The imprinted gene and parent-of-origin effect databas

Nucleic Acids Research

29, 275-276

DOI: 10.1093/nar/29.1.275

Citation Report

#	Article	IF	Citations
1	Imprinted genes and mental dysfunction. Annals of Medicine, 2001, 33, 428-436.	3.8	88
2	Cardiomyopathy in mice with paternal uniparental disomy for chromosome 12. Genesis, 2001, 30, 274-279.	1.6	6
3	Post-Zygotic Origin of Complete Maternal Chromosome 7 Isodisomy and Consequent Loss of Placental PEG1/MEST Expression. Placenta, 2001, 22, 813-821.	1.5	23
4	Characterization of the Methylation-sensitive Promoter of the Imprinted ZAC Gene Supports Its Role in Transient Neonatal Diabetes Mellitus. Journal of Biological Chemistry, 2001, 276, 18653-18656.	3.4	65
5	The Role of Imprinted Genes in Fetal Growth. Neonatology, 2002, 81, 217-228.	2.0	99
6	Genome Scan Reveals New Coat Color Loci in Exotic Pig Cross. , 2002, 93, 1-8.		28
7	5 The origins of genomic imprinting in mammals. Advances in Genetics, 2002, 46, 119-163.	1.8	81
8	Visualization of Transcription-Dependent Association of Imprinted Genes with the Nuclear Matrix. Experimental Cell Research, 2002, 274, 189-196.	2.6	10
9	Asb4, Ata3, and Dcn Are Novel Imprinted Genes Identified by High-Throughput Screening Using RIKEN cDNA Microarray. Biochemical and Biophysical Research Communications, 2002, 290, 1499-1505.	2.1	126
11	Testing for Genetic Linkage in Families by a Variance-Components Approach in the Presence of Genomic Imprinting. American Journal of Human Genetics, 2002, 70, 751-757.	6.2	61
12	A Parent-of-Origin Effect in Two Families with Retinoblastoma Is Associated with a Distinct Splice Mutation in the RB1 Gene. American Journal of Human Genetics, 2002, 71, 174-179.	6.2	63
13	Mesial Temporal Lobe Abnormalities in a Family With 15q26qter Trisomy. Archives of Neurology, 2002, 59, 1476-9.	4.5	8
14	A further look at quantitative trait loci affecting growth and fatness in a cross between Meishan and Large White pig populations. Genetics Selection Evolution, 2002, 34, 193-210.	3.0	47
15	Evidence for linkage of HLA loci in juvenile idiopathic oligoarthritis: Independent effects of HLA-A and HLA-DRB1. Arthritis and Rheumatism, 2002, 46, 2716-2720.	6.7	25
16	The distinguishing sequence characteristics of mouse imprinted genes. Mammalian Genome, 2002, 13, 639-645.	2.2	37
17	A novel approach for identifying candidate imprinted genes through sequence analysis of imprinted and control genes. Human Genetics, 2002, 111, 511-520.	3.8	24
18	Glutamate Receptor Genes. Molecular Neurobiology, 2002, 25, 191-212.	4.0	43
19	Lay Understandings of Sex/Gender and Genetics: A Methodology That Preserves Polyvocal Coder Input. Sex Roles, 2003, 49, 557-570.	2.4	3

