Anne C Ferguson-Smith

List of Publications by Year
in descending order

87 papers	12,516 citations	81434 41 h-index	62345 84 g-index
99 all docs	99 docs citations	99 times ranked	17683 citing authors

#	Article	IF	Citations
1	Preimplantation genetic testing for a chr14q32 microdeletion in a family with Kagami-Ogata syndrome and Temple syndrome. Journal of Medical Genetics, 2022, 59, 253-261.	1.5	5
2	Epigenetic changes induced by in utero dietary challenge result in phenotypic variability in successive generations of mice. Nature Communications, 2022, 13, 2464.	5.8	13
3	Subnuclear localisation is associated with gene expression more than parental origin at the imprinted Dlk1-Dio3 locus. PLoS Genetics, 2022, 18, e1010186.	1.5	0
4	Mendelâ€™s laws of heredity on his 200th birthday: What have we learned by considering exceptions?. Heredity, 2022, 129, 1-3.	1.2	8
5	Genomic properties of variably methylated retrotransposons in mouse. Mobile DNA, 2021, 12, 6.	1.3	17
6	A spontaneous genetically induced epiallele at a retrotransposon shapes host genome function. ELife, 2021, 10, .	2.8	9
7	<i>Dlk1</i> dosage regulates hippocampal neurogenesis and cognition. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	16
8	Defective folate metabolism causes germline epigenetic instability and distinguishes Hira as a phenotype inheritance biomarker. Nature Communications, 2021, 12, 3714.	5.8	12
9	Variably methylated retrotransposons are refractory to a range of environmental perturbations. Nature Genetics, 2021, 53, 1233-1242.	9.4	23
10	Imprinting methylation predicts hippocampal volumes and hyperintensities and the change with age in later life. Scientific Reports, 2021, 11, 943.	1.6	10
11	Epigenetic Mechanisms of ART-Related Imprinting Disorders: Lessons From iPSC and Mouse Models. Genes, 2021, 12, 1704.	1.0	10
12	Metastable epialleles and their contribution to epigenetic inheritance in mammals. Seminars in Cell and Developmental Biology, 2020, 97, 93-105.	2.3	34
13	The evolution of genomic imprinting: Epigenetic control of mammary gland development and postnatal resource control. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2020, 12, e1476.	6.6	9
14	KRAB zinc finger protein diversification drives mammalian interindividual methylation variability. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 31290-31300.	3.3	25
15	Strain-Specific Epigenetic Regulation of Endogenous Retroviruses: The Role of Trans-Acting Modifiers. Viruses, 2020, 12, 810.	1.5	11
16	Trappc9 deficiency causes parent-of-origin dependent microcephaly and obesity. PLoS Genetics, 2020, 16, e1008916.	1.5	22
17	Obstacles to detecting isoforms using full-length scRNA-seq data. Genome Biology, 2020, 21, 74.	3.8	36
18	ZFP57 regulation of transposable elements and gene expression within and beyond imprinted domains. Epigenetics and Chromatin, 2019, 12, 49.	1.8	42

#	Article	IF	Citations
19	Imprinting methylation in SNRPN and MEST1 in adult blood predicts cognitive ability. PLoS ONE, 2019, 14, e0211799.	1.1	13
20	TET3 prevents terminal differentiation of adult NSCs by a non-catalytic action at Snrpn. Nature Communications, 2019, 10, 1726.	5.8	29
21	Genomic Imprinting and Physiological Processes in Mammals. Cell, 2019, 176, 952-965.	13.5	395
22	ZNF445 is a primary regulator of genomic imprinting. Genes and Development, 2019, 33, 49-54.	2.7	138
23	The origins of genomic imprinting in mammals. Reproduction, Fertility and Development, 2019, 31, 1203.	0.1	14
24	The mammalian LINC complex component SUN1 regulates muscle regeneration by modulating drosha activity. ELife, 2019, 8, .	2.8	12
25	Targeted deletion of a 170-kb cluster of LINE-1 repeats and implications for regional control. Genome Research, 2018, 28, 345-356.	2.4	12
26	The discovery and importance of genomic imprinting. ELife, 2018, 7, .	2.8	50
27	Simulation-based benchmarking of isoform quantification in single-cell RNA-seq. Genome Biology, 2018, 19, 191.	3.8	25
28	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. Nature Genetics, 2018, 50, 1574-1583.	9.4	169
29	The imprinted gene Pw1/Peg3 regulates skeletal muscle growth, satellite cell metabolic state, and self-renewal. Scientific Reports, 2018, 8, 14649.	1.6	17
30	Identification, Characterization, and Heritability of Murine Metastable Epialleles: Implications for Non-genetic Inheritance. Cell, 2018, 175, 1259-1271.e13.	13.5	124
31	Dadâ€™s diet â€“ smRNA methylation signatures in sperm pass on disease risk. Nature Reviews Endocrinology, 2018, 14, 446-447.	4.3	1
32	Visualizing Changes in Cdkn1c Expression Links Early-Life Adversity to Imprint Mis-regulation in Adults. Cell Reports, 2017, 18, 1090-1099.	2.9	43
33	Epigenetic Mechanisms of Transmission of Metabolic Disease across Generations. Cell Metabolism, 2017, 25, 559-571.	7.2	179
34	Interplay of cis and trans mechanisms driving transcription factor binding and gene expression evolution. Nature Communications, 2017, 8, 1092.	5.8	60
35	Genomic Imprinting and the Regulation of Postnatal Neurogenesis. Brain Plasticity, 2017, 3, 89-98.	1.9	12
36	Role of the BAHD1 Chromatin-Repressive Complex in Placental Development and Regulation of Steroid Metabolism. PLoS Genetics, 2016, 12, e1005898.	1.5	34

