Robert P Feil

List of Publications by Year
in descending order

117 papers	18,130 citations	28274 55 h-index	24982 109 g-index
123 all docs	123 docs citations	123 times ranked	21236 citing authors

#	Article	IF	Citations
1	A Bivalent Chromatin Structure Marks Key Developmental Genes in Embryonic Stem Cells. Cell, 2006, 125, 315-326.	28.9	4,773
2	Epigenetics and the environment: emerging patterns and implications. Nature Reviews Genetics, 2012, 13, 97-109.	16.3	1,524
3	Putative X-linked adrenoleukodystrophy gene shares unexpected homology with ABC transporters. Nature, 1993, 361, 726-730.	27.8	1,157
4	The Air Noncoding RNA Epigenetically Silences Transcription by Targeting G9a to Chromatin. Science, 2008, 322, 1717-1720.	12.6	883
5	Child Health, Developmental Plasticity, and Epigenetic Programming. Endocrine Reviews, 2011, 32, 159-224.	20.1	533
6	Culture of Preimplantation Mouse Embryos Affects Fetal Development and the Expression of Imprinted Genes1. Biology of Reproduction, 2001, 64, 918-926.	2.7	532
7	Genomic Imprinting and Physiological Processes in Mammals. Cell, 2019, 176, 952-965.	28.9	395
8	Imprinting on distal chromosome 7 in the placenta involves repressive histone methylation independent of DNA methylation. Nature Genetics, 2004, 36, 1291-1295.	21.4	394
9	Imprinting along the Kcnq1 domain on mouse chromosome 7 involves repressive histone methylation and recruitment of Polycomb group complexes. Nature Genetics, 2004, 36, 1296-1300.	21.4	386
10	Epigenetic regulation of mammalian genomic imprinting. Current Opinion in Genetics and Development, 2004, 14, 188-195.	3.3	346
11	Multiple imprinted sense and antisense transcripts, differential methylation and tandem repeats in a putative imprinting control region upstream of mouseâ€‰Igf2. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 12509-12514.	7.1	248
12	Convergent evolution of genomic imprinting in plants and mammals. Trends in Genetics, 2007, 23, 192-199.	6.7	238
13	The cell proliferation antigen Ki-67 organises heterochromatin. ELife, 2016, 5, e13722.	6.0	237
14	Culture of preimplantation embryos and its long-term effects on gene expression and phenotype. Human Reproduction Update, 2001, 7, 419-427.	10.8	228
15	Limited evolutionary conservation of imprinting in the human placenta. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 6623-6628.	7.1	226
16	Global hypomethylation of the genome in XX embryonic stem cells. Nature Genetics, 2005, 37, 1274-1279.	21.4	222
17	Epigenetic Transitions in Germ Cell Development and Meiosis. Developmental Cell, 2010, 19, 675-686.	7.0	212
18	Allele-specific histone lysine methylation marks regulatory regions at imprinted mouse genes. EMBO Journal, 2002, 21, 6560-6570.	7.8	198

