Wolf Reik

List of Publications by Year
in descending order

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272	64,149	668	871
papers	citations	122 h-index	243 g-index

309	309	309	48588
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Evolution and Functions of Long Noncoding RNAs. Cell, 2009, 136, 629-641.	13.5	4,480
2	Epigenetic Reprogramming in Mammalian Development. Science, 2001, 293, 1089-1093.	6.0	2,706
3	Genomic imprinting: parental influence on the genome. Nature Reviews Genetics, 2001, 2, 21-32.	7.7	2,120
4	Stability and flexibility of epigenetic gene regulation in mammalian development. Nature, 2007, 447, 425-432.	13.7	1,728
5	The Human Cell Atlas. ELife, 2017, 6, .	2.8	1,547
6	Epigenetic reprogramming in mammals. Human Molecular Genetics, 2005, 14, R47-R58.	1.4	1,140
7	Dynamic Reprogramming of DNA Methylation in the Early Mouse Embryo. Developmental Biology, 2002, 241, 172-182.	0.9	1,099
8	Epigenetic reprogramming in mouse primordial germ cells. Mechanisms of Development, 2002, 117, 15-23.	1.7	1,091
9	Epigenetic Reprogramming in Plant and Animal Development. Science, 2010, 330, 622-627.	6.0	1,042
10	Dynamic regulation of 5-hydroxymethylcytosine in mouse ES cells and during differentiation. Nature, 2011, 473, 398-402.	13.7	1,035
11	Placental-specific IGF-II is a major modulator of placental and fetal growth. Nature, 2002, 417, 945-948.	13.7	961
12	Single-cell genome-wide bisulfite sequencing for assessing epigenetic heterogeneity. Nature Methods, 2014, 11, 817-820.	9.0	954
13	Active genes dynamically colocalize to shared sites of ongoing transcription. Nature Genetics, 2004, 36, 1065-1071.	9.4	942
14	Active demethylation of the paternal genome in the mouse zygote. Current Biology, 2000, 10, 475-478.	1.8	935
15	Conservation of methylation reprogramming in mammalian development: Aberrant reprogramming in cloned embryos. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 13734-13738.	3.3	894
16	Quantitative Sequencing of 5-Methylcytosine and 5-Hydroxymethylcytosine at Single-Base Resolution. Science, 2012, 336, 934-937.	6.0	850
17	The Dynamics of Genome-wide DNA Methylation Reprogramming in Mouse Primordial Germ Cells. Molecular Cell, 2012, 48, 849-862.	4.5	837
18	Resetting Transcription Factor Control Circuitry toward Ground-State Pluripotency in Human. Cell, 2014, 158, 1254-1269.	13.5	784

#	Article	IF	Citations
19	Genome-wide erasure of DNA methylation in mouse primordial germ cells is affected by AID deficiency. Nature, 2010, 463, 1101-1105.	13.7	777
20	The H19 lincRNA is a developmental reservoir of miR-675 that suppresses growth and Igf1r. Nature Cell Biology, 2012, 14, 659-665.	4.6	747
21	5-Hydroxymethylcytosine in the mammalian zygote is linked with epigenetic reprogramming. Nature Communications, 2011, 2, 241.	5.8	674
22	Uncovering the role of 5-hydroxymethylcytosine in the epigenome. Nature Reviews Genetics, 2012, 13, 7-13.	7.7	658
23	A single-cell molecular map of mouse gastrulation and early organogenesis. Nature, 2019, 566, 490-495.	13.7	658
24	Parallel single-cell sequencing links transcriptional and epigenetic heterogeneity. Nature Methods, 2016, 13, 229-232.	9.0	602
25	Resistance of IAPs to methylation reprogramming may provide a mechanism for epigenetic inheritance in the mouse. Genesis, 2003, 35, 88-93.	0.8	599
26	DNA methylation aging clocks: challenges and recommendations. Genome Biology, 2019, 20, 249.	3.8	552
27	In utero undernourishment perturbs the adult sperm methylome and intergenerational metabolism. Science, 2014, 345, 1255903.	6.0	535
28	Culture of Preimplantation Mouse Embryos Affects Fetal Development and the Expression of Imprinted Genes1. Biology of Reproduction, 2001, 64, 918-926.	1.2	532
29	Beckwith-Wiedemann syndrome and assisted reproduction technology (ART). Journal of Medical Genetics, 2003, 40, 62-64.	1.5	524
30	scNMT-seq enables joint profiling of chromatin accessibility DNA methylation and transcription in single cells. Nature Communications, 2018, 9, 781.	5.8	513
31	Epigenetic Marking Correlates with Developmental Potential in Cloned Bovine Preimplantation Embryos. Current Biology, 2003, 13, 1116-1121.	1.8	491
32	Interaction between differentially methylated regions partitions the imprinted genes Igf2 and H19 into parent-specific chromatin loops. Nature Genetics, 2004, 36, 889-893.	9.4	483
33	Genomic imprinting determines methylation of parental alleles in transgenic mice. Nature, 1987, 328, 248-251.	13.7	480
34	CTCF binding at the H19 imprinting control region mediates maternally inherited higher-order chromatin conformation to restrict enhancer access to Igf2. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 10684-10689.	3.3	465
35	Activation-induced Cytidine Deaminase Deaminates 5-Methylcytosine in DNA and Is Expressed in Pluripotent Tissues. Journal of Biological Chemistry, 2004, 279, 52353-52360.	1.6	441
36	Epigenetic dynamics of stem cells and cell lineage commitment: digging Waddington's canal. Nature Reviews Molecular Cell Biology, 2009, 10, 526-537.	16.1	441

