# Andrew Feinberg

## List of Publications by Citations



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|---|---|---|---|
| 241 papers | 70,981 citations | 98 h-index | 266 g-index |
| 270 ext. papers | 76,526 ext. citations | 15.4 avg, IF | 7.99 L-index |

| # | Paper | IF | Citations |
|---|---|---|---|
| 241 | A technique for radiolabeling DNA restriction endonuclease fragments to high specific activity. *Analytical Biochemistry*, **1983**, 132, 6-13 | 3.1 | 20314 |
| 240 | "A technique for radiolabeling DNA restriction endonuclease fragments to high specific activity". Addendum. *Analytical Biochemistry*, **1984**, 137, 266-7 | 3.1 | 6032 |
| 239 | Minfi: a flexible and comprehensive Bioconductor package for the analysis of Infinium DNA methylation microarrays. *Bioinformatics*, **2014**, 30, 1363-9 | 7.2 | 1941 |
| 238 | Hypomethylation distinguishes genes of some human cancers from their normal counterparts. *Nature*, **1983**, 301, 89-92 | 50.4 | 1906 |
| 237 | The history of cancer epigenetics. *Nature Reviews Cancer*, **2004**, 4, 143-53 | 31.3 | 1803 |
| 236 | Epigenetic memory in induced pluripotent stem cells. *Nature*, **2010**, 467, 285-90 | 50.4 | 1729 |
| 235 | The human colon cancer methylome shows similar hypo- and hypermethylation at conserved tissue-specific CpG island shores. *Nature Genetics*, **2009**, 41, 178-186 | 36.3 | 1681 |
| 234 | The epigenetic progenitor origin of human cancer. *Nature Reviews Genetics*, **2006**, 7, 21-33 | 30.1 | 1417 |
| 233 | Phenotypic plasticity and the epigenetics of human disease. *Nature*, **2007**, 447, 433-40 | 50.4 | 1288 |
| 232 | DNMT1 and DNMT3b cooperate to silence genes in human cancer cells. *Nature*, **2002**, 416, 552-6 | 50.4 | 1008 |
| 231 | 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, 1350-3 | 36.3 | 936 |
| 230 | Increased methylation variation in epigenetic domains across cancer types. *Nature Genetics*, **2011**, 43, 768-75 | 36.3 | 825 |
| 229 | Association of in vitro fertilization with Beckwith-Wiedemann syndrome and epigenetic alterations of LIT1 and H19. *American Journal of Human Genetics*, **2003**, 72, 156-60 | 11 | 762 |
| 228 | Hypomethylation of DNA from benign and malignant human colon neoplasms. *Science*, **1985**, 228, 187-90 | 33.3 | 724 |
| 227 | Epigenetic silencing of tumour suppressor gene p15 by its antisense RNA. *Nature*, **2008**, 451, 202-6 | 50.4 | 710 |
| 226 | Relaxation of imprinted genes in human cancer. *Nature*, **1993**, 362, 747-9 | 50.4 | 708 |
| 225 | Epigenome-wide association data implicate DNA methylation as an intermediary of genetic risk in rheumatoid arthritis. *Nature Biotechnology*, **2013**, 31, 142-7 | 44.5 | 691 |

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| 224 | DNA methylation age of blood predicts all-cause mortality in later life. *Genome Biology*, **2015**, 16, 25 | 18.3 | 670 |
| 223 | Loss of IGF2 imprinting: a potential marker of colorectal cancer risk. *Science*, **2003**, 299, 1753-5 | 33.3 | 634 |
| 222 | Intra-individual change over time in DNA methylation with familial clustering. *JAMA - Journal of the American Medical Association*, **2008**, 299, 2877-83 | 27.4 | 533 |
| 221 | DNA methylation-based measures of biological age: meta-analysis predicting time to death. *Aging*, **2016**, 8, 1844-1865 | 5.6 | 531 |
| 220 | Epigenetic modulators, modifiers and mediators in cancer aetiology and progression. *Nature Reviews Genetics*, **2016**, 17, 284-99 | 30.1 | 490 |
| 219 | DNA Methylation in Newborns and Maternal Smoking in Pregnancy: Genome-wide Consortium Meta-analysis. *American Journal of Human Genetics*, **2016**, 98, 680-96 | 11 | 489 |
