	2.7	11
146	Simple purification of human chromosomes to homogeneity using muntjac hybrid cells. Nature Genetics, 1994, 7, 29-33.	21.4	10
147	Wilms' Tumor as a Model for Cancer Biology. , 2003, 222, 239-248.		10
148	Addition of H19 â€˜Loss of Methylation Testingâ€™ for Beckwith-Wiedemann Syndrome (BWS) Increases the Diagnostic Yield. Journal of Molecular Diagnostics, 2010, 12, 576-588.	2.8	10
149	A Loss of Epigenetic Control Can Promote Cell Death through Reversing the Balance of Pathways in a Signaling Network. Molecular Cell, 2018, 72, 60-70.e3.	9.7	10
150	Converging genetic and epigenetic drivers of paediatric acute lymphoblastic leukaemia identified by an information-theoretic analysis. Nature Biomedical Engineering, 2021, 5, 360-376.	22.5	10
151	Inheritance pattern of Beckwith-Wiedemann syndrome is heterogeneous in 291 families with an affected proband. American Journal of Medical Genetics, Part A, 2005, 137A, 16-21.	1.2	8
152	The Nucleolus Gets the Silent Treatment. Cell Stem Cell, 2014, 15, 675-676.	11.1	6
153	Lack of parental origin specificity of altered alleles at 11p15 in testicular germ cell tumors. Cancer Genetics and Cytogenetics, 2003, 147, 1-8.	1.0	4
154	Estimating DNA methylation potential energy landscapes from nanopore sequencing data. Scientific Reports, 2021, 11, 21619.	3.3	2
155	A third-generation method reveals cell lineage ancestry. Nature Methods, 2013, 10, 117-118.	19.0	1
156	Cancer Epigenomics. , 2009, , 385-395.		1
157	Beckwith-Wiedemann Syndrome. , 1998, , 1047-1052.		1
158	Genomic Imprinting. , 2011, , 1536-1538.		0
159	Genomic Imprinting. , 2016, , 1888-1891.		0