Andrew Feinberg

List of Publications by Year in Descending Order

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	Abstract IA009: Cancer is a disease of epigenetic stochasticity. *Cancer Research*, **2022**, 82, IA009-IA009	10.1	
240	Estimating DNA methylation potential energy landscapes from nanopore sequencing data. *Scientific Reports*, **2021**, 11, 21619	4.9	1
239	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	6.1	1
238	Converging genetic and epigenetic drivers of paediatric acute lymphoblastic leukaemia identified by an information-theoretic analysis. *Nature Biomedical Engineering*, **2021**, 5, 360-376	19	3
237	Human brain region-specific variably methylated regions are enriched for heritability of distinct neuropsychiatric traits. *Genome Biology*, **2021**, 22, 116	18.3	1
236	Statistical mechanics meets single-cell biology. *Nature Reviews Genetics*, **2021**, 22, 459-476	30.1	11
235	Independent Methylome-Wide Association Studies of Schizophrenia Detect Consistent Case-Control Differences. *Schizophrenia Bulletin*, **2020**, 46, 319-327	1.3	3
234	A Dysregulated DNA Methylation Landscape Linked to Gene Expression in MLL-Rearranged AML. *Epigenetics*, **2020**, 15, 841-858	5.7	7
233	DIPG-12. TARGETING EPIGENETIC MODIFIERS TO INDUCE IMMUNE SIGNALING IN DIPG. *Neuro-Oncology*, **2020**, 22, iii289-iii289	1	78
232	Detection of haplotype-dependent allele-specific DNA methylation in WGBS data. *Nature Communications*, **2020**, 11, 5238	17.4	6
231	Ranking genomic features using an information-theoretic measure of epigenetic discordance. *BMC Bioinformatics*, **2019**, 20, 175	3.6	7
230	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
229	Epigenetic marks of prenatal air pollution exposure found in multiple tissues relevant for child health. *Environment International*, **2019**, 126, 363-376	12.9	31
228	The NASA Twins Study: A multidimensional analysis of a year-long human spaceflight. *Science*, **2019**, 364,	33.3	300
227	Analyzing whole genome bisulfite sequencing data from highly divergent genotypes. *Nucleic Acids Research*, **2019**, 47, e117	20.1	8
226	Blood Leukocyte DNA Methylation Predicts Risk of Future Myocardial Infarction and Coronary Heart Disease. *Circulation*, **2019**, 140, 645-657	16.7	65
225	Neuronal brain-region-specific DNA methylation and chromatin accessibility are associated with neuropsychiatric trait heritability. *Nature Neuroscience*, **2019**, 22, 307-316	25.5	68

224	The Key Role of Epigenetics in Human Disease Prevention and Mitigation. *New England Journal of Medicine*, **2018**, 378, 1323-1334	59.2	290
223	An information-theoretic approach to the modeling and analysis of whole-genome bisulfite sequencing data. *BMC Bioinformatics*, **2018**, 19, 87	3.6	14
222	Arioc: GPU-accelerated alignment of short bisulfite-treated reads. *Bioinformatics*, **2018**, 34, 2673-2675	7.2	11
221	Case-control meta-analysis of blood DNA methylation and autism spectrum disorder. *Molecular Autism*, **2018**, 9, 40	6.5	48
220	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
219	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	17.6	7
218	Epigenomic reprogramming during pancreatic cancer progression links anabolic glucose metabolism to distant metastasis. *Nature Genetics*, **2017**, 49, 367-376	36.3	250
217	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
216	Potential energy landscapes identify the information-theoretic nature of the epigenome. *Nature Genetics*, **2017**, 49, 719-729	36.3	64
215	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
214	Cross-tissue integration of genetic and epigenetic data offers insight into autism spectrum disorder. *Nature Communications*, **2017**, 8, 1011	17.4	44
213	Smoking induces DNA methylation changes in Multiple Sclerosis patients with exposure-response relationship. *Scientific Reports*, **2017**, 7, 14589	4.9	41
212	Nanopore sequencing in microgravity. *Npj Microgravity*, **2016**, 2, 16035	5.3	50
211	Evaluation of techniques for performing cellular isolation and preservation during microgravity conditions. *Npj Microgravity*, **2016**, 2, 16025	5.3	7
210	"Gap hunting" to characterize clustered probe signals in Illumina methylation array data. *Epigenetics and Chromatin*, **2016**, 9, 56	5.8	34
209	Epigenetic modulators, modifiers and mediators in cancer aetiology and progression. *Nature Reviews Genetics*, **2016**, 17, 284-99	30.1	490
208	Presence of an epigenetic signature of prenatal cigarette smoke exposure in childhood. *Environmental Research*, **2016**, 144, 139-148	7.9	75
207	DNA methylation-based measures of biological age: meta-analysis predicting time to death. *Aging*, **2016**, 8, 1844-1865	5.6	531