| 218 | Comprehensive methylome map of lineage commitment from haematopoietic progenitors. *Nature*, **2010**, 467, 338-42 | 50.4 | 484 |
| 217 | Large histone H3 lysine 9 dimethylated chromatin blocks distinguish differentiated from embryonic stem cells. *Nature Genetics*, **2009**, 41, 246-50 | 36.3 | 469 |
| 216 | Donor cell type can influence the epigenome and differentiation potential of human induced pluripotent stem cells. *Nature Biotechnology*, **2011**, 29, 1117-9 | 44.5 | 443 |
| 215 | Bump hunting to identify differentially methylated regions in epigenetic epidemiology studies. *International Journal of Epidemiology*, **2012**, 41, 200-9 | 7.8 | 430 |
| 214 | Hypomethylation of ras oncogenes in primary human cancers. *Biochemical and Biophysical Research Communications*, **1983**, 111, 47-54 | 3.4 | 426 |
| 213 | Cancer as a dysregulated epigenome allowing cellular growth advantage at the expense of the host. *Nature Reviews Cancer*, **2013**, 13, 497-510 | 31.3 | 421 |
| 212 | 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, 13653-8 | 11.5 | 420 |
| 211 | Loss of imprinting of IGF2 is linked to reduced expression and abnormal methylation of H19 in Wilms' tumour. *Nature Genetics*, **1994**, 7, 433-9 | 36.3 | 418 |
| 210 | 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, 154-8 | 36.3 | 412 |
| 209 | Evolution in health and medicine Sackler colloquium: 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 Suppl 1, 1757-64 | 11.5 | 398 |
| 208 | Somatic deletion and duplication of genes on chromosome 11 in Wilms' tumours. *Nature*, **1984**, 309, 176-8 | 50.4 | 385 |
| 207 | An integrated epigenetic and genetic approach to common human disease. *Trends in Genetics*, **2004** , 20, 350-8 | 8.5 | 367 |

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|---|---|---|---|
| 206 | Reduced genomic 5-methylcytosine content in human colonic neoplasia. *Cancer Research*, **1988**, 48, 1159-61 | 11 | 358 |
| 205 | Comprehensive high-throughput arrays for relative methylation (CHARM). *Genome Research*, **2008**, 18, 780-90 | 9.7 | 350 |
| 204 | Use of restriction fragment length polymorphisms to determine the clonal origin of human tumors. *Science*, **1985**, 227, 642-5 | 33.3 | 337 |
| 203 | Human KVLQT1 gene shows tissue-specific imprinting and encompasses Beckwith-Wiedemann syndrome chromosomal rearrangements. *Nature Genetics*, **1997**, 15, 181-5 | 36.3 | 335 |
| 202 | A comparison of non-integrating reprogramming methods. *Nature Biotechnology*, **2015**, 33, 58-63 | 44.5 | 326 |
| 201 | Loss of imprinting of a paternally expressed transcript, with antisense orientation to KVLQT1, occurs frequently in Beckwith-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*, **1998**, 95, 5203-8 | 11.5 | 315 |
| 200 | Loss of genes on the short arm of chromosome 11 in bladder cancer. *Nature*, **1985**, 318, 377-80 | 50.4 | 312 |
| 199 | The NASA Twins Study: A multidimensional analysis of a year-long human spaceflight. *Science*, **2019**, 364, | 33.3 | 300 |
| 198 | Genome-scale epigenetic reprogramming during epithelial-to-mesenchymal transition. *Nature Structural and Molecular Biology*, **2011**, 18, 867-74 | 17.6 | 297 |
| 197 | The Key Role of Epigenetics in Human Disease Prevention and Mitigation. *New England Journal of Medicine*, **2018**, 378, 1323-1334 | 59.2 | 290 |
| 196 | An X chromosome gene, WTX, is commonly inactivated in Wilms tumor. *Science*, **2007**, 315, 642-5 | 33.3 | 288 |
| 195 | Loss of imprinting in colorectal cancer linked to hypomethylation of H19 and IGF2. *Cancer Research*, **2002**, 62, 6442-6 | 10.1 | 282 |
| 194 | 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, 6806-11 | 11.5 | 279 |
