Andrew Feinberg

List of Publications by Year
in descending order

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243 papers	84,942 citations	1704 104 h-index	1051 234 g-index
270 all docs	270 docs citations	270 times ranked	56020 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	A technique for radiolabeling DNA restriction endonuclease fragments to high specific activity. Analytical Biochemistry, 1984, 137, 266-267.	2.4	6,353
3	Minfi: a flexible and comprehensive Bioconductor package for the analysis of Infinium DNA methylation microarrays. Bioinformatics, 2014, 30, 1363-1369.	4.1	3,192
4	Hypomethylation distinguishes genes of some human cancers from their normal counterparts. Nature, 1983, 301, 89-92.	27.8	2,175
5	The history of cancer epigenetics. Nature Reviews Cancer, 2004, 4, 143-153.	28.4	2,061
6	Epigenetic memory in induced pluripotent stem cells. Nature, 2010, 467, 285-290.	27.8	2,011
7	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
8	The epigenetic progenitor origin of human cancer. Nature Reviews Genetics, 2006, 7, 21-33.	16.3	1,642
9	Phenotypic plasticity and the epigenetics of human disease. Nature, 2007, 447, 433-440.	27.8	1,475
10	DNMT1 and DNMT3b cooperate to silence genes in human cancer cells. Nature, 2002, 416, 552-556.	27.8	1,126
11	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
12	Increased methylation variation in epigenetic domains across cancer types. Nature Genetics, 2011, 43, 768-775.	21.4	968
13	DNA methylation age of blood predicts all-cause mortality in later life. Genome Biology, 2015, 16, 25.	8.8	928
14	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
15	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
16	Hypomethylation of DNA from Benign and Malignant Human Colon Neoplasms. Science, 1985, 228, 187-190.	12.6	786
17	DNA methylation-based measures of biological age: meta-analysis predicting time to death. Aging, 2016, 8, 1844-1865.	3.1	786
18	Relaxation of imprinted genes in human cancer. Nature, 1993, 362, 747-749.	27.8	780

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19	Epigenetic silencing of tumour suppressor gene p15 by its antisense RNA. Nature, 2008, 451, 202-206.	27.8	777
20	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
21	Loss of IGF2 Imprinting: A Potential Marker of Colorectal Cancer Risk. Science, 2003, 299, 1753-1755.	12.6	704
22	Epigenetic modulators, modifiers and mediators in cancer aetiology and progression. Nature Reviews Genetics, 2016, 17, 284-299.	16.3	679
23	Intra-individual Change Over Time in DNA Methylation With Familial Clustering. JAMA - Journal of the American Medical Association, 2008, 299, 2877.	7.4	602
24	The NASA Twins Study: A multidimensional analysis of a year-long human spaceflight. Science, 2019, 364, .	12.6	576
25	Bump hunting to identify differentially methylated regions in epigenetic epidemiology studies. International Journal of Epidemiology, 2012, 41, 200-209.	1.9	567
26	Comprehensive methylome map of lineage commitment from haematopoietic progenitors. Nature, 2010, 467, 338-342.	27.8	554
27	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
28	Large histone H3 lysine 9 dimethylated chromatin blocks distinguish differentiated from embryonic stem cells. Nature Genetics, 2009, 41, 246-250.	21.4	540
29	SIRT3, a human SIR2 homologue, is an NAD- dependent deacetylase localized to mitochondria. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 13653-13658.	7.1	496
30	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
31	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
32	Hypomethylation of ras oncogenes in primary human cancers. Biochemical and Biophysical Research Communications, 1983, 111, 47-54.	2.1	470
33	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
34	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
35	Somatic deletion and duplication of genes on chromosome 11 in Wilms' tumours. Nature, 1984, 309, 176-178.	27.8	426
36	A comparison of non-integrating reprogramming methods. Nature Biotechnology, 2015, 33, 58-63.	17.5	424