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19	Environmental and nutritional effects on the epigenetic regulation of genes. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2006, 600, 46-57.	1.0	198
20	Differential histone modifications mark mouse imprinting control regions during spermatogenesis. EMBO Journal, 2007, 26, 720-729.	7.8	198
21	New insights into establishment and maintenance of DNA methylation imprints in mammals. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20110336.	4.0	179
22	G9a Histone Methyltransferase Contributes to Imprinting in the Mouse Placenta. Molecular and Cellular Biology, 2008, 28, 1104-1113.	2.3	172
23	ATRX Plays a Key Role in Maintaining Silencing at Interstitial Heterochromatic Loci and Imprinted Genes. Cell Reports, 2015, 11, 405-418.	6.4	152
24	Genomic imprinting in mammals: an interplay between chromatin and DNA methylation?. Trends in Genetics, 1999, 15, 431-435.	6.7	142
25	Escape from gene silencing in ICF syndrome: evidence for advanced replication time as a major determinant. Human Molecular Genetics, 2000, 9, 2575-2587.	2.9	135
26	DNA Methylation Is Linked to Deacetylation of Histone H3, but Not H4, on the Imprinted Genes Snrpnand U2af1-rs1. Molecular and Cellular Biology, 2001, 21, 5426-5436.	2.3	130
27	Chromatin mechanisms in genomic imprinting. Mammalian Genome, 2009, 20, 544-556.	2.2	118
28	Genomic imprinting in the placenta. Cytogenetic and Genome Research, 2006, 113, 90-98.	1.1	116
29	Histone methylation is mechanistically linked to DNA methylation at imprinting control regions in mammals. Human Molecular Genetics, 2009, 18, 3375-3383.	2.9	115
30	Conservation of IGF2-H19 and IGF2R imprinting in sheep: effects of somatic cell nuclear transfer. Mechanisms of Development, 2003, 120, 1433-1442.	1.7	112
31	Epigenetic Properties and Identification of an Imprint Mark in the Nesp-Gnasxl Domain of the Mouse Gnas Imprinted Locus. Molecular and Cellular Biology, 2003, 23, 5475-5488.	2.3	110
32	Epigenetic deregulation of imprinting in congenital diseases of aberrant growth. BioEssays, 2006, 28, 453-459.	2.5	106
33	Long noncoding RNAs in human disease: emerging mechanisms and therapeutic strategies. Epigenomics, 2015, 7, 877-879.	2.1	104
34	Acetylation of histone H3 at lysine 64 regulates nucleosome dynamics and facilitates transcription. ELife, 2014, 3, e01632.	6.0	99
35	Methylation analysis on individual chromosomes: improved protocol for bisulphite genomic sequencing. Nucleic Acids Research, 1994, 22, 695-696.	14.5	92
36	Reciprocal imprinting of human GRB10 in placental trophoblast and brain: evolutionary conservation of reversed allelic expression. Human Molecular Genetics, 2009, 18, 3066-3074.	2.9	92

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37	Epigenetic deregulation of genomic imprinting in human disorders and following assisted reproduction. Birth Defects Research Part C: Embryo Today Reviews, 2005, 75, 81-97.	3.6	91
38	Genomic imprinting and human disease. Essays in Biochemistry, 2010, 48, 187-200.	4.7	91
39	Parental Allele-Specific Chromatin Configuration in a Boundaryâ€“Imprinting-Control Element Upstream of the Mouse H19 Gene. Molecular and Cellular Biology, 1999, 19, 2556-2566.	2.3	87
40	Site-Specific Analysis of Histone Methylation and Acetylation. , 2004, 287, 099-120.		84
41	Identification of the Imprinted KLF14 Transcription Factor Undergoing Human-Specific Accelerated Evolution. PLoS Genetics, 2007, 3, e65.	3.5	82
42	A mono-allelic bivalent chromatin domain controls tissue-specific imprinting at Grb10. EMBO Journal, 2008, 27, 2523-2532.	7.8	75
43	Heterochromatin delays CRISPR-Cas9 mutagenesis but does not influence the outcome of mutagenic DNA repair. PLoS Biology, 2018, 16, e2005595.	5.6	75
44	Small regulatory RNAs controlled by genomic imprinting and their contribution to human disease. Epigenetics, 2012, 7, 1341-1348.	2.7	73
45	ZFP57 maintains the parent-of-origin-specific expression of the imprinted genes and differentially affects non-imprinted targets in mouse embryonic stem cells. Nucleic Acids Research, 2016, 44, 8165-8178.	14.5	73
46	PRâ€SET7 and SUV4â€20H regulate H4 lysineâ€20 methylation at imprinting control regions in the mouse. EMBO Reports, 2008, 9, 998-1005.	4.5	72
47	Comparative analysis of human chromosome 7q21 and mouse proximal chromosome 6 reveals a placental-specific imprinted gene, TFPI2/Tfpi2, which requires EHMT2 and EED for allelic-silencing. Genome Research, 2008, 18, 1270-1281.	5.5	72
48	Perturbation of genomic imprinting in oligozoospermia. Epigenetics, 2009, 4, 27-30.	2.7	72
49	PRMT5-mediated histone H4 arginine-3 symmetrical dimethylation marks chromatin at G + C-rich regions of the mouse genome. Nucleic Acids Research, 2014, 42, 235-248.	14.5	72
50	Transcription and histone methylation changes correlate with imprint acquisition in male germ cells. EMBO Journal, 2012, 31, 606-615.	7.8	71
51	Placental abnormalities associated with post-natal mortality in sheep somatic cell clones. Theriogenology, 2006, 65, 1110-1121.	2.1	69
52	A 195-kb cosmid walk encompassing the human Xq28 color vision pigment genes. Genomics, 1990, 6, 367-373.	2.9	64
53	Genomic imprinting in ruminants: allele-specific gene expression in parthenogenetic sheep. Mammalian Genome, 1998, 9, 831-834.	2.2	64
54	ICR Noncoding RNA Expression Controls Imprinting and DNA Replication at the Dlk1-Dio3 Domain. Developmental Cell, 2014, 31, 19-33.	7.0	64