#	Article	IF	Citations
21	Fetal Development after Assisted Reproduction?A Review. Placenta, 2003, 24, S104-S113.	1.5	44
22	Natural Selection and the Evolution of Genome Imprinting. Annual Review of Genetics, 2003, 37, 349-370.	7.6	53
23	Epigenetic reprogramming in early embryonic development: effects of in-vitro production and somatic nuclear transfer. Reproductive BioMedicine Online, 2003, 7, 649-656.	2.4	68
24	Genomic Imprinting and Linkage Test for Quantitative-Trait Loci in Extended Pedigrees. American Journal of Human Genetics, 2003, 73, 933-938.	6.2	45
25	Imprinting. Advances in Experimental Medicine and Biology, 2003, 544, 159-168.	1.6	0
26	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
27	Discovery of Imprinted Transcripts in the Mouse Transcriptome Using Large-Scale Expression Profiling. Genome Research, 2003, 13, 1402-1409.	5.5	96
28	Identification of Novel Imprinted Genes in a Genome-Wide Screen for Maternal Methylation. Genome Research, 2003, 13, 558-569.	5.5	160
29	Formation of trisomies and their parental origin in hyperdiploid childhood acute lymphoblastic leukemia. Blood, 2003, 102, 3010-3015.	1.4	47
30	Characterization of quantitative trait loci for growth and meat quality in a cross between commercial breeds of swine1. Journal of Animal Science, 2004, 82, 2213-2228.	0.5	96
31	The Effect of Genetic Conflict on Genomic Imprinting and Modification of Expression at a Sex-Linked Locus. Genetics, 2004, 166, 565-579.	2.9	21
32	Identification and properties of imprinted genes and their control elements. Cytogenetic and Genome Research, 2004, 105, 335-345.	1.1	16
33	Resourceful imprinting. Nature, 2004, 432, 53-57.	27.8	257
34	Quantitative trait loci for meat yield and muscle distribution in a broiler layer cross. Livestock Science, 2004, 87, 143-151.	1.2	47
35	A parent-of-origin detectable polymorphism in the hypermethylated region upstream of the human H19 gene. International Journal of Legal Medicine, 2004, 118, 158-162.	2.2	12
36	Maternally and Paternally Silenced Imprinted Genes Differ in Their Intron Content. Comparative and Functional Genomics, 2004, 5, 572-583.	2.0	2
37	Characterization and chondrocyte differentiation stage-specific expression of KRAB zinc-finger protein gene ZNF470. Experimental Cell Research, 2004, 299, 137-147.	2.6	14
38	Maternal effect in multiple sclerosis. Lancet, The, 2004, 363, 1748-1749.	13.7	5

#	Article	IF	Citations
39	Genomic Imprinting in Plants: A Predominantly Maternal Affair. , 0, , 174-200.		16
40	No evidence for preferential maternal origin of duplicated chromosome 14 in hyperdiploid ALL. Blood, 2005, 105, 1837-1838.	1.4	2
41	Expression of imprinted genes is aberrant in deceased newborn cloned calves and relatively normal in surviving adult clones. Molecular Reproduction and Development, 2005, 71, 431-438.	2.0	108
42	Environmental signaling and evolutionary change: can exposure of pregnant mammals to environmental estrogens lead to epigenetically induced evolutionary changes in embryos?. Evolution & Development, 2005, 7, 341-350.	2.0	64
43	Identification of a cluster of X-linked imprinted genes in mice. Nature Genetics, 2005, 37, 620-624.	21.4	128
44	Imprinted genes and motherâ€“offspring interactions. Early Human Development, 2005, 81, 73-77.	1.8	120
45	A census of mammalian imprinting. Trends in Genetics, 2005, 21, 457-465.	6.7	612
46	Beckwithâ€“Wiedemann syndrome. American Journal of Medical Genetics, Part C: Seminars in Medical Genetics, 2005, 137C, 12-23.	1.6	263
47	Allelic expression of IGF2 in live-bearing, matrotrophic fishes. Development Genes and Evolution, 2005, 215, 207-212.	0.9	42
48	Linkage Analysis of Affected Sib Pairs Allowing for Parentâ€ofâ€Origin Effects. Annals of Human Genetics, 2005, 69, 113-126.	0.8	16
50	Mapping and Exclusion Mapping of Genomic Imprinting Effects in Mouse F2 Families. Journal of Heredity, 2005, 96, 329-338.	2.4	38
51	A Novel Variant of Inpp5f Is Imprinted in Brain, and Its Expression Is Correlated with Differential Methylation of an Internal CpG Island. Molecular and Cellular Biology, 2005, 25, 5514-5522.	2.3	63
52	Global gene expression profiles reveal significant nuclear reprogramming by the blastocyst stage after cloning. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 17582-17587.	7.1	184
53	Parametric Approach to Genomic Imprinting Analysis with Applications to Angelmanâ€™s Syndrome. Human Heredity, 2005, 59, 26-33.	0.8	15
54	APeg3, a novel paternally expressed gene 3 antisense RNA transcript specifically expressed in vasopressinergic magnocellular neurons in the rat supraoptic nucleus. Molecular Brain Research, 2005, 137, 143-151.	2.3	17
55	Characterization of three novel imprinted snoRNAs from mouse Irm gene. Biochemical and Biophysical Research Communications, 2006, 340, 1217-1223.	2.1	8
56	Expression profiling of uniparental mouse embryos is inefficient in identifying novel imprinted genes. Genomics, 2006, 87, 509-519.	2.9	34
57	Genomic Imprinting in Mammals: Emerging Themes and Established Theories. PLoS Genetics, 2006, 2, e147.	3.5	194