206	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. *Genome Biology*, **2016**, 17, 255	18.3	171
205	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	14.4	20
204	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
203	DNA methylation of cord blood cell types: Applications for mixed cell birth studies. *Epigenetics*, **2016**, 11, 354-62	5.7	196
202	Association of DNA Methylation Differences With Schizophrenia in an Epigenome-Wide Association Study. *JAMA Psychiatry*, **2016**, 73, 506-14	14.5	108
201	Whole-genome analysis of the methylome and hydroxymethylome in normal and malignant lung and liver. *Genome Research*, **2016**, 26, 1730-1741	9.7	61
200	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
199	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
198	Age and sun exposure-related widespread genomic blocks of hypomethylation in nonmalignant skin. *Genome Biology*, **2015**, 16, 80	18.3	83
197	DNA methylation age of blood predicts all-cause mortality in later life. *Genome Biology*, **2015**, 16, 25	18.3	670
196	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
195	An LSC epigenetic signature is largely mutation independent and implicates the HOXA cluster in AML pathogenesis. *Nature Communications*, **2015**, 6, 8489	17.4	79
194	Epigenetics at the Crossroads of Genes and the Environment. *JAMA - Journal of the American Medical Association*, **2015**, 314, 1129-30	27.4	62
193	A comparison of non-integrating reprogramming methods. *Nature Biotechnology*, **2015**, 33, 58-63	44.5	326
192	DNA methylation is stable during replication and cell cycle arrest. *Scientific Reports*, **2015**, 5, 17911	4.9	32
191	Mouse-human experimental epigenetic analysis unmasks dietary targets and genetic liability for diabetic phenotypes. *Cell Metabolism*, **2015**, 21, 138-49	24.6	76
190	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
189	Epigenetic stochasticity, nuclear structure and cancer: the implications for medicine. *Journal of Internal Medicine*, **2014**, 276, 5-11	10.8	40

188	Minfi: a flexible and comprehensive Bioconductor package for the analysis of Infinium DNA methylation microarrays. *Bioinformatics*, **2014**, 30, 1363-9	7.2	1941
187	Large hypomethylated blocks as a universal defining epigenetic alteration in human solid tumors. *Genome Medicine*, **2014**, 6, 61	14.4	120
186	DNA methylation in cancer: three decades of discovery. *Genome Medicine*, **2014**, 6, 36	14.4	12
185	A selective phenelzine analogue inhibitor of histone demethylase LSD1. *ACS Chemical Biology*, **2014**, 9, 1284-93	4.9	66
184	Large-scale hypomethylated blocks associated with Epstein-Barr virus-induced B-cell immortalization. *Genome Research*, **2014**, 24, 177-84	9.7	99
183	The nucleolus gets the silent treatment. *Cell Stem Cell*, **2014**, 15, 675-6	18	5
182	Common DNA methylation alterations in multiple brain regions in autism. *Molecular Psychiatry*, **2014**, 19, 862-71	15.1	219
181	Mutation in Wilms' Tumor 1 Induces DNA Hypermethylation of PRC2 Targets, Blocks Myelomonocytic Differentiation, and Defines a Novel Subtype of AML Responsive to EZH2 Inhibition. *Blood*, **2014**, 124, 780-780	2.2	
180	Epigenetic Signature of Leukemia Stem Cells Defines Subgroups Associated with Clinical Outcome and Cell of Origin in AML. *Blood*, **2014**, 124, 2147-2147	2.2	
179	Higher order chromatin organization in cancer. *Seminars in Cancer Biology*, **2013**, 23, 109-15	12.7	65
178	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
177	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
176	Measuring cell-type specific differential methylation in human brain tissue. *Genome Biology*, **2013**, 14, R94	18.3	78
175	A third-generation method reveals cell lineage ancestry. *Nature Methods*, **2013**, 10, 117-8	21.6	1
174	Increase in Science Research Commitment in a Didactic and Laboratory-Based Program Targeted to Gifted Minority High-School Students. *Roeper Review*, **2013**, 35, 18-26	1.4	12
173	The epigenetic basis of common human disease. *Transactions of the American Clinical and Climatological Association*, **2013**, 124, 84-93	0.9	10
172	Bump hunting to identify differentially methylated regions in epigenetic epidemiology studies. *International Journal of Epidemiology*, **2012**, 41, 200-9	7.8	430
171	Regulated noise in the epigenetic landscape of development and disease. *Cell*, **2012**, 148, 1123-31	56.2	166