| 193 | Epigenetics at the epicenter of modern medicine. *JAMA - Journal of the American Medical Association*, **2008**, 299, 1345-50 | 27.4 | 275 |
| 192 | Loss of imprinting of Igf2 alters intestinal maturation and tumorigenesis in mice. *Science*, **2005**, 307, 1976-8 | 33.3 | 272 |
| 191 | The epigenetics of cancer etiology. *Seminars in Cancer Biology*, **2004**, 14, 427-32 | 12.7 | 272 |
| 190 | Epigenetics and assisted reproductive technology: a call for investigation. *American Journal of Human Genetics*, **2004**, 74, 599-609 | 11 | 269 |
| 189 | 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, 3026-30 | 11.5 | 266 |

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| 188 | Poly(ADP-ribosyl)ation regulates CTCF-dependent chromatin insulation. *Nature Genetics*, **2004**, 36, 1105-10 | 36.3 | 261 |
| 187 | Personalized epigenomic signatures that are stable over time and covary with body mass index. *Science Translational Medicine*, **2010**, 2, 49ra67 | 17.5 | 254 |
| 186 | Epigenomic reprogramming during pancreatic cancer progression links anabolic glucose metabolism to distant metastasis. *Nature Genetics*, **2017**, 49, 367-376 | 36.3 | 250 |
| 185 | Loss of imprinting in normal tissue of colorectal cancer patients with microsatellite instability. *Nature Medicine*, **1998**, 4, 1276-80 | 50.5 | 249 |
| 184 | Genetic linkage of Beckwith-Wiedemann syndrome to 11p15. *American Journal of Human Genetics*, **1989**, 44, 720-3 | 11 | 239 |
| 183 | The emerging science of epigenomics. *Human Molecular Genetics*, **2006**, 15 Spec No 1, R95-101 | 5.6 | 238 |
| 182 | Reversible switching between epigenetic states in honeybee behavioral subcastes. *Nature Neuroscience*, **2012**, 15, 1371-3 | 25.5 | 237 |
| 181 | Epigenetic alterations of H19 and LIT1 distinguish patients with Beckwith-Wiedemann syndrome with cancer and birth defects. *American Journal of Human Genetics*, **2002**, 70, 604-11 | 11 | 236 |
| 180 | Targeted disruption of the Kvlqt1 gene causes deafness and gastric hyperplasia in mice. *Journal of Clinical Investigation*, **2000**, 106, 1447-55 | 15.9 | 234 |
| 179 | Multiple genetic alterations in distal and proximal colorectal cancer. *Lancet, The*, **1989**, 2, 353-6 | 40 | 230 |
| 178 | DNA methylation signatures within the human brain. *American Journal of Human Genetics*, **2007**, 81, 1304-15 | 11 | 228 |
| 177 | Common DNA methylation alterations in multiple brain regions in autism. *Molecular Psychiatry*, **2014**, 19, 862-71 | 15.1 | 219 |
| 176 | DNA methylation of cord blood cell types: Applications for mixed cell birth studies. *Epigenetics*, **2016**, 11, 354-62 | 5.7 | 196 |
| 175 | Loss of allelic heterozygosity at a second locus on chromosome 11 in sporadic Wilms' tumor cells. *Molecular and Cellular Biology*, **1989**, 9, 1799-803 | 4.8 | 193 |
| 174 | Association between Beckwith-Wiedemann syndrome and assisted reproductive technology: a case series of 19 patients. *Fertility and Sterility*, **2005**, 83, 349-54 | 4.8 | 191 |
| 173 | Microallelotyping defines the sequence and tempo of allelic losses at tumour suppressor gene loci during colorectal cancer progression. *Nature Medicine*, **1995**, 1, 902-9 | 50.5 | 184 |
| 172 | Tumor cell growth arrest caused by subchromosomal transferable DNA fragments from chromosome 11. *Science*, **1993**, 260, 361-4 | 33.3 | 174 |
| 171 | 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, 1209-17 | 5.6 | 172 |

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| 170 | DNA methylation and genomic imprinting: insights from cancer into epigenetic mechanisms. *Seminars in Cancer Biology*, **2002**, 12, 389-98 | 12.7 | 171 |