#	Article	IF	Citations
58	Determinants of intrauterine growth. , 2006, , 23-31.		4
60	Quantifying Genomic Imprinting in the Presence of Linkage. Biometrics, 2006, 62, 1071-1080.	1.4	8
61	Parentally imprinted allele typing at a short tandem repeat locus in intron 1a of imprinted gene KCNQ1. Legal Medicine, 2006, 8, 139-143.	1.3	5
62	TLINKAGE-IMPRINT: A Model-Based Approach to Performing Two-Locus Genetic Imprinting Analysis. Human Heredity, 2006, 62, 145-156.	0.8	3
63	Maximum likelihood inference of imprinting and allele-specific expression from EST data. Bioinformatics, 2006, 22, 3032-3039.	4.1	12
64	The imprinted gene and parent-of-origin effect database now includes parental origin of de novo mutations. Nucleic Acids Research, 2006, 34, D29-D31.	14.5	57
65	GeneChips in Stem Cell Research. Methods in Enzymology, 2006, 420, 162-224.	1.0	4
66	Perspectives: The Possible Influence of Assisted Reproductive Technologies on Transgenerational Reproductive Effects of Environmental Endocrine Disruptors. Toxicological Sciences, 2006, 96, 218-226.	3.1	17
67	Genome-wide survey of imprinted genes. Cytogenetic and Genome Research, 2006, 113, 144-152.	1.1	18
68	Chromosome-Wise Dissection of the Genome of the Extremely Big Mouse Line DU6i. Genetics, 2006, 172, 401-410.	2.9	17
69	An Extension of the Transmission Disequilibrium Test Incorporating Imprinting. Genetics, 2007, 175, 1489-1504.	2.9	12
70	Trisomy 8Âas theÂsole chromosomal aberration inÂacute myeloid leukemia andÂmyelodysplastic syndromes. Pathologie Et Biologie, 2007, 55, 37-48.	2.2	89
71	Distinct sets of developmentally regulated genes that are expressed by human oocytes and human embryonic stem cells. Fertility and Sterility, 2007, 87, 677-690.	1.0	39
72	Overexpression of IGF2R and IGF1R mRNA in SCNT-produced Goats Survived to Adulthood. Journal of Genetics and Genomics, 2007, 34, 709-719.	3.9	5
73	Genomic Imprinting as a Mechanism of Reproductive Isolation in Mammals. Journal of Mammalogy, 2007, 88, 5-23.	1.3	54
74	The transmission disequilibrium test and imprinting effects test based on caseâ€parent pairs. Genetic Epidemiology, 2007, 31, 273-287.	1.3	13
75	Data mining of RNA expression and DNA genotype data: Presentation Group 5 contributions to Genetic Analysis Workshop 15. Genetic Epidemiology, 2007, 31, S43-S50.	1.3	1
76	Dominance and parent-of-origin effects of coding and non-coding alleles at the acylCoA-diacylglycerol-acyltransferase (DGAT1) gene on milk production traits in German Holstein cows. BMC Genetics, 2007, 8, 62.	2.7	41