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55	Histone H3K9 Methyltransferase G9a in Oocytes Is Essential for Preimplantation Development but Dispensable for CG Methylation Protection. Cell Reports, 2019, 27, 282-293.e4.	6.4	62
56	Stochastic imprinting in the progeny of Dnmt3Lâˆ'/âˆ' females. Human Molecular Genetics, 2006, 15, 589-598.	2.9	60
57	Epigenetic asymmetry in the zygote and mammalian development. International Journal of Developmental Biology, 2009, 53, 191-201.	0.6	60
58	EHMT2 directs DNA methylation for efficient gene silencing in mouse embryos. Genome Research, 2016, 26, 192-202.	5.5	60
59	Nuclei of Nonviable Ovine Somatic Cells Develop into Lambs after Nuclear Transplantation. Biology of Reproduction, 2002, 67, 126-132.	2.7	56
60	Regulatory links between imprinted genes: evolutionary predictions and consequences. Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20152760.	2.6	56
61	CTCF modulates allele-specific sub-TAD organization and imprinted gene activity at the mouse Dlk1-Dio3 and Igf2-H19 domains. Genome Biology, 2019, 20, 272.	8.8	56
62	Meg3 Non-coding RNA Expression Controls Imprinting by Preventing Transcriptional Upregulation in cis. Cell Reports, 2018, 23, 337-348.	6.4	54
63	Chromatin mechanisms in the developmental control of imprinted gene expression. International Journal of Biochemistry and Cell Biology, 2015, 67, 139-147.	2.8	53
64	ZFP57 recognizes multiple and closely spaced sequence motif variants to maintain repressive epigenetic marks in mouse embryonic stem cells. Nucleic Acids Research, 2016, 44, 1118-1132.	14.5	50
65	Parental Chromosome-specific Chromatin Conformation in the Imprinted U2af1-rs1 Gene in the Mouse. Journal of Biological Chemistry, 1997, 272, 20893-20900.	3.4	49
66	Environmental effects on genomic imprinting in mammals. Toxicology Letters, 2001, 120, 143-150.	0.8	47
67	Allelic inactivation of the pseudoautosomal gene SYBL1 is controlled by epigenetic mechanisms common to the X and Y chromosomes. Human Molecular Genetics, 2002, 11, 3191-3198.	2.9	47
68	Synergic reprogramming of mammalian cells by combined exposure to mitotic Xenopus egg extracts and transcription factors. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 17331-17336.	7.1	47
69	Quantitative FLIM-FRET Microscopy to Monitor Nanoscale Chromatin Compaction InÂVivo Reveals Structural Roles of Condensin Complexes. Cell Reports, 2017, 18, 1791-1803.	6.4	45
70	Parallels between Mammalian Mechanisms of Monoallelic Gene Expression. Trends in Genetics, 2018, 34, 954-971.	6.7	44
71	Imprinted gene expression in hybrids: perturbed mechanisms and evolutionary implications. Heredity, 2014, 113, 167-175.	2.6	43
72	Epigenetic stability of embryonic stem cells and developmental potential. Trends in Biotechnology, 2007, 25, 556-562.	9.3	42