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37	The Key Role of Epigenetics in Human Disease Prevention and Mitigation. New England Journal of Medicine, 2018, 378, 1323-1334.	27.0	419
38	An integrated epigenetic and genetic approach to common human disease. Trends in Genetics, 2004, 20, 350-358.	6.7	408
39	Reduced genomic 5-methylcytosine content in human colonic neoplasia. Cancer Research, 1988, 48, 1159-61.	0.9	395
40	Use of restriction fragment length polymorphisms to determine the clonal origin of human tumors. Science, 1985, 227, 642-645.	12.6	383
41	Comprehensive high-throughput arrays for relative methylation (CHARM). Genome Research, 2008, 18, 780-790.	5.5	379
42	Epigenomic reprogramming during pancreatic cancer progression links anabolic glucose metabolism to distant metastasis. Nature Genetics, 2017, 49, 367-376.	21.4	365
43	Human KVLQT1 gene shows tissue-specific imprinting and encompasses Beckwith-Wiedemann syndrome chromosomal rearrangements. Nature Genetics, 1997, 15, 181-185.	21.4	354
44	Loss of imprinting of a paternally expressed transcript, with antisense orientation to K _V LQT1, occurs frequently in Beckwithâ€“Wiedemann syndrome and is independent of insulin-like growth factor II imprinting. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 5203-5208.	7.1	350
45	Genome-scale epigenetic reprogramming during epithelial-to-mesenchymal transition. Nature Structural and Molecular Biology, 2011, 18, 867-874.	8.2	340
46	Loss of genes on the short arm of chromosome 11 in bladder cancer. Nature, 1985, 318, 377-380.	27.8	334
47	Epigenetics at the Epicenter of Modern Medicine. JAMA - Journal of the American Medical Association, 2008, 299, 1345.	7.4	331
48	An X Chromosome Gene, WTX , Is Commonly Inactivated in Wilms Tumor. Science, 2007, 315, 642-645.	12.6	321
49	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
50	Loss of Imprinting of Igf2 Alters Intestinal Maturation and Tumorigenesis in Mice. Science, 2005, 307, 1976-1978.	12.6	312
51	Epigenetics and Assisted Reproductive Technology: A Call for Investigation. American Journal of Human Genetics, 2004, 74, 599-609.	6.2	311
52	Reversible switching between epigenetic states in honeybee behavioral subcastes. Nature Neuroscience, 2012, 15, 1371-1373.	14.8	305
53	Loss of imprinting in colorectal cancer linked to hypomethylation of H19 and IGF2. Cancer Research, 2002, 62, 6442-6.	0.9	305
54	The epigenetics of cancer etiology. Seminars in Cancer Biology, 2004, 14, 427-432.	9.6	300

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55	Personalized Epigenomic Signatures That Are Stable Over Time and Covary with Body Mass Index. Science Translational Medicine, 2010, 2, 49ra67.	12.4	292
56	Imprinting of the gene encoding a human cyclin-dependent kinase inhibitor, p57KIP2, on chromosome 11p15.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 3026-3030.	7.1	290
57	The emerging science of epigenomics. Human Molecular Genetics, 2006, 15, R95-R101.	2.9	283
58	Poly(ADP-ribosyl)ation regulates CTCF-dependent chromatin insulation. Nature Genetics, 2004, 36, 1105-1110.	21.4	282
59	Loss of imprinting in normal tissue of colorectal cancer patients with microsatellite instability. Nature Medicine, 1998, 4, 1276-1280.	30.7	279
60	Common DNA methylation alterations in multiple brain regions in autism. Molecular Psychiatry, 2014, 19, 862-871.	7.9	279
61	Targeted disruption of the Kvlqt1 gene causes deafness and gastric hyperplasia in mice. Journal of Clinical Investigation, 2000, 106, 1447-1455.	8.2	269
62	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
63	MULTIPLE GENETIC ALTERATIONS IN DISTAL AND PROXIMAL COLORECTAL CANCER. Lancet, The, 1989, 334, 353-356.	13.7	257
64	DNA Methylation Signatures within the Human Brain. American Journal of Human Genetics, 2007, 81, 1304-1315.	6.2	256
65	DNA methylation of cord blood cell types: Applications for mixed cell birth studies. Epigenetics, 2016, 11, 354-362.	2.7	256
66	Genetic linkage of Beckwith-Wiedemann syndrome to 11p15. American Journal of Human Genetics, 1989, 44, 720-3.	6.2	254
67	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. Genome Biology, 2016, 17, 255.	8.8	251
68	Association of Body Mass Index with DNA Methylation and Gene Expression in Blood Cells and Relations to Cardiometabolic Disease: A Mendelian Randomization Approach. PLoS Medicine, 2017, 14, e1002215.	8.4	246
69	Regulated Noise in the Epigenetic Landscape of Development and Disease. Cell, 2012, 148, 1123-1131.	28.9	220
70	LIT1, an imprinted antisense RNA in the human KvLQT1 locus identified by screening for differentially expressed transcripts using monochromosomal hybrids. Human Molecular Genetics, 1999, 8, 1209-1217.	2.9	214
71	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
72	Loss of allelic heterozygosity at a second locus on chromosome 11 in sporadic Wilms' tumor cells.. Molecular and Cellular Biology, 1989, 9, 1799-1803.	2.3	204