| 169 | DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. *Genome Biology*, **2016**, 17, 255 | 18.3 | 171 |
| 168 | Regulated noise in the epigenetic landscape of development and disease. *Cell*, **2012**, 148, 1123-31 | 56.2 | 166 |
| 167 | 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 | 11.6 | 162 |
| 166 | Moving AHEAD with an international human epigenome project. *Nature*, **2008**, 454, 711-5 | 50.4 | 158 |
| 165 | Distinct effects on gene expression of chemical and genetic manipulation of the cancer epigenome revealed by a multimodality approach. *Cancer Cell*, **2004**, 6, 361-71 | 24.3 | 157 |
| 164 | Tissue, developmental, and tumor-specific expression of divergent transcripts in Wilms tumor. *Science*, **1990**, 250, 991-4 | 33.3 | 150 |
| 163 | Mutation affecting the 12th amino acid of the c-Ha-ras oncogene product occurs infrequently in human cancer. *Science*, **1983**, 220, 1175-7 | 33.3 | 148 |
| 162 | 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, 1698-703 | 9.7 | 142 |
| 161 | Low frequency of p57KIP2 mutation in Beckwith-Wiedemann syndrome. *American Journal of Human Genetics*, **1997**, 61, 304-9 | 11 | 138 |
| 160 | Concerted nonsyntenic allelic loss in human colorectal carcinoma. *Science*, **1988**, 241, 961-5 | 33.3 | 134 |
| 159 | Cancer epigenetics takes center stage. *Proceedings of the National Academy of Sciences of the United States of America*, **2001**, 98, 392-4 | 11.5 | 130 |
| 158 | Tumor-associated zinc finger mutations in the CTCF transcription factor selectively alter tts DNA-binding specificity. *Cancer Research*, **2002**, 62, 48-52 | 10.1 | 130 |
| 157 | Redefining CpG islands using hidden Markov models. *Biostatistics*, **2010**, 11, 499-514 | 3.7 | 122 |
| 156 | Large hypomethylated blocks as a universal defining epigenetic alteration in human solid tumors. *Genome Medicine*, **2014**, 6, 61 | 14.4 | 120 |
| 155 | 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, 10366-70 | 11.5 | 118 |
| 154 | Microdeletion of LIT1 in familial Beckwith-Wiedemann syndrome. *American Journal of Human Genetics*, **2004**, 75, 844-9 | 11 | 113 |
| 153 | Genome-wide DNA methylation scan in major depressive disorder. *PLoS ONE*, **2012**, 7, e34451 | 3.7 | 113 |

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| 152 | Loss of imprinting of IGF2: a common epigenetic modifier of intestinal tumor risk. *Cancer Research*, **2005**, 65, 11236-40 | 10.1 | 111 |
| 151 | Loss of imprinting of insulin growth factor II gene: a potential heritable biomarker for colon neoplasia predisposition. *Gastroenterology*, **2004**, 126, 964-70 | 13.3 | 110 |
| 150 | Association of DNA Methylation Differences With Schizophrenia in an Epigenome-Wide Association Study. *JAMA Psychiatry*, **2016**, 73, 506-14 | 14.5 | 108 |
| 149 | A genome-wide screen for normally methylated human CpG islands that can identify novel imprinted genes. *Genome Research*, **2002**, 12, 543-54 | 9.7 | 104 |
| 148 | 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 | 5.1 | 102 |
| 147 | Loss of imprinting in hepatoblastoma. *Cancer Research*, **1995**, 55, 1836-8 | 10.1 | 100 |
| 146 | Large-scale hypomethylated blocks associated with Epstein-Barr virus-induced B-cell immortalization. *Genome Research*, **2014**, 24, 177-84 | 9.7 | 99 |
| 145 | Hot-stop PCR: a simple and general assay for linear quantitation of allele ratios. *Nature Genetics*, **2000**, 25, 375-6 | 36.3 | 99 |
| 144 | Sequence and comparative analysis of the mouse 1-megabase region orthologous to the human 11p15 imprinted domain. *Genome Research*, **2000**, 10, 1697-710 | 9.7 | 94 |