#	Article	IF	Citations
77	A simple method for detection of imprinting effects based on caseâ€“parents trios. Heredity, 2007, 98, 85-91.	2.6	5
78	Review article: Epigenetic control of fetal gene expression. BJOG: an International Journal of Obstetrics and Gynaecology, 2008, 115, 158-168.	2.3	172
79	Hypothesis: Dysregulation of methylation of brainâ€expressed genes on the X chromosome and autism spectrum disorders. American Journal of Medical Genetics, Part A, 2008, 146A, 2213-2220.	1.2	22
80	Epimutations of the KCNQ1OT1 imprinting center of chromosome 11 in early human embryolethality. Russian Journal of Genetics, 2008, 44, 1394-1399.	0.6	14
81	Parentally imprinted allele (PIA) typing in the differentially methylated region upstream of the human H19 gene. Forensic Science International: Genetics, 2008, 2, 286-291.	3.1	7
82	Unwitting hosts fall victim to imprinting. Epigenetics, 2008, 3, 258-260.	2.7	20
83	Maternal Transmission of Multiple Sclerosis in a Dutch Population. Archives of Neurology, 2008, 65, 345-8.	4.5	58
84	Investigating Parent of Origin Effects in Studies of Type 2 Diabetes and Obesity. Current Diabetes Reviews, 2008, 4, 329-339.	1.3	36
85	Detection of Parent-of-Origin Effects Based on Complete and Incomplete Nuclear Families with Multiple Affected Children. Human Heredity, 2009, 67, 1-12.	0.8	20
86	Differential methylation persists at the mouseRasgrf1DMR in tissues displaying monoallelic and biallelic expression. Epigenetics, 2009, 4, 241-247.	2.7	18
87	Detecting parent of origin and dominant QTL in a two-generation commercial poultry pedigree using variance component methodology. Genetics Selection Evolution, 2009, 41, 6.	3.0	19
88	Expression profile and transcription factor binding site exploration of imprinted genes in human and mouse. BMC Genomics, 2009, 10, 144.	2.8	27
89	Parental origin of sequence variants associated with complex diseases. Nature, 2009, 462, 868-874.	27.8	521
90	Effect of Alcohol Consumption on CpG Methylation in the Differentially Methylated Regions of H19 and IGâ€DMR in Male Gametesâ€”Implications for Fetal Alcohol Spectrum Disorders. Alcoholism: Clinical and Experimental Research, 2009, 33, 1615-1627.	2.4	224
91	The TDRD9-MIWI2 Complex Is Essential for piRNA-Mediated Retrotransposon Silencing in the Mouse Male Germline. Developmental Cell, 2009, 17, 775-787.	7.0	297
92	Family-Based Association Studies. , 2009, , 191-240.		2
93	Multiple sclerosis: clinical features, pathophysiology, neuroimaging and future therapies. Future Neurology, 2009, 4, 229-246.	0.5	9
94	Imprinting disorders and assisted reproductive technology. Current Opinion in Endocrinology, Diabetes and Obesity, 2010, 17, 517-522.	2.3	88

#	Article	IF	Citations
95	Divergence of imprinted genes during mammalian evolution. BMC Evolutionary Biology, 2010, 10, 116.	3.2	19
96	DNA sequence polymorphisms in a panel of eight candidate bovine imprinted genes and their association with performance traits in Irish Holstein-Friesian cattle. BMC Genetics, 2010, 11, 93.	2.7	49
97	Distinguishing epigenetic marks of developmental and imprinting regulation. Epigenetics and Chromatin, 2010, 3, 2.	3.9	69
98	Differential decay of parent-of-origin-specific genomic sharing in cystic fibrosis-affected sib pairs maps a paternally imprinted locus to 7q34. European Journal of Human Genetics, 2010, 18, 553-559.	2.8	2
99	Characterization of the methylation patterns of MS4A2 in atopic cases and controls. Allergy: European Journal of Allergy and Clinical Immunology, 2010, 65, 333-337.	5.7	10
100	Genome-wide Gene Expression Profiling Reveals Aberrant MAPK and Wnt Signaling Pathways Associated with Early Parthenogenesis. Journal of Molecular Cell Biology, 2010, 2, 333-344.	3.3	37
101	ncRNAimprint: A comprehensive database of mammalian imprinted noncoding RNAs. Rna, 2010, 16, 1889-1901.	3.5	49
102	Nutrition, Epigenetics, and Developmental Plasticity: Implications for Understanding Human Disease. Annual Review of Nutrition, 2010, 30, 315-339.	10.1	332
103	Genomic imprinting in diabetes. Genome Medicine, 2010, 2, 55.	8.2	11
104	Alterations in sperm DNA methylation patterns at imprinted loci in two classes of infertility. Fertility and Sterility, 2010, 94, 1728-1733.	1.0	259
105	Introduction into the analysis of high-throughput-sequencing based epigenome data. Briefings in Bioinformatics, 2010, 11, 512-523.	6.5	27
106	DNA methylation patterns associate with genetic and gene expression variation in HapMap cell lines. Genome Biology, 2011, 12, R10.	8.8	754
107	DNA sequence polymorphisms within the bovine guanine nucleotide-binding protein Gs subunit alpha (Gsî±)-encoding (GNAS) genomic imprinting domain are associated with performance traits. BMC Genetics, 2011, 12, 4.	2.7	32
108	Dynamic changes in gene expression during human early embryo development: from fundamental aspects to clinical applications. Human Reproduction Update, 2011, 17, 272-290.	10.8	121
109	Epigenetics in Male Reproduction: A Practical Introduction to the Informatics of Next Generation Sequencing. Epigenetics and Human Health, 2011, , 231-258.	0.2	0
110	Gene expression in placentation of farm animals: An overview of gene function during development. Theriogenology, 2011, 76, 589-597.	2.1	11
111	A comparative analysis of DNA methylation across human embryonic stem cell lines. Genome Biology, 2011, 12, R62.	9.6	86
112	The molecular and cellular basis of variable craniofacial phenotypes and their genetic rescue in Twisted gastrulation mutant mice. Developmental Biology, 2011, 355, 21-31.	2.0	13