170	Euchromatin islands in large heterochromatin domains are enriched for CTCF binding and differentially DNA-methylated regions. *BMC Genomics*, **2012**, 13, 566	4.5	33
169	Reversible switching between epigenetic states in honeybee behavioral subcastes. *Nature Neuroscience*, **2012**, 15, 1371-3	25.5	237
168	Stem cell differentiation as a renewal-reward process: predictions and validation in the colonic crypt. *Advances in Experimental Medicine and Biology*, **2012**, 736, 199-209	3.6	
167	Significance analysis and statistical dissection of variably methylated regions. *Biostatistics*, **2012**, 13, 166-78	3.7	75
166	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
165	Genome-wide DNA methylation scan in major depressive disorder. *PLoS ONE*, **2012**, 7, e34451	3.7	113
164	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
163	Increased methylation variation in epigenetic domains across cancer types. *Nature Genetics*, **2011**, 43, 768-75	36.3	825
162	Genome-scale epigenetic reprogramming during epithelial-to-mesenchymal transition. *Nature Structural and Molecular Biology*, **2011**, 18, 867-74	17.6	297
161	Accurate genome-scale percentage DNA methylation estimates from microarray data. *Biostatistics*, **2011**, 12, 197-210	3.7	62
160	Adaptation of the CHARM DNA methylation platform for the rat genome reveals novel brain region-specific differences. *Epigenetics*, **2011**, 6, 1378-90	5.7	17
159	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
158	Epigenetic memory in induced pluripotent stem cells. *Nature*, **2010**, 467, 285-90	50.4	1729
157	Comprehensive methylome map of lineage commitment from haematopoietic progenitors. *Nature*, **2010**, 467, 338-42	50.4	484
156	Epigenomics reveals a functional genome anatomy and a new approach to common disease. *Nature Biotechnology*, **2010**, 28, 1049-52	44.5	92
155	Reply to Reassessing the abundance of H3K9me2 chromatin domains in embryonic stem cells *Nature Genetics*, **2010**, 42, 5-6	36.3	22
154	Parent-of-origin effects in autism identified through genome-wide linkage analysis of 16,000 SNPs. *PLoS ONE*, **2010**, 5, e12513	3.7	28
153	Personalized epigenomic signatures that are stable over time and covary with body mass index. *Science Translational Medicine*, **2010**, 2, 49ra67	17.5	254

152	Redefining CpG islands using hidden Markov models. *Biostatistics*, **2010**, 11, 499-514	3.7	122
151	Comprehensive high-throughput arrays for relative methylation (CHARM). *Current Protocols in Human Genetics*, **2010**, Chapter 20, Unit 20.1.1-19	3.2	23
150	Addition of H19 'loss of methylation testing' for Beckwith-Wiedemann syndrome (BWS) increases the diagnostic yield. *Journal of Molecular Diagnostics*, **2010**, 12, 576-88	5.1	9
149	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
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	A new link between epigenetic progenitor lesions in cancer and the dynamics of signal transduction. *Cell Cycle*, **2009**, 8, 383-90	4.7	31
146	Temporal stability and age-related prevalence of loss of imprinting of the insulin-like growth factor-2 gene. *Epigenetics*, **2009**, 4, 114-8	5.7	19
145	A species-generalized probabilistic model-based definition of CpG islands. *Mammalian Genome*, **2009**, 20, 674-80	3.2	47
144	Large histone H3 lysine 9 dimethylated chromatin blocks distinguish differentiated from embryonic stem cells. *Nature Genetics*, **2009**, 41, 246-50	36.3	469
143	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
142	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
141	Nanoelectromechanics of methylated DNA in a synthetic nanopore. *Biophysical Journal*, **2009**, 96, L32-4	2.9	54
140	Cancer Epigenomics **2009**, 385-395		1
139	Epigenetic silencing of tumour suppressor gene p15 by its antisense RNA. *Nature*, **2008**, 451, 202-6	50.4	710
138	Moving AHEAD with an international human epigenome project. *Nature*, **2008**, 454, 711-5	50.4	158
137	Epigenetics at the epicenter of modern medicine. *JAMA - Journal of the American Medical Association*, **2008**, 299, 1345-50	27.4	275
136	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
135	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