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37	Asymmetric regulation of imprinting on the maternal and paternal chromosomes at the Dlk1-Gtl2 imprinted cluster on mouse chromosome 12. Nature Genetics, 2003, 35, 97-102.	9.4	438
38	A maternally methylated CpG island in KvLQT1 is associated with an antisense paternal transcript and loss of imprinting in Beckwith-Wiedemann syndrome. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 8064-8069.	3.3	399
39	Imprinting on distal chromosome 7 in the placenta involves repressive histone methylation independent of DNA methylation. Nature Genetics, 2004, 36, 1291-1295.	9.4	394
40	NANOG-dependent function of TET1 and TET2 in establishment of pluripotency. Nature, 2013, 495, 370-374.	13.7	376
41	Reprogramming DNA methylation in the mammalian life cycle: building and breaking epigenetic barriers. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20110330.	1.8	374
42	FGF Signaling Inhibition in ESCs Drives Rapid Genome-wide Demethylation to the Epigenetic Ground State of Pluripotency. Cell Stem Cell, 2013, 13, 351-359.	5.2	371
43	Dynamic chromatin modifications characterise the first cell cycle in mouse embryos. Developmental Biology, 2005, 280, 225-236.	0.9	368
44	DeepCpG: accurate prediction of single-cell DNA methylation states using deep learning. Genome Biology, 2017, 18, 67.	3.8	361
45	Altered imprinted gene methylation and expression in completely ES cell-derived mouse fetuses: association with aberrant phenotypes. Development (Cambridge), 1998, 125, 2273-2282.	1.2	347
46	Single-cell epigenomics: Recording the past and predicting the future. Science, 2017, 358, 69-75.	6.0	343
47	Multi-tissue DNA methylation age predictor in mouse. Genome Biology, 2017, 18, 68.	3.8	341
48	Regulation of supply and demand for maternal nutrients in mammals by imprinted genes. Journal of Physiology, 2003, 547, 35-44.	1.3	328
49	Epigenetic restriction of embryonic cell lineage fate by methylation of Elf5. Nature Cell Biology, 2008, 10, 1280-1290.	4.6	326
50	BLUEPRINT to decode the epigenetic signature written in blood. Nature Biotechnology, 2012, 30, 224-226.	9.4	323
51	Global Mapping of DNA Methylation in Mouse Promoters Reveals Epigenetic Reprogramming of Pluripotency Genes. PLoS Genetics, 2008, 4, e1000116.	1.5	317
52	Transactivation of Igf2 in a mouse model of Beckwithâ€“Wiedemann syndrome. Nature, 1997, 389, 809-815.	13.7	312
53	Naive Pluripotent Stem Cells Derived Directly from Isolated Cells of the Human Inner Cell Mass. Stem Cell Reports, 2016, 6, 437-446.	2.3	310
54	Multi-omics profiling of mouse gastrulation at single-cell resolution. Nature, 2019, 576, 487-491.	13.7	307