#	Article	IF	Citations
113	The Characterisation of Three Types of Genes that Overlie Copy Number Variable Regions. PLoS ONE, 2011, 6, e14814.	2.5	24
114	Developmental plasticity and developmental origins of non-communicable disease: Theoretical considerations and epigenetic mechanisms. Progress in Biophysics and Molecular Biology, 2011, 106, 272-280.	2.9	248
115	Parental ages and levels of DNA methylation in the newborn are correlated. BMC Medical Genetics, 2011, 12, 47.	2.1	86
116	Detection of Parent-of-Origin Effects for Quantitative Traits in Complete and Incomplete Nuclear Families With Multiple Children. American Journal of Epidemiology, 2011, 174, 226-233.	3.4	12
117	A powerful approach for association analysis incorporating imprinting effects. Bioinformatics, 2011, 27, 2571-2577.	4.1	11
118	Assisted reproduction treatment and epigenetic inheritance. Human Reproduction Update, 2012, 18, 171-197.	10.8	161
119	A powerful parent-of-origin effects test for qualitative traits incorporating control children in nuclear families. Journal of Human Genetics, 2012, 57, 500-507.	2.3	8
120	CD45-deficient severe combined immunodeficiency caused by uniparental disomy. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 10456-10461.	7.1	39
121	The human imprintome vl.O: Over 120 imprinted genes in the human genome impose a major review on previous censuses. , 2012, , .		1
122	Parthenogenesis in non-rodent species: developmental competence and differentiation plasticity. Theriogenology, 2012, 77, 766-772.	2.1	18
123	dsPIG: a tool to predict imprinted genes from the deep sequencing of whole transcriptomes. BMC Bioinformatics, 2012, 13, 271.	2.6	12
124	A survey of tissue-specific genomic imprinting in mammals. Molecular Genetics and Genomics, 2012, 287, 621-630.	2.1	84
125	Localizing Transcriptional Regulatory Elements at the Mouse Dlk1 Locus. PLoS ONE, 2012, 7, e36483.	2.5	13
126	Porcine Tissue-Specific Regulatory Networks Derived from Meta-Analysis of the Transcriptome. PLoS ONE, 2012, 7, e46159.	2.5	23
127	Likelihood Approach for Detecting Imprinting and In Utero Maternal Effects Using General Pedigrees from Prospective Familyâ€Based Association Studies. Biometrics, 2012, 68, 477-485.	1.4	8
128	Investigation of six testicular germ cell tumor susceptibility genes suggests a parent-of-origin effect in SPRY4. Human Molecular Genetics, 2013, 22, 3373-3380.	2.9	26
129	Joint detection of association, imprinting and maternal effects using all children and their parents. European Journal of Human Genetics, 2013, 21, 1449-1456.	2.8	11
130	DNA Methylation Profiling of Placental Villi from Karyotypically Normal Miscarriage and Recurrent Miscarriage. American Journal of Pathology, 2013, 182, 2276-2284.	3.8	37