134	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
133	SNP-specific array-based allele-specific expression analysis. *Genome Research*, **2008**, 18, 771-9	9.7	56
132	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
131	Comprehensive high-throughput arrays for relative methylation (CHARM). *Genome Research*, **2008**, 18, 780-90	9.7	350
130	Gene-based SNP mapping of a psychotic bipolar affective disorder linkage region on 22q12.3: association with HMG2L1 and TOM1. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2008**, 147B, 59-67	3.5	15
129	Overlapping euchromatin/heterochromatin- associated marks are enriched in imprinted gene regions and predict allele-specific modification. *Genome Research*, **2008**, 18, 1806-13	9.7	27
128	Genetics and epigenetics--nature's pen-and-pencil set. *New England Journal of Medicine*, **2007**, 356, 731-3	59.2	60
127	The commonality of plasticity underlying multipotent tumor cells and embryonic stem cells. *Journal of Cellular Biochemistry*, **2007**, 101, 908-17	4.7	51
126	Phenotypic plasticity and the epigenetics of human disease. *Nature*, **2007**, 447, 433-40	50.4	1288
125	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
124	An X chromosome gene, WTX, is commonly inactivated in Wilms tumor. *Science*, **2007**, 315, 642-5	33.3	288
123	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
122	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
121	An epigenetic approach to cancer etiology. *Cancer Journal (Sudbury, Mass)*, **2007**, 13, 70-4	2.2	42
120	DNA methylation signatures within the human brain. *American Journal of Human Genetics*, **2007**, 81, 1304-15	11	228
119	The emerging science of epigenomics. *Human Molecular Genetics*, **2006**, 15 Spec No 1, R95-101	5.6	238
118	The epigenetic progenitor origin of human cancer. *Nature Reviews Genetics*, **2006**, 7, 21-33	30.1	1417
117	Loss of imprinting of IGF2: a common epigenetic modifier of intestinal tumor risk. *Cancer Research*, **2005**, 65, 11236-40	10.1	111

116	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
115	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
114	Loss of imprinting of Igf2 alters intestinal maturation and tumorigenesis in mice. *Science*, **2005**, 307, 1976-8	33.3	272
113	Cancer epigenetics is no Mickey Mouse. *Cancer Cell*, **2005**, 8, 267-8	24.3	37
112	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
111	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
110	Inheritance pattern of Beckwith-Wiedemann syndrome is heterogeneous in 291 families with an affected proband. *American Journal of Medical Genetics, Part A*, **2005**, 137, 16-21	2.5	8
109	A genetic approach to cancer epigenetics. *Cold Spring Harbor Symposia on Quantitative Biology*, **2005**, 70, 335-41	3.9	23
108	Poly(ADP-ribosyl)ation regulates CTCF-dependent chromatin insulation. *Nature Genetics*, **2004**, 36, 1105-10	36.3	261
107	The history of cancer epigenetics. *Nature Reviews Cancer*, **2004**, 4, 143-53	31.3	1803
106	An integrated epigenetic and genetic approach to common human disease. *Trends in Genetics*, **2004** , 20, 350-8	8.5	367
105	The epigenetics of cancer etiology. *Seminars in Cancer Biology*, **2004**, 14, 427-32	12.7	272
104	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
103	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
102	Epigenetics and assisted reproductive technology: a call for investigation. *American Journal of Human Genetics*, **2004**, 74, 599-609	11	269
101	Microdeletion of LIT1 in familial Beckwith-Wiedemann syndrome. *American Journal of Human Genetics*, **2004**, 75, 844-9	11	113
100	The new field of epigenomics: implications for cancer and other common disease research. *Cold Spring Harbor Symposia on Quantitative Biology*, **2004**, 69, 447-56	3.9	21
99	Wilms' tumor as a model for cancer biology. *Methods in Molecular Biology*, **2003**, 222, 239-48	1.4	7

