List of Publications by Year in descending order

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		38742	51608
181	8,959	50	86
papers	citations	h-index	g-index
212	212	212	10213
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Additional annotation enhances potential for biologically-relevant analysis of the Illumina Infinium HumanMethylation450 BeadChip array. Epigenetics and Chromatin, 2013, 6, 4.	3.9	412
2	Cytogenetic analysis of miscarriages from couples with recurrent miscarriage: a case-control study. Human Reproduction, 2002, 17, 446-451.	0.9	381
3	Mechanisms leading to uniparental disomy and their clinical consequences. BioEssays, 2000, 22, 452-459.	2.5	296
4	Uniparental disomy 7 in Silver—Russell syndrome and primordial growth retardation. Human Molecular Genetics, 1995, 4, 583-587.	2.9	289
5	Small nuclear ribonucleoprotein polypeptide N (SNRPN), an expressed gene in the Prader–Willi syndrome critical region. Nature Genetics, 1992, 2, 265-269.	21.4	271
6	The human placenta methylome. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6037-6042.	7.1	256
7	Molecular diagnosis of the Prader-Willi and Angelman syndromes by detection of parent-of-origin specific DNA methylation in 15q11-13. Human Genetics, 1992, 90, 313-5.	3.8	195
8	DNA methylation profiling of human placentas reveals promoter hypomethylation of multiple genes in early-onset preeclampsia. European Journal of Human Genetics, 2010, 18, 1006-1012.	2.8	189
9	Widespread DNA hypomethylation at gene enhancer regions in placentas associated with early-onset pre-eclampsia. Molecular Human Reproduction, 2013, 19, 697-708.	2.8	187
10	FMR1 repeat sizes in the gray zone and high end of the normal range are associated with premature ovarian failure. Human Genetics, 2005, 117, 376-382.	3.8	170
11	Evidence for widespread changes in promoter methylation profile in human placenta in response to increasing gestational age and environmental/stochastic factors. BMC Genomics, 2011, 12, 529.	2.8	164
12	Fertility and aging: do reproductive-aged Canadian women know what they need to know?. Fertility and Sterility, 2010, 93, 2162-2168.	1.0	162
13	Androgenetic/biparental mosaicism causes placental mesenchymal dysplasia. Journal of Medical Genetics, 2005, 43, 187-192.	3.2	161
14	HLA–Bw60 increases susceptibility to ankylosing spondylitis in HLA–B27+ patients. Arthritis and Rheumatism, 1989, 32, 1135-1141.	6.7	158
15	Decreased Placental Methylation at the H19/IGF2 Imprinting Control Region is Associated with Normotensive Intrauterine Growth Restriction but not Preeclampsia. Placenta, 2010, 31, 197-202.	1.5	148
16	Genotype-phenotype correlation in a series of 167 deletion and non-deletion patients with Prader-Willi syndrome. Human Genetics, 1995, 96, 638-643.	3.8	147
17	Modification of 15q11 — q13 DNA methylation imprints in unique Angelman and Prader — Willi patients. Human Molecular Genetics, 1993, 2, 1377-1382.	2.9	144
18	DNA methylation changes in whole blood is associated with exposure to the environmental contaminants, mercury, lead, cadmium and bisphenol A, in women undergoing ovarian stimulation for IVF. Human Reproduction, 2012, 27, 1401-1410.	0.9	142

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19	Skewed X-Chromosome Inactivation Is Common in Fetuses or Newborns Associated with Confined Placental Mosaicism. American Journal of Human Genetics, 1997, 61, 1353-1361.	6.2	114
20	Chromosome-wide DNA methylation analysis predicts human tissue-specific X inactivation. Human Genetics, 2011, 130, 187-201.	3.8	111
21	<i>MECP2</i> promoter methylation and X chromosome inactivation in autism. Autism Research, 2008, 1, 169-178.	3.8	107
22	Pervasive polymorphic imprinted methylation in the human placenta. Genome Research, 2016, 26, 756-767.	5.5	107
23	Sex-specific meiotic recombination in the PraderWilli/Angelman syndrome imprinted region. Human Molecular Genetics, 1995, 4, 801-806.	2.9	105
24	Telomere length and reproductive aging. Human Reproduction, 2009, 24, 1206-1211.	0.9	101
25	Early Onset Pre-Eclampsia Is Associated with Altered DNA Methylation of Cortisol-Signalling and Steroidogenic Genes in the Placenta. PLoS ONE, 2013, 8, e62969.	2.5	98
26	Identification of copy number variants in miscarriages from couples with idiopathic recurrent pregnancy loss. Human Reproduction, 2010, 25, 2913-2922.	0.9	95
27	A skewed view of X chromosome inactivation. Journal of Clinical Investigation, 2008, 118, 20-23.	8.2	94
28	Different measures of "genome-wide―DNA methylation exhibit unique properties in placental and somatic tissues. Epigenetics, 2012, 7, 652-663.	2.7	85
29	Genome-wide mapping of imprinted differentially methylated regions by DNA methylation profiling of human placentas from triploidies. Epigenetics and Chromatin, 2011, 4, 10.	3.9	84
30	Prenatal and Perinatal Environmental Influences on the Human Fetal and Placental Epigenome. Clinical Pharmacology and Therapeutics, 2012, 92, 716-726.	4.7	84
31	Extremely Skewed X-Chromosome Inactivation Is Increased in Women with Recurrent Spontaneous Abortion. American Journal of Human Genetics, 1999, 65, 913-917.	6.2	82
32	Hypoxia alters the epigenetic profile in cultured human placental trophoblasts. Epigenetics, 2013, 8, 192-202.	2.7	80
33	Placental epigenetic clocks: estimating gestational age using placental DNA methylation levels. Aging, 2019, 11, 4238-4253.	3.1	79
34	The Human Placental Methylome. Cold Spring Harbor Perspectives in Medicine, 2015, 5, a023044-a023044.	6.2	77
35	Origin and outcome of pregnancies affected by androgenetic/biparental chimerism. Human Reproduction, 2007, 22, 1114-1122.	0.9	75
36	Evaluating DNA methylation and gene expression variability in the human term placenta. Placenta, 2010, 31, 1070-1077.	1.5	75