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55	Adaptation of nutrient supply to fetal demand in the mouse involves interaction between the Igf2 gene and placental transporter systems. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 19219-19224.	3.3	306
56	Reprogramming the Methylome: Erasing Memory and Creating Diversity. Cell Stem Cell, 2014, 14, 710-719.	5.2	301
57	Epigenetic inheritance in the mouse. Current Biology, 1997, 7, 277-280.	1.8	298
58	Dynamics of the epigenetic landscape during the maternal-to-zygotic transition. Nature Reviews Molecular Cell Biology, 2018, 19, 436-450.	16.1	298
59	Cohesin Is Required for Higher-Order Chromatin Conformation at the Imprinted IGF2-H19 Locus. PLoS Genetics, 2009, 5, e1000739.	1.5	296
60	Oxidative bisulfite sequencing of 5-methylcytosine and 5-hydroxymethylcytosine. Nature Protocols, 2013, 8, 1841-1851.	5.5	291
61	Single-Cell Landscape of Transcriptional Heterogeneity and Cell Fate Decisions during Mouse Early Gastrulation. Cell Reports, 2017, 20, 1215-1228.	2.9	290
62	Molecular subtypes and phenotypic expression of Beckwithâ€“Wiedemann syndrome. European Journal of Human Genetics, 2005, 13, 1025-1032.	1.4	284
63	Global Reorganization of the Nuclear Landscape in Senescent Cells. Cell Reports, 2015, 10, 471-483.	2.9	282
64	Placental-specific insulin-like growth factor 2 (Igf2) regulates the diffusional exchange characteristics of the mouse placenta. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 8204-8208.	3.3	281
65	Imprinting Mechanisms. Genome Research, 1998, 8, 881-900.	2.4	275
66	Beckwith-Wiedemann syndrome: imprinting in clusters revisited. Journal of Clinical Investigation, 2000, 105, 247-845.	3.9	274
67	Methylome analysis using MeDIP-seq with low DNA concentrations. Nature Protocols, 2012, 7, 617-636.	5.5	270
68	A screen for hydroxymethylcytosine and formylcytosine binding proteins suggests functions in transcription and chromatin regulation. Genome Biology, 2013, 14, R119.	13.9	269
69	Methylation levels of maternal and paternal genomes during preimplantation development. Development (Cambridge), 1991, 113, 119-127.	1.2	269
70	Parental imprinting: potentially active chromatin of the repressed maternal allele of the mouse insulin-like growth factor II (Igf2) gene.. Genes and Development, 1992, 6, 1843-1856.	2.7	264
71	Establishment of porcine and human expanded potential stem cells. Nature Cell Biology, 2019, 21, 687-699.	4.6	261
72	Transgenes as probes for active chromosomal domains in mouse development. Nature, 1988, 333, 852-855.	13.7	257