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73	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
74	DNA methylation and genomic imprinting: insights from cancer into epigenetic mechanisms. Seminars in Cancer Biology, 2002, 12, 389-398.	9.6	196
75	Tumor cell growth arrest caused by subchromosomal transferable DNA fragments from chromosome 11. Science, 1993, 260, 361-364.	12.6	187
76	Genomic imprinting and gene activation in cancer. Nature Genetics, 1993, 4, 110-113.	21.4	182
77	Moving AHEAD with an international human epigenome project. Nature, 2008, 454, 711-715.	27.8	177
78	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
79	Large hypomethylated blocks as a universal defining epigenetic alteration in human solid tumors. Genome Medicine, 2014, 6, 61.	8.2	170
80	Tissue, Developmental, and Tumor-Specific Expression of Divergent Transcripts in Wilms Tumor. Science, 1990, 250, 991-994.	12.6	160
81	Mutation Affecting the 12th Amino Acid of the c-Ha- ras Oncogene Product Occurs Infrequently in Human Cancer. Science, 1983, 220, 1175-1177.	12.6	159
82	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
83	Redefining CpG islands using hidden Markov models. Biostatistics, 2010, 11, 499-514.	1.5	151
84	Association of DNA Methylation Differences With Schizophrenia in an Epigenome-Wide Association Study. JAMA Psychiatry, 2016, 73, 506.	11.0	151
85	Blood Leukocyte DNA Methylation Predicts Risk of Future Myocardial Infarction and Coronary Heart Disease. Circulation, 2019, 140, 645-657.	1.6	151
86	Loss of Imprinting of Insulin-Like Growth Factor-II (IGF2) Gene in Distinguishing Specific Biologic Subtypes of Wilms Tumor. Journal of the National Cancer Institute, 2001, 93, 1698-1703.	6.3	150
87	Low Frequency of p57KIP2 Mutation in Beckwith-Wiedemann Syndrome. American Journal of Human Genetics, 1997, 61, 304-309.	6.2	148
88	Cancer epigenetics takes center stage. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 392-394.	7.1	148
89	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
90	Concerted nonsyntenic allelic loss in human colorectal carcinoma. Science, 1988, 241, 961-965.	12.6	145

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91	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
92	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
93	Large-scale hypomethylated blocks associated with Epstein-Barr virusâ€“induced B-cell immortalization. Genome Research, 2014, 24, 177-184.	5.5	130
94	Microdeletion of LIT1 in Familial Beckwith-Wiedemann Syndrome. American Journal of Human Genetics, 2004, 75, 844-849.	6.2	126
95	Limited up-regulation of DNA methyltransferase in human colon cancer reflecting increased cell proliferation.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 10366-10370.	7.1	125
96	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
97	An LSC epigenetic signature is largely mutation independent and implicates the HOXA cluster in AML pathogenesis. Nature Communications, 2015, 6, 8489.	12.8	121
98	Neuronal brain-region-specific DNA methylation and chromatin accessibility are associated with neuropsychiatric trait heritability. Nature Neuroscience, 2019, 22, 307-316.	14.8	120
99	Genome-Wide DNA Methylation Scan in Major Depressive Disorder. PLoS ONE, 2012, 7, e34451.	2.5	120
100	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
101	Loss of Imprinting of IGF2: A Common Epigenetic Modifier of Intestinal Tumor Risk. Cancer Research, 2005, 65, 11236-11240.	0.9	119
102	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
103	Potential energy landscapes identify the information-theoretic nature of the epigenome. Nature Genetics, 2017, 49, 719-729.	21.4	114
104	Age and sun exposure-related widespread genomic blocks of hypomethylation in nonmalignant skin. Genome Biology, 2015, 16, 80.	8.8	111
105	Loss of imprinting in hepatoblastoma. Cancer Research, 1995, 55, 1836-8.	0.9	111
106	Multiple genetic loci within 11p15 defined by Beckwith-Wiedemann syndrome rearrangement breakpoints and subchromosomal transferable fragments.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 12456-12460.	7.1	108
107	Sequence and Comparative Analysis of the Mouse 1-Megabase Region Orthologous to the Human 11p15 Imprinted Domain. Genome Research, 2000, 10, 1697-1710.	5.5	107
108	Hot-stop PCR: a simple and general assay for linear quantitation of allele ratios. Nature Genetics, 2000, 25, 375-376.	21.4	106