| 143 | 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, 12456-60 | 11.5 | 93 |
| 142 | Epigenomics reveals a functional genome anatomy and a new approach to common disease. *Nature Biotechnology*, **2010**, 28, 1049-52 | 44.5 | 92 |
| 141 | Paternal sperm DNA methylation associated with early signs of autism risk in an autism-enriched cohort. *International Journal of Epidemiology*, **2015**, 44, 1199-210 | 7.8 | 91 |
| 140 | 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 | 10.1 | 91 |
| 139 | Enhanced sensitivity to IGF-II signaling links loss of imprinting of IGF2 to increased cell proliferation and tumor risk. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 20926-31 | 11.5 | 90 |
| 138 | Epigenetic specificity of loss of imprinting of the IGF2 gene in Wilms tumors. *Journal of the National Cancer Institute*, **2007**, 99, 1270-3 | 9.7 | 89 |
| 137 | Imprinting of a genomic domain of 11p15 and loss of imprinting in cancer: an introduction. *Cancer Research*, **1999**, 59, 1743s-1746s | 10.1 | 87 |
| 136 | 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 | 5.3 | 85 |
| 135 | Age and sun exposure-related widespread genomic blocks of hypomethylation in nonmalignant skin. *Genome Biology*, **2015**, 16, 80 | 18.3 | 83 |

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|---|---|---|---|
| 134 | DNA methylation as a mediator of HLA-DRB1*15:01 and a protective variant in multiple sclerosis. *Nature Communications*, **2018**, 9, 2397 | 17.4 | 81 |
| 133 | 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, 1149-59 | 5.6 | 81 |
| 132 | Butyrophenone influences on the opiate receptor. *European Journal of Pharmacology*, **1976**, 36, 231-5 | 5.3 | 80 |
| 131 | Meta-analysis of epigenome-wide association studies in neonates reveals widespread differential DNA methylation associated with birthweight. *Nature Communications*, **2019**, 10, 1893 | 17.4 | 79 |
| 130 | An LSC epigenetic signature is largely mutation independent and implicates the HOXA cluster in AML pathogenesis. *Nature Communications*, **2015**, 6, 8489 | 17.4 | 79 |
| 129 | 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 | 4.3 | 79 |
| 128 | Measuring cell-type specific differential methylation in human brain tissue. *Genome Biology*, **2013**, 14, R94 | 18.3 | 78 |
| 127 | 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, 16759-64 | 11.5 | 78 |
| 126 | DIPG-12. TARGETING EPIGENETIC MODIFIERS TO INDUCE IMMUNE SIGNALING IN DIPG. *Neuro-Oncology*, **2020**, 22, iii289-iii289 | 1 | 78 |
| 125 | GeMes, clusters of DNA methylation under genetic control, can inform genetic and epigenetic analysis of disease. *American Journal of Human Genetics*, **2014**, 94, 485-95 | 11 | 76 |
| 124 | Mouse-human experimental epigenetic analysis unmasks dietary targets and genetic liability for diabetic phenotypes. *Cell Metabolism*, **2015**, 21, 138-49 | 24.6 | 76 |
| 123 | Presence of an epigenetic signature of prenatal cigarette smoke exposure in childhood. *Environmental Research*, **2016**, 144, 139-148 | 7.9 | 75 |
| 122 | Significance analysis and statistical dissection of variably methylated regions. *Biostatistics*, **2012**, 13, 166-78 | 3.7 | 75 |
| 121 | Loss of Imprinting in Disease Progression in Chronic Myelogenous Leukemia. *Blood*, **1998**, 91, 3144-3147 | 2.2 | 71 |
| 120 | BAT3 and SET1A form a complex with CTCFL/BORIS to modulate H3K4 histone dimethylation and gene expression. *Molecular and Cellular Biology*, **2008**, 28, 6720-9 | 4.8 | 68 |
| 119 | Neuronal brain-region-specific DNA methylation and chromatin accessibility are associated with neuropsychiatric trait heritability. *Nature Neuroscience*, **2019**, 22, 307-316 | 25.5 | 68 |