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73	Resourceful imprinting. Nature, 2004, 432, 53-57.	13.7	257
74	Single-cell epigenomics: powerful new methods for understanding gene regulation and cell identity. Genome Biology, 2016, 17, 72.	3.8	253
75	Developmental control of allelic methylation in the imprinted mouse Igf2 and H19 genes. Development (Cambridge), 1994, 120, 2933-2943.	1.2	252
76	Co-evolution of X-chromosome inactivation and imprinting in mammals. Nature Reviews Genetics, 2005, 6, 403-410.	7.7	251
77	Multiple imprinted sense and antisense transcripts, differential methylation and tandem repeats in a putative imprinting control region upstream of mouse Igf2. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 12509-12514.	3.3	248
78	Epigenetic reprogramming in early mammalian development and following somatic nuclear transfer. Seminars in Cell and Developmental Biology, 2003, 14, 93-100.	2.3	240
79	Data Resource Profile: Accessible Resource for Integrated Epigenomic Studies (ARIES). International Journal of Epidemiology, 2015, 44, 1181-1190.	0.9	238
80	Imprinting mutations in the Beckwithâ€"Wiedemann syndrome suggested by an altered imprinting pattern in the IGF2â€"H19 domain. Human Molecular Genetics, 1995, 4, 2379-2385.	1.4	235
81	DNA demethylation by DNA repair. Trends in Genetics, 2009, 25, 82-90.	2.9	232
82	Culture of preimplantation embryos and its long-term effects on gene expression and phenotype. Human Reproduction Update, 2001, 7, 419-427.	5.2	228
83	Tracking the embryonic stem cell transition from ground state pluripotency. Development (Cambridge), 2017, 144, 1221-1234.	1.2	226
84	5-Formylcytosine can be a stable DNA modification in mammals. Nature Chemical Biology, 2015, 11, 555-557.	3.9	225
85	Epigenetic resetting of human pluripotency. Development (Cambridge), 2017, 144, 2748-2763.	1.2	225
86	Efficient targeted DNA methylation with chimeric dCas9â€"Dnmt3aâ€"Dnmt3L methyltransferase. Nucleic Acids Research, 2017, 45, 1703-1713.	6.5	224
87	Establishment of mouse expanded potential stem cells. Nature, 2017, 550, 393-397.	13.7	223
88	Imprinting in clusters: lessons from Beckwith-Wiedemann syndrome. Trends in Genetics, 1997, 13, 330-334.	2.9	222
89	Evolution of imprinting mechanisms: the battle of the sexes begins in the zygote. Nature Genetics, 2001, 27, 255-256.	9.4	209
90	Germline Mutation in NLRP2 (NALP2) in a Familial Imprinting Disorder (Beckwith-Wiedemann) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62 T	1.5	208

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91	Placental overgrowth in mice lacking the imprinted gene Ipl. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 7490-7495.	3.3	207
92	Genome-wide distribution of 5-formylcytosine in embryonic stem cells is associated with transcription and depends on thymine DNA glycosylase. Genome Biology, 2012, 13, R69.	13.9	205
93	Dnmt2-dependent methylomes lack defined DNA methylation patterns. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 8627-8631.	3.3	204
94	Imprinted Genes, Placental Development and Fetal Growth. Hormone Research in Paediatrics, 2006, 65, 50-58.	0.8	203
95	Comparison of whole-genome bisulfite sequencing library preparation strategies identifies sources of biases affecting DNA methylation data. Genome Biology, 2018, 19, 33.	3.8	201
96	Genome-wide base-resolution mapping of DNA methylation in single cells using single-cell bisulfite sequencing (scBS-seq). Nature Protocols, 2017, 12, 534-547.	5.5	199
97	Molecular signatures of plastic phenotypes in two eusocial insect species with simple societies. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13970-13975.	3.3	192
98	Impairment of DNA Methylation Maintenance Is the Main Cause of Global Demethylation in Naive Embryonic Stem Cells. Molecular Cell, 2016, 62, 848-861.	4.5	189
99	Deletion of a silencer element in Igf2 results in loss of imprinting independent of H19. Nature Genetics, 2000, 26, 203-206.	9.4	188
100	Clinical and molecular genetic features of Beckwith-Wiedemann syndrome associated with assisted reproductive technologies. Human Reproduction, 2008, 24, 741-747.	0.4	186
101	How imprinting centres work. Cytogenetic and Genome Research, 2006, 113, 81-89.	0.6	185
102	Redundant Mechanisms to Form Silent Chromatin at Pericentromeric Regions Rely on BEND3 and DNA Methylation. Molecular Cell, 2014, 56, 580-594.	4.5	185
103	Regulation of Placental Efficiency for Nutrient Transport by Imprinted Genes. Placenta, 2006, 27, 98-102.	0.7	184
104	The long noncoding RNA Kcnq1ot1 organises a lineage-specific nuclear domain for epigenetic gene silencing. Development (Cambridge), 2009, 136, 525-530.	1.2	182
105	Evidence That Paternal Expression of the Îµ-Sarcoglycan Gene Accounts for Reduced Penetrance in Myoclonus-Dystonia. American Journal of Human Genetics, 2002, 71, 1303-1311.	2.6	178
106	MERVL/Zscan4 Network Activation Results in Transient Genome-wide DNA Demethylation of mESCs. Cell Reports, 2016, 17, 179-192.	2.9	174
107	Epigenotype-phenotype correlations in Beckwith-Wiedemann syndrome. Journal of Medical Genetics, 2000, 37, 921-926.	1.5	170
108	Conservation of the H19 noncoding RNA and H19-IGF2 imprinting mechanism in therians. Nature Genetics, 2008, 40, 971-976.	9.4	169