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109	Parental Imprinting of Human Chromosome Region 11p15.3-pter Involved in the Beckwith-Wiedemann Syndrome and Various Human Neoplasia. European Journal of Human Genetics, 1994, 2, 3-23.	2.8	103
110	Loss of imprinting of insulin-like growth factor-II in Wilms' tumor commonly involves altered methylation but not mutations of CTCF or its binding site. Cancer Research, 2001, 61, 4947-50.	0.9	103
111	Epigenomics reveals a functional genome anatomy and a new approach to common disease. Nature Biotechnology, 2010, 28, 1049-1052.	17.5	99
112	Mouse-Human Experimental Epigenetic Analysis Unmasks Dietary Targets and Genetic Liability for Diabetic Phenotypes. Cell Metabolism, 2015, 21, 138-149.	16.2	98
113	Syntenic Organization of the Mouse Distal Chromosome 7 Imprinting Cluster and the Beckwith-Wiedemann Syndrome Region in Chromosome 11p15.5. Human Molecular Genetics, 1998, 7, 1149-1159.	2.9	97
114	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
115	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
116	Presence of an epigenetic signature of prenatal cigarette smoke exposure in childhood. Environmental Research, 2016, 144, 139-148.	7.5	96
117	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
118	Butyrophenone influences on the opiate receptor. European Journal of Pharmacology, 1976, 36, 231-235.	3.5	92
119	Significance analysis and statistical dissection of variably methylated regions. Biostatistics, 2012, 13, 166-178.	1.5	92
120	Measuring cell-type specific differential methylation in human brain tissue. Genome Biology, 2013, 14, R94.	9.6	92
121	Whole-genome analysis of the methylome and hydroxymethylome in normal and malignant lung and liver. Genome Research, 2016, 26, 1730-1741.	5.5	91
122	A Selective Phenelzine Analogue Inhibitor of Histone Demethylase LSD1. ACS Chemical Biology, 2014, 9, 1284-1293.	3.4	88
123	Imprinting of a genomic domain of 11p15 and loss of imprinting in cancer: an introduction. Cancer Research, 1999, 59, 1743s-1746s.	0.9	88
124	Genomic Imprinting and Cancer. , 2001, , 358-362.		87
125	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
126	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

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127	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
128	Higher order chromatin organization in cancer. Seminars in Cancer Biology, 2013, 23, 109-115.	9.6	83
129	Methylation meets genomics. Nature Genetics, 2001, 27, 9-10.	21.4	78
130	Interferon-alpha restores the deficient expression of the cytoadhesion molecule lymphocyte function antigen-3 by chronic myelogenous leukemia progenitor cells.. Journal of Clinical Investigation, 1991, 88, 2131-2136.	8.2	78
131	Epigenetics at the Crossroads of Genes and the Environment. JAMA - Journal of the American Medical Association, 2015, 314, 1129.	7.4	77
132	Loss of Imprinting in Disease Progression in Chronic Myelogenous Leukemia. Blood, 1998, 91, 3144-3147.	1.4	76
133	Nanopore sequencing in microgravity. Npj Microgravity, 2016, 2, 16035.	3.7	76
134	Case-control meta-analysis of blood DNA methylation and autism spectrum disorder. Molecular Autism, 2018, 9, 40.	4.9	74
135	DNA methylation shows genome-wide association ofNFIX,RAPGEF2andMSRB3with gestational age at birth. International Journal of Epidemiology, 2012, 41, 188-199.	1.9	71
136	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
137	Genetics and Epigenetics â€" Nature's Pen-and-Pencil Set. New England Journal of Medicine, 2007, 356, 731-733.	27.0	69
138	Two Novel Genes in the Center of the 11p15 Imprinted Domain Escape Genomic Imprinting. Human Molecular Genetics, 1999, 8, 683-690.	2.9	68
139	Accurate genome-scale percentage DNA methylation estimates from microarray data. Biostatistics, 2011, 12, 197-210.	1.5	67
140	Cross-tissue integration of genetic and epigenetic data offers insight into autism spectrum disorder. Nature Communications, 2017, 8, 1011.	12.8	66
141	Statistical mechanics meets single-cell biology. Nature Reviews Genetics, 2021, 22, 459-476.	16.3	65
142	â€œGap huntingâ€•to characterize clustered probe signals in Illumina methylation array data. Epigenetics and Chromatin, 2016, 9, 56.	3.9	61
143	SNP-specific array-based allele-specific expression analysis. Genome Research, 2008, 18, 771-779.	5.5	60
144	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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145	The commonality of plasticity underlying multipotent tumor cells and embryonic stem cells. Journal of Cellular Biochemistry, 2007, 101, 908-917.	2.6	59
146	Epigenetic marks of prenatal air pollution exposure found in multiple tissues relevant for child health. Environment International, 2019, 126, 363-376.	10.0	58
147	Loss of Allelic Heterozygosity at a Second Locus on Chromosome 11 in Sporadic Wilmsâ€™ Tumor Cells. Molecular and Cellular Biology, 1989, 9, 1799-1803.	2.3	57
148	Smoking induces DNA methylation changes in Multiple Sclerosis patients with exposure-response relationship. Scientific Reports, 2017, 7, 14589.	3.3	55
149	Nanoelectromechanics of Methylated DNA in a Synthetic Nanopore. Biophysical Journal, 2009, 96, L32-L34.	0.5	54
150	Reduced expression of the cyclin-dependent kinase inhibitor gene p57KIP2 in Wilms' tumor. Cancer Research, 1996, 56, 5723-7.	0.9	54
151	Genomic Imprinting, DNA Methylation, and Cancer. Journal of the National Cancer Institute, 1994, 86, 753-759.	6.3	52
152	A species-generalized probabilistic model-based definition of CpG islands. Mammalian Genome, 2009, 20, 674-80.	2.2	52
153	Epigenetic stochasticity, nuclear structure and cancer: the implications for medicine. Journal of Internal Medicine, 2014, 276, 5-11.	6.0	52
154	DNA Methylation, Genomic Imprinting and Cancer. Current Topics in Microbiology and Immunology, 2000, 249, 87-99.	1.1	50
155	Targeted regulation of imprinted genes by synthetic zinc-finger transcription factors. Gene Therapy, 2003, 10, 513-522.	4.5	49
156	Alterations in DNA methylation in human colon neoplasia. Journal of Surgical Oncology, 1987, 3, 149-151.	1.4	48
157	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
158	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
159	Disruption of a Novel Imprinted Zinc-Finger Gene, ZNF215, in Beckwith-Wiedemann Syndrome. American Journal of Human Genetics, 2000, 66, 1473-1484.	6.2	47
160	Genomic imprinting of a human apoptosis gene homologue, TSSC3. Cancer Research, 1998, 58, 1052-6.	0.9	47
161	Cancer epigenetics is no Mickey Mouse. Cancer Cell, 2005, 8, 267-268.	16.8	46
162	Epigenetic effects in eukaryotic gene expression. Genesis, 1994, 15, 458-462.	2.1	45