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73	Imprinting control regions (ICRs) are marked by mono-allelic bivalent chromatin when transcriptionally inactive. Nucleic Acids Research, 2016, 44, 621-635.	14.5	41
74	Genomic Imprinting: A Chromatin Connection. American Journal of Human Genetics, 1997, 61, 1213-1219.	6.2	40
75	Genome-wide DNA demethylation in mammals. Genome Biology, 2010, 11, 110.	9.6	40
76	Epigenetic deregulation of genomic imprinting in humans: causal mechanisms and clinical implications. Epigenomics, 2013, 5, 715-728.	2.1	40
77	Exogenous Expression of Human Protamine 1 (hPrm1) Remodels Fibroblast Nuclei into Spermatid-like Structures. Cell Reports, 2015, 13, 1765-1771.	6.4	39
78	Differential patterns of histone methylation and acetylation distinguish active and repressed alleles at X-linked genes. Cytogenetic and Genome Research, 2002, 99, 66-74.	1.1	34
79	1q12 chromosome translocations form aberrant heterochromatic foci associated with changes in nuclear architecture and gene expression in B cell lymphoma. EMBO Molecular Medicine, 2010, 2, 159-171.	6.9	33
80	Chromatin structure and imprinting: Developmental control of DNase-I sensitivity in the mouse insulin-like growth factor 2 gene. Genesis, 1995, 17, 240-252.	2.1	32
81	Inhibition of Histone Deacetylases Alters Allelic Chromatin Conformation at the Imprinted U2af1-rs1 Locus in Mouse Embryonic Stem Cells. Journal of Biological Chemistry, 2002, 277, 11728-11734.	3.4	32
82	Increased H3K9 methylation and impaired expression of Protocadherins are associated with the cognitive dysfunctions of the Kleefstra syndrome. Nucleic Acids Research, 2018, 46, 4950-4965.	14.5	32
83	A KRAB Domain Zinc Finger Protein in Imprinting and Disease. Developmental Cell, 2008, 15, 487-488.	7.0	26
84	Chromatin Immunoprecipitation (ChIP) on Unfixed Chromatin from Cells and Tissues to Analyze Histone Modifications. Cold Spring Harbor Protocols, 2007, 2007, pdb.prot4767-pdb.prot4767.	0.3	24
85	The placental imprinted DLK1-DIO3 domain: a new link to prenatal and postnatal growth in humans. American Journal of Obstetrics and Gynecology, 2017, 217, 350.e1-350.e13.	1.3	23
86	Stability and Lability of Parental Methylation Imprints in Development and Disease. Genes, 2019, 10, 999.	2.4	23
87	Human imprinted retrogenes exhibit non-canonical imprint chromatin signatures and reside in non-imprinted host genes. Nucleic Acids Research, 2011, 39, 4577-4586.	14.5	22
88	Characterization of Novel Paternal ncRNAs at the Plagl1 Locus, Including Hymai, Predicted to Interact with Regulators of Active Chromatin. PLoS ONE, 2012, 7, e38907.	2.5	21
89	Differential 3D chromatin organization and gene activity in genomic imprinting. Current Opinion in Genetics and Development, 2020, 61, 17-24.	3.3	21
90	In Vitro Corticogenesis from Embryonic Stem Cells Recapitulates the In Vivo Epigenetic Control of Imprinted Gene Expression. Cerebral Cortex, 2017, 27, bhw102.	2.9	18