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109	Imprinting mechanisms in mammals. Current Opinion in Genetics and Development, 1998, 8, 154-164.	1.5	168
110	DNA methylation and mammalian epigenetics. Electrophoresis, 2001, 22, 2838-2843.	1.3	168
111	Single cell transcriptome analysis of human, marmoset and mouse embryos reveals common and divergent features of preimplantation development. Development (Cambridge), 2018, 145, .	1.2	167
112	Adult phenotype in the mouse can be affected by epigenetic events in the early embryo. Development (Cambridge), 1993, 119, 933-942.	1.2	166
113	Dietary restriction protects from age-associated DNA methylation and induces epigenetic reprogramming of lipid metabolism. Genome Biology, 2017, 18, 56.	3.8	164
114	Epigenetic modifications in an imprinting cluster are controlled by a hierarchy of DMRs suggesting long-range chromatin interactions. Human Molecular Genetics, 2003, 12, 295-305.	1.4	159
115	Ageing affects DNA methylation drift and transcriptional cell-to-cell variability in mouse muscle stem cells. Nature Communications, 2019, 10, 4361.	5.8	157
116	Integration of spatial and single-cell transcriptomic data elucidates mouse organogenesis. Nature Biotechnology, 2022, 40, 74-85.	9.4	152
117	Selective impairment of methylation maintenance is the major cause of DNA methylation reprogramming in the early embryo. Epigenetics and Chromatin, 2015, 8, 1.	1.8	149
118	Genomic imprinting and genetic disorders in man. Trends in Genetics, 1989, 5, 332-336.	2.9	147
119	Dppa2 and Dppa4 directly regulate the Dux-driven zygotic transcriptional program. Genes and Development, 2019, 33, 194-208.	2.7	144
120	Structural differences in centromeric heterochromatin are spatially reconciled on fertilisation in the mouse zygote. Chromosoma, 2007, 116, 403-415.	1.0	143
121	An association between variants in the IGF2 gene and Beckwith-Wiedemann syndrome: interaction between genotype and epigenotype. Human Molecular Genetics, 2003, 13, 247-255.	1.4	140
122	Retinol and ascorbate drive erasure of epigenetic memory and enhance reprogramming to naÃ¯ve pluripotency by complementary mechanisms. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 12202-12207.	3.3	139
123	An intragenic methylated region in the imprintedIgf2gene augments transcription. EMBO Reports, 2001, 2, 1101-1106.	2.0	137
124	Silencing of CDKN1C (p57KIP2) is associated with hypomethylation at KvDMR1 in Beckwith-Wiedemann syndrome. Journal of Medical Genetics, 2003, 40, 797-801.	1.5	135
125	Imprinting of IGF2 P0 transcript and novel alternatively spliced INS-IGF2 isoforms show differences between mouse and human. Human Molecular Genetics, 2006, 15, 1259-1269.	1.4	133
126	Promoter DNA methylation couples genome-defence mechanisms to epigenetic reprogramming in the mouse germline. Development (Cambridge), 2012, 139, 3623-3632.	1.2	130