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37	Transgenerational inheritance: Models and mechanisms of nonâ€“DNA sequenceâ€“based inheritance. Science, 2016, 354, 59-63.	6.0	288
38	Fetus-derived DLK1 is required for maternal metabolic adaptations to pregnancy and is associated with fetal growth restriction. Nature Genetics, 2016, 48, 1473-1480.	9.4	79
39	Novel Primate Model of Serotonin Transporter Genetic Polymorphisms Associated with Gene Expression, Anxiety and Sensitivity to Antidepressants. Neuropsychopharmacology, 2016, 41, 2366-2376.	2.8	29
40	Non-CG DNA methylation is a biomarker for assessing endodermal differentiation capacity in pluripotent stem cells. Nature Communications, 2016, 7, 10458.	5.8	38
41	Trim28 Haploinsufficiency Triggers Bi-stable Epigenetic Obesity. Cell, 2016, 164, 353-364.	13.5	161
42	The Dlk1-Gtl2 Locus Preserves LT-HSC Function by Inhibiting the PI3K-mTOR Pathway to Restrict Mitochondrial Metabolism. Cell Stem Cell, 2016, 18, 214-228.	5.2	149
43	Allele-specific binding of ZFP57 in the epigenetic regulation of imprinted and non-imprinted monoallelic expression. Genome Biology, 2015, 16, 112.	3.8	150
44	CRISPR-Cas9-Mediated Genetic Screening in Mice with Haploid Embryonic Stem Cells Carrying a Guide RNA Library. Cell Stem Cell, 2015, 17, 221-232.	5.2	91
45	A trans-homologue interaction between reciprocally imprinted <i>miR-127</i> and <i>Rtl1</i> regulates placenta development. Development (Cambridge), 2015, 142, 2425-30.	1.2	62
46	Germline and somatic imprinting in the nonhuman primate highlights species differences in oocyte methylation. Genome Research, 2015, 25, 611-623.	2.4	25
47	<i>ZFP57</i>and the Targeted Maintenance of Postfertilization Genomic Imprints. Cold Spring Harbor Symposia on Quantitative Biology, 2015, 80, 177-187.	2.0	29
48	Functional and Molecular Consequences of the Dnmt3aR882H Mutation in Acute Myeloid Leukaemia. Blood, 2015, 126, 2424-2424.	0.6	3
49	Parent-of-Origin Effects Implicate Epigenetic Regulation of Experimental Autoimmune Encephalomyelitis and Identify Imprinted Dlk1 as a Novel Risk Gene. PLoS Genetics, 2014, 10, e1004265.	1.5	16
50	Phenotypic Outcomes of Imprinted Gene Models in Mice: Elucidation of Pre- and Postnatal Functions of Imprinted Genes. Annual Review of Genomics and Human Genetics, 2014, 15, 93-126.	2.5	84
51	DLK1/PREF1 regulates nutrient metabolism and protects from steatosis. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 16088-16093.	3.3	54
52	Insulin and insulin-like growth factor 1 receptors are required for normal expression of imprinted genes. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 14512-14517.	3.3	43
53	In utero undernourishment perturbs the adult sperm methylome and intergenerational metabolism. Science, 2014, 345, 1255903.	6.0	535
54	Epigenetic Control of the Genomeâ€"Lessons from Genomic Imprinting. Genes, 2014, 5, 635-655.	1.0	73