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91	Epigenetics, an emerging discipline with broad implications. Comptes Rendus - Biologies, 2008, 331, 837-843.	0.2	17
92	Chromosome Loops, Insulators, and Histone Methylation: New Insights into Regulation of Imprinting in Clusters. Cold Spring Harbor Symposia on Quantitative Biology, 2004, 69, 29-38.	1.1	16
93	MEDEA Takes Control of Its Own Imprinting. Cell, 2006, 124, 468-470.	28.9	16
94	Environmental effects on chromatin repression at imprinted genes and endogenous retroviruses. Current Opinion in Chemical Biology, 2018, 45, 139-147.	6.1	15
95	Nucleotide Sequence of a 28-kb Mouse Genomic Region Comprising the Imprinted Igf2 Gene. DNA Research, 1996, 3, 331-335.	3.4	14
96	Early-embryonic culture and manipulation could affect genomic imprinting. Trends in Molecular Medicine, 2001, 7, 245-246.	6.7	14
97	Ready for the marks. Nature, 2009, 461, 359-360.	27.8	13
98	Insertion of an Imprinted Insulator into the IgH Locus Reveals Developmentally Regulated, Transcription-Dependent Control of V(D)J Recombination. Molecular and Cellular Biology, 2015, 35, 529-543.	2.3	12
99	Methylation of the C19MC microRNA locus in the placenta: association with maternal and childhood body size. International Journal of Obesity, 2020, 44, 13-22.	3.4	10
100	Exploring chromatin structural roles of non-coding RNAs at imprinted domains. Biochemical Society Transactions, 2021, 49, 1867-1879.	3.4	10
101	Oocyte-derived histone H3 lysine 27 methylation controls gene expression in the early embryo. Nature Structural and Molecular Biology, 2017, 24, 685-686.	8.2	7
102	Zfp57 inactivation illustrates the role of ICR methylation in imprinted gene expression during neural differentiation of mouse ESCs. Scientific Reports, 2021, 11, 13802.	3.3	7
103	A Role for Caenorhabditis elegans COMPASS in Germline Chromatin Organization. Cells, 2020, 9, 2049.	4.1	6
104	Imprinted Small RNAs Unraveled: Maternal MicroRNAs Antagonize a Paternal-Genome-Driven Gene Expression Network. Molecular Cell, 2020, 78, 3-5.	9.7	6
105	Chromosomal rearrangement segregating with adrenoleukodystrophy: a molecular analysis.. Proceedings of the National Academy of Sciences of the United States of America, 1993, 90, 9489-9493.	7.1	5
106	Cbx-rs2 (M31), a mouse homolog of the Drosophila Heterochromatin protein 1 gene, maps to distal Chromosome 11 and is nonallelic to Om. Mammalian Genome, 1995, 6, 469-471.	2.2	5
107	Probing Chromatin Structure with Nuclease Sensitivity Assays. , 2002, 181, 269-284.		5
108	PCR-Based Analysis of Immunoprecipitated Chromatin. Cold Spring Harbor Protocols, 2007, 2007, pdb.prot4768-pdb.prot4768.	0.3	3

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109	Genomic Imprinting and Its Effects on Genes and Chromosomes in Mammals. , 2004, 240, 53-76.		2
110	Emerging chromatin structural roles of the methyl-CpG binding protein MeCP2. Epigenomics, 2021, 13, 405-409.	2.1	2
111	Epigenetic Mechanisms in Mammals and Their Effects on Cloning Procedures. , 2009, , 559-579.		2
112	A probe from an Xâ€“Y homology region detects RFLPs in Xq13â€“q22. Nucleic Acids Research, 1989, 17, 1279-1279.	14.5	1
113	Environmental Effects on Genomic Imprinting in Development and Disease. , 2019, , 3-23.		1
114	PRC-mediated interaction networks of repressed genes: emerging insights and possible roles. Epigenomics, 2016, 8, 733-735.	2.1	0
115	Ovine Somatic Cell Nuclear Transfer. , 2005, , .		0
116	Noncoding RNAs and Chromatin Modifications in the Developmental Control of Imprinted Genes. Epigenetics and Human Health, 2016, , 19-40.	0.2	0
117	Environmental Effects on Genomic Imprinting in Development and Disease. , 2017, , 1-21.		0