#	Article	IF	Citations
131	Intrauterine calorie restriction affects placental DNA methylation and gene expression. Physiological Genomics, 2013, 45, 565-576.	2.3	84
132	The Presence of Methylation Quantitative Trait Loci Indicates a Direct Genetic Influence on the Level of DNA Methylation in Adipose Tissue. PLoS ONE, 2013, 8, e55923.	2.5	83
133	Evolution of genomic imprinting as a coordinator of coadapted gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5085-5090.	7.1	30
134	Imprinting at the PLAGL1 domain is contained within a 70-kb CTCF/cohesin-mediated non-allelic chromatin loop. Nucleic Acids Research, 2013, 41, 2171-2179.	14.5	25
135	Paternally expressed genes predominate in the placenta. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 10705-10710.	7.1	137
136	Robust partial likelihood approach for detecting imprinting and maternal effects using case-control families. Annals of Applied Statistics, 2013, 7, .	1.1	10
137	Diagnosis of an imprintedâ€gene syndrome by a novel bioinformatics analysis of wholeâ€genome sequences from a family trio. Molecular Genetics & Genomic Medicine, 2014, 2, 530-538.	1.2	14
138	SNP-guided identification of monoallelic DNA-methylation events from enrichment-based sequencing data. Nucleic Acids Research, 2014, 42, e157-e157.	14.5	6
139	Genomeâ€wide association analyses of child genotype effects and parentâ€ofâ€origin effects in specific language impairment. Genes, Brain and Behavior, 2014, 13, 418-429.	2.2	76
140	Sperm DNA Methylation Analysis in Swine Reveals Conserved and Species-Specific Methylation Patterns and Highlights an Altered Methylation at the GNAS Locus in Infertile Boars1. Biology of Reproduction, 2014, 91, 137.	2.7	27
141	Clinical and genomic evaluation of 201 patients with Phelanâ€“McDermid syndrome. Human Genetics, 2014, 133, 847-859.	3.8	142
142	Using next-generation RNA sequencing to identify imprinted genes. Heredity, 2014, 113, 156-166.	2.6	108
143	Microarray analysis of gene expression in parthenotes and inÂvitroâ€“derived goat embryos. Theriogenology, 2014, 81, 854-860.	2.1	6
144	Flexible analysis of RNA-seq data using mixed effects models. Bioinformatics, 2014, 30, 180-188.	4.1	73
145	Nonparametric method for detecting imprinting effect using all members of general pedigrees with missing data. Journal of Human Genetics, 2014, 59, 541-548.	2.3	0
146	Imprinted loci in domestic livestock species as epigenomic targets for artificial selection of complex traits. Animal Genetics, 2014, 45, 25-39.	1.7	21
147	Different yet similar: evolution of imprinting in flowering plants and mammals. F1000prime Reports, 2014, 6, 63.	5.9	45
148	Allele-specific binding of ZFP57 in the epigenetic regulation of imprinted and non-imprinted monoallelic expression. Genome Biology, 2015, 16, 112.	8.8	150

#	Article	IF	Citations
149	The direction of cross affects obesity after puberty in male but not female offspring. BMC Genomics, 2015, 16, 904.	2.8	6
150	Allelome.PRO, a pipeline to define allele-specific genomic features from high-throughput sequencing data. Nucleic Acids Research, 2015, 43, gkv727.	14.5	26
151	A powerful association test for qualitative traits incorporating imprinting effects using general pedigree data. Journal of Human Genetics, 2015, 60, 77-83.	2.3	1
152	The landscape of genomic imprinting across diverse adult human tissues. Genome Research, 2015, 25, 927-936.	5.5	216
153	Epigenetic events regulating monoallelic gene expression. Critical Reviews in Biochemistry and Molecular Biology, 2015, 50, 337-358.	5.2	22
154	Genetic conflict reflected in tissue-specific maps of genomic imprinting in human and mouse. Nature Genetics, 2015, 47, 544-549.	21.4	221
155	Genomic imprinting effects on complex traits in domesticated animal species. Frontiers in Genetics, 2015, 6, 156.	2.3	25
156	Exercise-associated DNA methylation change in skeletal muscle and the importance of imprinted genes: a bioinformatics meta-analysis. British Journal of Sports Medicine, 2015, 49, 1567-1578.	6.7	108
157	Epigenetics in Exercise Science and Sports Medicine. , 2016, , 515-530.		5
158	A uniform survey of allele-specific binding and expression over 1000-Genomes-Project individuals. Nature Communications, 2016, 7, 11101.	12.8	78
159	DNA Methylation Profiling of Uniparental Disomy Subjects Provides a Map of Parental Epigenetic Bias in the Human Genome. American Journal of Human Genetics, 2016, 99, 555-566.	6.2	66
160	Loss of RNA expression and allele-specific expression associated with congenital heart disease. Nature Communications, 2016, 7, 12824.	12.8	51
161	Phenotypic subregions within the split-hand/foot malformation 1 locus. Human Genetics, 2016, 135, 345-357.	3.8	15
162	Nutrition in Early Life, Epigenetics, and Health. , 2016, , 135-158.		1
163	Allelic Dropout During Polymerase Chain Reaction due to G-Quadruplex Structures and DNA Methylation Is Widespread at Imprinted Human Loci. G3: Genes, Genomes, Genetics, 2017, 7, 1019-1025.	1.8	17
164	Detection of Imprinting Effects for Quantitative Traits on X Chromosome Using Nuclear Families with Multiple Daughters. Annals of Human Genetics, 2017, 81, 147-160.	0.8	2
165	Analysis of case-parent trios for imprinting effect using a loglinear model with adjustment for sex-of-parent-specific transmission ratio distortion. Human Genetics, 2017, 136, 951-961.	3.8	2
166	Maternal residential air pollution and placental imprinted gene expression. Environment International, 2017, 108, 204-211.	10.0	26