| 118 | A selective phenelzine analogue inhibitor of histone demethylase LSD1. *ACS Chemical Biology*, **2014**, 9, 1284-93 | 4.9 | 66 |
| 117 | Blood Leukocyte DNA Methylation Predicts Risk of Future Myocardial Infarction and Coronary Heart Disease. *Circulation*, **2019**, 140, 645-657 | 16.7 | 65 |

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|---|---|---|---|
| 116 | Higher order chromatin organization in cancer. *Seminars in Cancer Biology*, **2013**, 23, 109-15 | 12.7 | 65 |
| 115 | Potential energy landscapes identify the information-theoretic nature of the epigenome. *Nature Genetics*, **2017**, 49, 719-729 | 36.3 | 64 |
| 114 | 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, 2131-6 | 15.9 | 63 |
| 113 | Epigenetics at the Crossroads of Genes and the Environment. *JAMA - Journal of the American Medical Association*, **2015**, 314, 1129-30 | 27.4 | 62 |
| 112 | Accurate genome-scale percentage DNA methylation estimates from microarray data. *Biostatistics*, **2011**, 12, 197-210 | 3.7 | 62 |
| 111 | Two novel genes in the center of the 11p15 imprinted domain escape genomic imprinting. *Human Molecular Genetics*, **1999**, 8, 683-90 | 5.6 | 62 |
| 110 | Whole-genome analysis of the methylome and hydroxymethylome in normal and malignant lung and liver. *Genome Research*, **2016**, 26, 1730-1741 | 9.7 | 61 |
| 109 | DNA methylation shows genome-wide association of NFIX, RAPGEF2 and MSRB3 with gestational age at birth. *International Journal of Epidemiology*, **2012**, 41, 188-99 | 7.8 | 60 |
| 108 | Genetics and epigenetics--nature's pen-and-pencil set. *New England Journal of Medicine*, **2007**, 356, 731-3 | 59.2 | 60 |
| 107 | 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, 10599-604 | 11.5 | 59 |
| 106 | SNP-specific array-based allele-specific expression analysis. *Genome Research*, **2008**, 18, 771-9 | 9.7 | 56 |
| 105 | Nanoelectromechanics of methylated DNA in a synthetic nanopore. *Biophysical Journal*, **2009**, 96, L32-4 | 2.9 | 54 |
| 104 | The commonality of plasticity underlying multipotent tumor cells and embryonic stem cells. *Journal of Cellular Biochemistry*, **2007**, 101, 908-17 | 4.7 | 51 |
| 103 | Nanopore sequencing in microgravity. *Npj Microgravity*, **2016**, 2, 16035 | 5.3 | 50 |
| 102 | Prenatal mercury concentration is associated with changes in DNA methylation at TCEANC2 in newborns. *International Journal of Epidemiology*, **2015**, 44, 1249-62 | 7.8 | 48 |
| 101 | Case-control meta-analysis of blood DNA methylation and autism spectrum disorder. *Molecular Autism*, **2018**, 9, 40 | 6.5 | 48 |
| 100 | A species-generalized probabilistic model-based definition of CpG islands. *Mammalian Genome*, **2009**, 20, 674-80 | 3.2 | 47 |
| 99 | Targeted regulation of imprinted genes by synthetic zinc-finger transcription factors. *Gene Therapy*, **2003**, 10, 513-22 | 4 | 47 |

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|---|---|---|---|
| 98 | Alterations in DNA methylation in human colon neoplasia. *Journal of Surgical Oncology*, **1987**, 3, 149-51 | | 47 |
| 97 | Detailed DNA methylation profiles of the E-cadherin promoter in the NCI-60 cancer cells. *Molecular Cancer Therapeutics*, **2007**, 6, 391-403 | 6.1 | 46 |
| 96 | Genomic imprinting of a human apoptosis gene homologue, TSSC3. *Cancer Research*, **1998**, 58, 1052-6 | 10.1 | 46 |
| 95 | Loss of allelic heterozygosity at a second locus on chromosome 11 in sporadic Wilms' tumor cells. *Molecular and Cellular Biology*, **1989**, 9, 1799-1803 | 4.8 | 45 |
| 94 | Reduced expression of the cyclin-dependent kinase inhibitor gene p57KIP2 in Wilms' tumor. *Cancer Research*, **1996**, 56, 5723-7 | 10.1 | 45 |