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163	A novel human homologue of yeast nucleosome assembly protein, 65 kb centromeric to the p57KIP2 gene, is biallelically expressed in fetal and adult tissues. Human Molecular Genetics, 1996, 5, 1743-1748.	2.9	45
164	An Epigenetic Approach to Cancer Etiology. Cancer Journal (Sudbury, Mass), 2007, 13, 70-74.	2.0	45
165	Mutant WT1 is associated with DNA hypermethylation of PRC2 targets in AML and responds to EZH2 inhibition. Blood, 2015, 125, 316-326.	1.4	45
166	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
167	DNA methylation is stable during replication and cell cycle arrest. Scientific Reports, 2016, 5, 17911.	3.3	44
168	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
169	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
170	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
171	Euchromatin islands in large heterochromatin domains are enriched for CTCF binding and differentially DNA-methylated regions. BMC Genomics, 2012, 13, 566.	2.8	40
172	Strain-Dependent Developmental Relaxation of Imprinting of an Endogenous Mouse Gene, Kvlqt1. Genomics, 1998, 53, 395-399.	2.9	35
173	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
174	A new link between epigenetic progenitor lesions in cancer and the dynamics of signal transduction. Cell Cycle, 2009, 8, 383-390.	2.6	33
175	Parent-Of-Origin Effects in Autism Identified through Genome-Wide Linkage Analysis of 16,000 SNPs. PLoS ONE, 2010, 5, e12513.	2.5	33
176	Reply to â€œReassessing the abundance of H3K9me2 chromatin domains in embryonic stem cellsâ€• Nature Genetics, 2010, 42, 5-6.	21.4	32
177	Epigenetic variability and the evolution of human cancer. Advances in Cancer Research, 2003, 88, 145-168.	5.0	31
178	Somatic mutation of TSSC5, a novel imprinted gene from human chromosome 11p15.5. Cancer Research, 1998, 58, 4155-9.	0.9	31
179	An Integrated Physical Map of 210 Markers Assigned to the Short Arm of Human Chromosome 11. Genomics, 1994, 21, 538-550.	2.9	30
180	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

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181	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
182	The two-domain hypothesis in Beckwith-Wiedemann syndrome. Journal of Clinical Investigation, 2000, 106, 739-740.	8.2	26
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