#	Article	IF	Citations
167	Linking Hematopoietic Differentiation to Co-Expressed Sets of Pluripotency-Associated and Imprinted Genes and to Regulatory microRNA-Transcription Factor Motifs. PLoS ONE, 2017, 12, e0166852.	2.5	7
168	Generalized disequilibrium test for association in qualitative traits incorporating imprinting effects based on extended pedigrees. BMC Genetics, 2017, 18, 90.	2.7	0
169	Novel imprinted single CpG sites found by global DNA methylation analysis in human parthenogenetic induced pluripotent stem cells. Epigenetics, 2018, 13, 343-351.	2.7	8
170	Identification of potential regulatory mutations using multi-omics analysis and haplotyping of lung adenocarcinoma cell lines. Scientific Reports, 2018, 8, 4926.	3.3	9
171	Two Powerful Tests for Parent-of-Origin Effects at Quantitative Trait Loci on the X Chromosome. Human Heredity, 2018, 83, 250-273.	0.8	0
173	Insights into imprinting from parent-of-origin phased methylomes and transcriptomes. Nature Genetics, 2018, 50, 1542-1552.	21.4	94
174	Effects of maternal nutrition on the expression of genomic imprinted genes in ovine fetuses. Epigenetics, 2018, 13, 793-807.	2.7	12
175	Genome-wide survey of parent-of-origin effects on DNA methylation identifies candidate imprinted loci in humans. Human Molecular Genetics, 2018, 27, 2927-2939.	2.9	22
176	Functional Genomics. , 2019, , 118-133.		5
177	Overgrowth Syndrome. Veterinary Clinics of North America - Food Animal Practice, 2019, 35, 265-276.	1.2	25
178	Genomic Imprinting As a Window into Human Language Evolution. BioEssays, 2019, 41, 1800212.	2.5	5
179	Epigenetic transgenerational inheritance of parent-of-origin allelic transmission of outcross pathology and sperm epimutations. Developmental Biology, 2020, 458, 106-119.	2.0	32
180	Immediate and durable effects of maternal tobacco consumption alter placental DNA methylation in enhancer and imprinted gene-containing regions. BMC Medicine, 2020, 18, 306.	5.5	24
181	Trappc9 deficiency causes parent-of-origin dependent microcephaly and obesity. PLoS Genetics, 2020, 16, e1008916.	3.5	22
182	Genomic Imprinting Is Critical for Understanding the Development and Adaptive Design of Psychological Mechanisms in Humans and Other Animals. , 2020, , 276-283.		0
183	Evolutionary Aspects of Genomic Imprinting. Molecular Biology, 2021, 55, 1-15.	1.3	7
186	PhenoDB, GeneMatcher and VariantMatcher, tools for analysis and sharing of sequence data. Orphanet Journal of Rare Diseases, 2021, 16, 365.	2.7	24
187	Loss of ZNF215 imprinting is associated with poor five-year survival in patients with cytogenetically abnormal-acute myeloid leukemia. Blood Cells, Molecules, and Diseases, 2021, 90, 102577.	1.4	7