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127	Sequence and functional comparison in the Beckwith-Wiedemann region: implications for a novel imprinting centre and extended imprinting. Human Molecular Genetics, 2000, 9, 2691-2706.	1.4	128
128	Sequence conservation and variability of imprinting in the Beckwith-Wiedemann syndrome gene cluster in human and mouse. Human Molecular Genetics, 2000, 9, 1829-1841.	1.4	118
129	Genome-wide Bisulfite Sequencing in Zygotes Identifies Demethylation Targets and Maps the Contribution of TET3 Oxidation. Cell Reports, 2014, 9, 1990-2000.	2.9	116
130	Analysis of germline CDKN1C (p57KIP2) mutations in familial and sporadic Beckwith-Wiedemann syndrome (BWS) provides a novel genotype-phenotype correlation. Journal of Medical Genetics, 1999, 36, 518-23.	1.5	115
131	Mammalian epigenomics: reprogramming the genome for development and therapy. Theriogenology, 2003, 59, 21-32.	0.9	114
132	Active turnover of DNA methylation during cell fate decisions. Nature Reviews Genetics, 2021, 22, 59-66.	7.7	113
133	Loss of the maternal H19 gene induces changes in Igf2 methylation in both cis and trans. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 10243-10248.	3.3	112
134	Overexpression of Insulin-Like Growth Factor-II in Transgenic Mice Is Associated with Pancreatic Islet Cell Hyperplasia*. Endocrinology, 1999, 140, 2353-2363.	1.4	111
135	Mice Deficient in APOBEC2 and APOBEC3. Molecular and Cellular Biology, 2005, 25, 7270-7277.	1.1	110
136	Transgenes as molecular probes for genomic imprinting. Trends in Genetics, 1988, 4, 59-62.	2.9	109
137	Transcriptional Heterogeneity in Naive and Primed Human Pluripotent Stem Cells at Single-Cell Resolution. Cell Reports, 2019, 26, 815-824.e4.	2.9	109
138	LifeTime and improving European healthcare through cell-based interceptive medicine. Nature, 2020, 587, 377-386.	13.7	108
139	Maternal DNA Methylation Regulates Early Trophoblast Development. Developmental Cell, 2016, 36, 152-163.	3.1	107
140	Imprinting mutation in the Beckwith-Wiedemann syndrome leads to biallelic IGF2 expression through an H19-independent pathway. Human Molecular Genetics, 1996, 5, 2027-2032.	1.4	103
141	Conceptual links between DNA methylation reprogramming in the early embryo and primordial germ cells. Current Opinion in Cell Biology, 2013, 25, 281-288.	2.6	103
142	Comparative Principles of DNA Methylation Reprogramming during Human and Mouse InÂVitro Primordial Germ Cell Specification. Developmental Cell, 2016, 39, 104-115.	3.1	102
143	Imprinting of IGF2 and H19: lack of reciprocity in sporadic Beckwith- Wiedemann syndrome. Human Molecular Genetics, 1997, 6, 1543-1548.	1.4	100
144	DNA methylation homeostasis in human and mouse development. Current Opinion in Genetics and Development, 2017, 43, 101-109.	1.5	99

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145	Active demethylation in mouse zygotes involves cytosine deamination and base excision repair. Epigenetics and Chromatin, 2013, 6, 39.	1.8	98
146	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.	1.4	97
147	Epigenetic asymmetry in the mammalian zygote and early embryo: relationship to lineage commitment?. Philosophical Transactions of the Royal Society B: Biological Sciences, 2003, 358, 1403-1409.	1.8	96
148	Silence across the border. Nature, 2000, 405, 408-409.	13.7	95
149	Altered imprinted gene methylation and expression in completely ES cell-derived mouse fetuses: association with aberrant phenotypes. Development (Cambridge), 1998, 125, 2273-82.	1.2	95
150	Evaluation of epigenetic marks in human embryos derived from IVF and ICSI. Human Reproduction, 2010, 25, 2387-2395.	0.4	93
151	Methylation analysis on individual chromosomes: improved protocol for bisulphite genomic sequencing. Nucleic Acids Research, 1994, 22, 695-696.	6.5	92
152	Genetic conflict in early development: parental imprinting in normal and abnormal growth. Reproduction, 1996, 1, 73-77.	2.0	92
153	Forget the Parents: Epigenetic Reprogramming in Human Germ Cells. Cell, 2015, 161, 1248-1251.	13.5	92
154	Genomic imprinting and embryonal tumours. Nature, 1989, 338, 112-113.	13.7	89
155	Epigenetic dynamics of the Kcnq1 imprinted domain in the early embryo. Development (Cambridge), 2006, 133, 4203-4210.	1.2	87
156	Epigenetic modification and uniparental inheritance of H19 in Beckwith-Wiedemann syndrome.. Journal of Medical Genetics, 1997, 34, 353-359.	1.5	86
157	Germline and Pluripotent Stem Cells. Cold Spring Harbor Perspectives in Biology, 2015, 7, a019422.	2.3	86
158	Allelic methylation of H19 and IGF2 in the Beckwith â€" Wiedemann syndrome. Human Molecular Genetics, 1994, 3, 1297-1301.	1.4	85
159	Developmental control of allelic methylation in the imprinted mouse Igf2 and H19 genes. Development (Cambridge), 1994, 120, 2933-43.	1.2	85
160	An upstream repressor element plays a role in Igf2 imprinting. EMBO Journal, 2001, 20, 3518-3525.	3.5	83
161	Frequent RASSF1A tumour suppressor gene promoter methylation in Wilms' tumour and colorectal cancer. Oncogene, 2002, 21, 7277-7282.	2.6	82
162	Methylation levels of maternal and paternal genomes during preimplantation development. Development (Cambridge), 1991, 113, 119-27.	1.2	82