98	Lack of parental origin specificity of altered alleles at 11p15 in testicular germ cell tumors. *Cancer Genetics and Cytogenetics*, **2003**, 147, 1-8		4
97	Targeted regulation of imprinted genes by synthetic zinc-finger transcription factors. *Gene Therapy*, **2003**, 10, 513-22	4	47
96	Loss of IGF2 imprinting: a potential marker of colorectal cancer risk. *Science*, **2003**, 299, 1753-5	33.3	634
95	Epigenetic variability and the evolution of human cancer. *Advances in Cancer Research*, **2003**, 88, 145-68	5.9	24
94	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
93	DNA methylation and genomic imprinting: insights from cancer into epigenetic mechanisms. *Seminars in Cancer Biology*, **2002**, 12, 389-98	12.7	171
92	DNMT1 and DNMT3b cooperate to silence genes in human cancer cells. *Nature*, **2002**, 416, 552-6	50.4	1008
91	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
90	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
89	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
88	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
87	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
86	A Genome-Wide Screen for Normally Methylated Human CpG Islands That Can Identify Novel Imprinted Genes. *Genome Research*, **2002**, 12, 543-554	9.7	3
85	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
84	Loss of imprinting in colorectal cancer linked to hypomethylation of H19 and IGF2. *Cancer Research*, **2002**, 62, 6442-6	10.1	282
83	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
82	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
81	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

80	Hot-stop PCR: a simple and general assay for linear quantitation of allele ratios. *Nature Genetics*, **2000**, 25, 375-6	36.3	99
79	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
78	Cloning and chromosomal localization of the human BARX2 homeobox protein gene. *Gene*, **2000**, 250, 171-80	3.8	21
77	Disruption of a novel imprinted zinc-finger gene, ZNF215, in Beckwith-Wiedemann syndrome. *American Journal of Human Genetics*, **2000**, 66, 1473-84	11	37
76	Targeted disruption of the Kvlqt1 gene causes deafness and gastric hyperplasia in mice. *Journal of Clinical Investigation*, **2000**, 106, 1447-55	15.9	234
75	The two-domain hypothesis in Beckwith-Wiedemann syndrome. *Journal of Clinical Investigation*, **2000**, 106, 739-40	15.9	20
74	DNA methylation, genomic imprinting and cancer. *Current Topics in Microbiology and Immunology*, **2000**, 249, 87-99	3.3	43
73	Two novel genes in the center of the 11p15 imprinted domain escape genomic imprinting. *Human Molecular Genetics*, **1999**, 8, 683-90	5.6	62
72	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*, **1999**, 96, 5203-8	11.5	315
71	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
70	Imprinting of a genomic domain of 11p15 and loss of imprinting in cancer: an introduction. *Cancer Research*, **1999**, 59, 1743s-1746s	10.1	87
69	Mosaic allelic insulin-like growth factor 2 expression patterns reveal a link between Wilms' tumorigenesis and epigenetic heterogeneity. *Cancer Research*, **1999**, 59, 3889-92	10.1	23
68	Loss of imprinting in normal tissue of colorectal cancer patients with microsatellite instability. *Nature Medicine*, **1998**, 4, 1276-80	50.5	249
67	Identification and mapping of human histone acetylation modifier gene homologues. *Genomics*, **1998**, 51, 262-9	4.3	16
66	Strain-dependent developmental relaxation of imprinting of an endogenous mouse gene, Kvlqt1. *Genomics*, **1998**, 53, 395-9	4.3	31
65	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
64	Loss of Imprinting in Disease Progression in Chronic Myelogenous Leukemia. *Blood*, **1998**, 91, 3144-3147	2.2	71
63	Loss of Imprinting in Disease Progression in Chronic Myelogenous Leukemia. *Blood*, **1998**, 91, 3144-3147	2.2	6

62	Beckwith-Wiedemann Syndrome **1998**, 1047-1052		1
61	Genomic imprinting of a human apoptosis gene homologue, TSSC3. *Cancer Research*, **1998**, 58, 1052-6	10.1	46
60	Somatic mutation of TSSC5, a novel imprinted gene from human chromosome 11p15.5. *Cancer Research*, **1998**, 58, 4155-9	10.1	28
59	Low frequency of p57KIP2 mutation in Beckwith-Wiedemann syndrome. *American Journal of Human Genetics*, **1997**, 61, 304-9	11	138
58	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
57	Construction of chicken x human microcell hybrids for human gene targeting. *Cytogenetic and Genome Research*, **1997**, 76, 72-6	1.9	15
56	Human KVLQT1 gene shows tissue-specific imprinting and encompasses Beckwith-Wiedemann syndrome chromosomal rearrangements. *Nature Genetics*, **1997**, 15, 181-5	36.3	335
55	Reversal of loss of imprinting in tumor cells by 5-aza-2'-deoxycytidine. *Cancer Research*, **1997**, 57, 48-50	10.1	25
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