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55	Considerations when investigating lncRNA function in vivo. ELife, 2014, 3, e03058.	2.8	309
56	Distinct fibroblast lineages determine dermal architecture in skin development and repair. Nature, 2013, 504, 277-281.	13.7	946
57	Mutation in Folate Metabolism Causes Epigenetic Instability and Transgenerational Effects on Development. Cell, 2013, 155, 81-93.	13.5	225
58	An Unbiased Assessment of the Role of Imprinted Genes in an Intergenerational Model of Developmental Programming. PLoS Genetics, 2012, 8, e1002605.	1.5	105
59	Imprinted Gene Dosage Is Critical for the Transition to Independent Life. Cell Metabolism, 2012, 15, 209-221.	7.2	72
60	<i>Trim28</i> Is Required for Epigenetic Stability During Mouse Oocyte to Embryo Transition. Science, 2012, 335, 1499-1502.	6.0	287
61	BLUEPRINT to decode the epigenetic signature written in blood. Nature Biotechnology, 2012, 30, 224-226.	9.4	323
62	Mammalian Genomic Imprinting. Cold Spring Harbor Perspectives in Biology, 2011, 3, a002592-a002592.	2.3	423
63	Postnatal loss of Dlk1 imprinting in stem cells and niche astrocytes regulates neurogenesis. Nature, 2011, 475, 381-385.	13.7	247
64	You Are What Your Dad Ate. Cell Metabolism, 2011, 13, 115-117.	7.2	87
65	Genomic imprinting: the emergence of an epigenetic paradigm. Nature Reviews Genetics, 2011, 12, 565-575.	7.7	736
66	Genomic imprinting as an adaptative model of developmental plasticity. FEBS Letters, 2011, 585, 2059-2066.	1.3	54
67	Nonallelic Transcriptional Roles of CTCF and Cohesins at Imprinted Loci. Molecular and Cellular Biology, 2011, 31, 3094-3104.	1.1	44
68	Intergenerational Transmission of Glucose Intolerance and Obesity by In Utero Undernutrition in Mice. Diabetes, 2009, 58, 460-468.	0.3	277
69	Gene Dosage Effects of the Imprinted Delta-Like Homologue 1 (Dlk1/Pref1) in Development: Implications for the Evolution of Imprinting. PLoS Genetics, 2009, 5, e1000392.	1.5	88
70	Genomic imprinting at the mammalian Dlk1-Dio3 domain. Trends in Genetics, 2008, 24, 306-316.	2.9	362
71	The <i>Air</i> Noncoding RNA Epigenetically Silences Transcription by Targeting G9a to Chromatin. Science, 2008, 322, 1717-1720.	6.0	883
72	A Maternal-Zygotic Effect Gene, Zfp57, Maintains Both Maternal and Paternal Imprints. Developmental Cell, 2008, 15, 547-557.	3.1	565

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73	Restricted co-expression of Dlk1 and the reciprocally imprinted non-coding RNA, Gtl2: Implications for cis-acting control. Developmental Biology, 2007, 306, 810-823.	0.9	70
74	Mechanisms regulating imprinted genes in clusters. Current Opinion in Cell Biology, 2007, 19, 281-289.	2.6	373
75	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
76	Regulation of Gene Activity and Repression: A Consideration of Unifying Themes. Current Topics in Developmental Biology, 2004, 60, 197-213.	1.0	14
77	X Inactivation: Pre- or Post-Fertilisation Turn-off?. Current Biology, 2004, 14, R323-R325.	1.8	10
78	Genomic imprintingâ€"insights from studies in mice. Seminars in Cell and Developmental Biology, 2003, 14, 43-49.	2.3	27
79	Epigenetic analysis of the Dlk1-Gtl2 imprinted domain on mouse chromosome 12: implications for imprinting control from comparison with Igf2-H19. Human Molecular Genetics, 2002, 11, 77-86.	1.4	211
80	Placental-specific IGF-II is a major modulator of placental and fetal growth. Nature, 2002, 417, 945-948.	13.7	961
81	Relationship between DNA methylation, histone H4 acetylation and gene expression in the mouse imprintedIgf2-H19domain. FEBS Letters, 2001, 488, 165-169.	1.3	83
82	DNA methylation in genomic imprinting, development, and disease. Journal of Pathology, 2001, 195, 97-110.	2.1	244
83	The mouseGtl2 gene is differentially expressed during embryonic development, encodes multiple alternatively spliced transcripts, and may act as an RNA. , 1998, 212, 214-228.		144
84	Developmental effects of genomic imprinting on mouse chromosome 12. Genetical Research, 1998, 72, 59-72.	0.3	0
85	The mouse Gtl2 gene is differentially expressed during embryonic development, encodes multiple alternatively spliced transcripts, and may act as an RNA. , 1998, 212, 214.		2
86	Imprinting moves to the centre. Nature Genetics, 1996, 14, 119-121.	9.4	25
87	Parental-origin-specific epigenetic modification of the mouse H19 gene. Nature, 1993, 362, 751-755.	13.7	415