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163	Dynamic methylation adjustment and counting as part of imprinting mechanisms.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 6371-6376.	3.3	78
164	Developmental consequences of imprinting of parental chromosomes by DNA methylation. Philosophical Transactions of the Royal Society of London Series B, Biological Sciences, 1990, 326, 313-327.	2.4	75
165	Multi-omic rejuvenation of human cells by maturation phase transient reprogramming. ELife, 2022, 11, .	2.8	75
166	Common polymorphism in H19 associated with birthweight and cord blood IGF-II levels in humans. BMC Genetics, 2005, 6, 22.	2.7	72
167	Genome-Scale Oscillations in DNA Methylation during Exit from Pluripotency. Cell Systems, 2018, 7, 63-76.e12.	2.9	70
168	Safeguarding parental identity: Dnmt1 maintains imprints during epigenetic reprogramming in early embryogenesis: Figure 1.. Genes and Development, 2008, 22, 1567-1571.	2.7	67
169	Low rates of mutation in clinical grade human pluripotent stem cells under different culture conditions. Nature Communications, 2020, 11, 1528.	5.8	67
170	Screening for genes that accelerate the epigenetic aging clock in humans reveals a role for the H3K36 methyltransferase NSD1. Genome Biology, 2019, 20, 146.	3.8	66
171	An endosiRNA-Based Repression Mechanism Counteracts Transposon Activation during Global DNA Demethylation in Embryonic Stem Cells. Cell Stem Cell, 2017, 21, 694-703.e7.	5.2	65
172	Igf2 imprinting in development and disease. International Journal of Developmental Biology, 2000, 44, 145-50.	0.3	65
173	Incomplete methylation reprogramming in SCNT embryos. Nature Genetics, 2012, 44, 965-966.	9.4	64
174	Systematic elimination of parthenogenetic cells in mouse chimeras. Development (Cambridge), 1989, 106, 29-35.	1.2	64
175	The two-domain hypothesis in Beckwithâ€“Wiedemann syndrome: autonomous imprinting of the telomeric domain of the distal chromosome 7 cluster. Human Molecular Genetics, 2005, 14, 503-511.	1.4	63
176	Developmental adaptations to increased fetal nutrient demand in mouse genetic models of Igf2â€mediated overgrowth. FASEB Journal, 2011, 25, 1737-1745.	0.2	62
177	8C-like cells capture the human zygotic genome activation program inÂvitro. Cell Stem Cell, 2022, 29, 449-459.e6.	5.2	62
178	Multiâ€omic rejuvenation of naturally aged tissues by a single cycle of transient reprogramming. Aging Cell, 2022, 21, e13578.	3.0	60
179	Genomic imprinting: a possible mechanism for the parental origin effect in Huntington's chorea.. Journal of Medical Genetics, 1988, 25, 805-808.	1.5	59
180	Epigenetic reprogramming: Back to the beginning. Nature, 2002, 420, 127-127.	13.7	59

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181	A Single-Cell Transcriptomics CRISPR-Activation Screen Identifies Epigenetic Regulators of the Zygotic Genome Activation Program. Cell Systems, 2020, 11, 25-41.e9.	2.9	59
182	In vivo genome-wide profiling reveals a tissue-specific role for 5-formylcytosine. Genome Biology, 2016, 17, 141.	3.8	58
183	Spatial profiling of early primate gastrulation in utero. Nature, 2022, 609, 136-143.	13.7	56
184	Shifting behaviour: epigenetic reprogramming in eusocial insects. Current Opinion in Cell Biology, 2012, 24, 367-373.	2.6	54
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