| 93 | Cross-tissue integration of genetic and epigenetic data offers insight into autism spectrum disorder. *Nature Communications*, **2017**, 8, 1011 | 17.4 | 44 |
| 92 | Genomic imprinting, DNA methylation, and cancer. *Journal of the National Cancer Institute*, **1994**, 86, 753-9 | 9.7 | 44 |
| 91 | DNA methylation, genomic imprinting and cancer. *Current Topics in Microbiology and Immunology*, **2000**, 249, 87-99 | 3.3 | 43 |
| 90 | An epigenetic approach to cancer etiology. *Cancer Journal (Sudbury, Mass )*, **2007**, 13, 70-4 | 2.2 | 42 |
| 89 | Smoking induces DNA methylation changes in Multiple Sclerosis patients with exposure-response relationship. *Scientific Reports*, **2017**, 7, 14589 | 4.9 | 41 |
| 88 | Epigenetic stochasticity, nuclear structure and cancer: the implications for medicine. *Journal of Internal Medicine*, **2014**, 276, 5-11 | 10.8 | 40 |
| 87 | 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, 1743-8 | 5.6 | 38 |
| 86 | Cancer epigenetics is no Mickey Mouse. *Cancer Cell*, **2005**, 8, 267-8 | 24.3 | 37 |
| 85 | 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, 155-61 | 5 | 37 |
| 84 | Disruption of a novel imprinted zinc-finger gene, ZNF215, in Beckwith-Wiedemann syndrome. *American Journal of Human Genetics*, **2000**, 66, 1473-84 | 11 | 37 |
| 83 | 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 | 5.7 | 36 |
| 82 | Mutant WT1 is associated with DNA hypermethylation of PRC2 targets in AML and responds to EZH2 inhibition. *Blood*, **2015**, 125, 316-26 | 2.2 | 35 |
| 81 | "Gap hunting" to characterize clustered probe signals in Illumina methylation array data. *Epigenetics and Chromatin*, **2016**, 9, 56 | 5.8 | 34 |

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| 80 | CTCFL/BORIS is a methylation-independent DNA-binding protein that preferentially binds to the paternal H19 differentially methylated region. *Cancer Research*, **2008**, 68, 5546-51 | 10.1 | 34 |
| 79 | 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, 187-91 | 2.5 | 34 |
| 78 | Euchromatin islands in large heterochromatin domains are enriched for CTCF binding and differentially DNA-methylated regions. *BMC Genomics*, **2012**, 13, 566 | 4.5 | 33 |
| 77 | DNA methyltransferase 1 and 3B activate BAG-1 expression via recruitment of CTCFL/BORIS and modulation of promoter histone methylation. *Cancer Research*, **2008**, 68, 2726-35 | 10.1 | 33 |
| 76 | DNA methylation is stable during replication and cell cycle arrest. *Scientific Reports*, **2015**, 5, 17911 | 4.9 | 32 |
| 75 | Epigenetic effects in eukaryotic gene expression. *Genesis*, **1994**, 15, 458-62 | | 32 |
| 74 | Epigenetic marks of prenatal air pollution exposure found in multiple tissues relevant for child health. *Environment International*, **2019**, 126, 363-376 | 12.9 | 31 |
| 73 | A new link between epigenetic progenitor lesions in cancer and the dynamics of signal transduction. *Cell Cycle*, **2009**, 8, 383-90 | 4.7 | 31 |
| 72 | Strain-dependent developmental relaxation of imprinting of an endogenous mouse gene, Kvlqt1. *Genomics*, **1998**, 53, 395-9 | 4.3 | 31 |
| 71 | Children with idiopathic hemihypertrophy and beckwith-wiedemann syndrome have different constitutional epigenotypes associated with wilms tumor. *American Journal of Human Genetics*, **2005**, 77, 887-91 | 11 | 29 |
| 70 | Parent-of-origin effects in autism identified through genome-wide linkage analysis of 16,000 SNPs. *PLoS ONE*, **2010**, 5, e12513 | 3.7 | 28 |
| 69 | An integrated physical map of 210 markers assigned to the short arm of human chromosome 11. *Genomics*, **1994**, 21, 538-50 | 4.3 | 28 |
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