#	Article	IF	Citations
188	Epigenetics in exercise science and sports medicine. , 2021, , 491-509.		1
189	Genomic Imprinting â€“ A Model for Roles of Histone Modifications in Epigenetic Control. , 2009, , 235-258.		5
191	Equality of the Sexes? Parent-of-Origin Effects on Transcription and de novo Mutations. , 2009, , 485-513.		1
192	Epigenetic Mechanisms in the Developmental Origins of Adult Disease. , 2011, , 187-204.		2
193	Mapping the epigenome â€” impact for toxicology. Exs, 2009, 99, 259-288.	1.4	13
194	On the Detection of Imprinted Quantitative Trait Loci in Experimental Crosses of Outbred Species. Genetics, 2002, 161, 931-938.	2.9	80
195	Toward a Marker-Dense Meiotic Map of the Potato Genome: Lessons From Linkage Group I. Genetics, 2003, 165, 2107-2116.	2.9	63
197	Allele-Specific, Age-Dependent and BMI-Associated DNA Methylation of Human MCHR1. PLoS ONE, 2011, 6, e17711.	2.5	43
198	Cellular Functions of Genetically Imprinted Genes in Human and Mouse as Annotated in the Gene Ontology. PLoS ONE, 2012, 7, e50285.	2.5	8
199	Hybrid Mice Reveal Parent-of-Origin and Cis- and Trans-Regulatory Effects in the Retina. PLoS ONE, 2014, 9, e109382.	2.5	22
200	Embryonic signature distinguishes pediatric and adult rhabdoid tumors from other SMARCB1-deficient cancers. Oncotarget, 2017, 8, 34245-34257.	1.8	13
202	Genome-Wide Assessment Characteristics of Genes Overlapping Copy Number Variation Regions in Duroc Purebred Population. Frontiers in Genetics, 2021, 12, 753748.	2.3	9
203	Imprinted Chromosomal Regions of the Human Genome Have Unusually High Recombination Rates. Genetics, 2003, 165, 1629-1632.	2.9	39
208	Epigenetic Profiling of Gliomas. , 2009, , 615-650.		1
209	The Importance of Aberrant DNA Methylation in Cancer. , 0, , .		1
211	Epigenetic Control of Genome Expression. , 2015, , 187-220.		0
212	EFFECTS OF AROCLOR 1254 ON THE DNA METHYLATION OF IMPRINTED GENES IN THE ADULT MOUSE SPERM. Applied Ecology and Environmental Research, 2017, 15, 999-1012.	0.5	1
215	AIJ: joint test for simultaneous detection of imprinting and non-imprinting allelic expression imbalance. Mathematical Biosciences and Engineering, 2020, 17, 366-386.	1.9	0

#	Article	IF	Citations
221	Genetics and familial distribution of multiple sclerosis: A review. Revue Neurologique, 2022, 178, 512-520.	1.5	4
222	Astroblastomas exhibit radial glia stem cell lineages and differential expression of imprinted and X-inactivation escape genes. Nature Communications, 2022, 13, 2083.	12.8	3
225	Detection of Parent-of-Origin Effects for the Variants Associated With Behavioral Disinhibition in the MCTFR Data. Frontiers in Genetics, 2022, 13, 831685.	2.3	0
226	Detection of Genomic Imprinting for Carcass Traits in Cattle Using Imputed High-Density Genotype Data. Frontiers in Genetics, 0, 13, .	2.3	1
227	Genome-wide detection of imprinted differentially methylated regions using nanopore sequencing. ELife, 0, 11, .	6.0	21
228	Increased copy number of imprinted genes in the chromosomal region 20q11-q13.32 is associated with resistance to antitumor agents in cancer cell lines. Clinical Epigenetics, 2022, 14, .	4.1	0
231	DNA Methylation Near DLGAP2 May Mediate the Relationship between Family History of Type 1 Diabetes and Type 1 Diabetes Risk. Pediatric Diabetes, 2023, 2023, 1-11.	2.9	0
232	Altered expression of imprinted genes in patients with cytogenetically normalâ€‘acute myeloid leukemia: Implications for leukemogenesis and survival outcomes. Molecular and Clinical Oncology, 2023, 19, .	1.0	0
233	Epigenomic mechanisms and episignature biomarkers in rare diseases. , 2024, , 1031-1076.		0