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37	Human Placental-Specific Epipolymorphism and its Association with Adverse Pregnancy Outcomes. PLoS ONE, 2009, 4, e7389.	2.5	71
38	The genotypic and phenotypic spectrum of PIGA deficiency. Orphanet Journal of Rare Diseases, 2015, 10, 23.	2.7	70
39	Inactive X chromosome-specific reduction in placental DNA methylation. Human Molecular Genetics, 2009, 18, 3544-3552.	2.9	66
40	Adjusting for Batch Effects in DNA Methylation Microarray Data, a Lesson Learned. Frontiers in Genetics, 2018, 9, 83.	2.3	66
41	Global analysis of DNA methylation changes during progression of oral cancer. Oral Oncology, 2013, 49, 1033-1042.	1.5	64
42	Comparison of phenotype in uniparental disomy and deletion Prader-Willi syndrome: Sex specific differences. , 1996, 65, 133-136.		63
43	Epigenetic regulation of placental gene expression in transcriptional subtypes of preeclampsia. Clinical Epigenetics, 2018, 10, 28.	4.1	63
44	Estrogen receptor α gene polymorphisms are associated with idiopathic premature ovarian failure. Fertility and Sterility, 2008, 89, 318-324.	1.0	62
45	Cell-specific characterization of the placental methylome. BMC Genomics, 2021, 22, 6.	2.8	62
46	MATERNAL UNIPARENTAL DISOMY OF CHROMOSOME 2 AND CONFINED PLACENTAL MOSAICISM FOR TRISOMY 2 IN A FETUS WITH INTRAUTERINE GROWTH RESTRICTION, HYPOSPADIAS, AND OLIGOHYDRAMNIOS. Prenatal Diagnosis, 1997, 17, 443-450.	2.3	60
47	Somatic segregation errors predominantly contribute to the gain or loss of a paternal chromosome leading to uniparental disomy for chromosome 15. Clinical Genetics, 2000, 57, 349-358.	2.0	58
48	Hypomethylation of the LEP gene in placenta and elevated maternal leptin concentration in early onset pre-eclampsia. Molecular and Cellular Endocrinology, 2013, 367, 64-73.	3.2	58
49	Extensive epigenetic reprogramming in human somatic tissues between fetus and adult. Epigenetics and Chromatin, 2011, 4, 7.	3.9	57
50	Maternal Uniparental Disomy of Chromosome 1 with No Apparent Phenotypic Effects. American Journal of Human Genetics, 1998, 63, 1216-1220.	6.2	56
51	Homozygous parent affected sib pair method for detecting disease predisposing variants: Application to insulin dependent diabetes mellitus. Genetic Epidemiology, 1993, 10, 273-288.	1.3	53
52	Postnatal followâ€up of prenatally diagnosed trisomy 16 mosaicism. Prenatal Diagnosis, 2006, 26, 548-558.	2.3	52
53	Origin of amnion and implications for evaluation of the fetal genotype in cases of mosaicism. Prenatal Diagnosis, 2002, 22, 1076-1085.	2.3	51
54	ADAM12-directed ectodomain shedding of E-cadherin potentiates trophoblast fusion. Cell Death and Differentiation, 2015, 22, 1970-1984.	11.2	51

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55	Assessing the role of placental trisomy in preeclampsia and intrauterine growth restriction. Prenatal Diagnosis, 2010, 30, 1-8.	2.3	50
56	Glucose as a fetal nutrient: dynamic regulation of several glucose transporter genes by DNA methylation in the human placenta across gestation. Journal of Nutritional Biochemistry, 2013, 24, 282-288.	4.2	50
57	Mining DNA methylation alterations towards a classification of placental pathologies. Human Molecular Genetics, 2018, 27, 135-146.	2.9	50
58	Review: A high capacity of the human placenta for genetic and epigenetic variation: Implications for assessing pregnancy outcome. Placenta, 2011, 32, S136-S141.	1.5	48
59	Detection of aberrant DNA methylation in unique Prader — Willi syndrome patients and its diagnostic implications. Human Molecular Genetics, 1994, 3, 893-895.	2.9	47
60	Nucleated red blood cells impact DNA methylation and expression analyses of cord blood hematopoietic cells. Clinical Epigenetics, 2015, 7, 95.	4.1	47
61	Beckwith–Wiedemann and Silver–Russell syndromes: opposite developmental imbalances in imprinted regulators of placental function and embryonic growth. Clinical Genetics, 2013, 84, 326-334.	2.0	42
62	Developmental transcription factor NFIB is a putative target of oncofetal miRNAs and is associated with tumour aggressiveness in lung adenocarcinoma. Journal of Pathology, 2016, 240, 161-172.	4.5	42
63	An empirically driven data reduction method on the human 450K methylation array to remove tissue specific non-variable CpGs. Clinical Epigenetics, 2017, 9, 11.	4.1	42
64	Placenta-specific Expression of the Interleukin-2 (IL-2) Receptor Î ² Subunit from an Endogenous Retroviral Promoter. Journal of Biological Chemistry, 2011, 286, 35543-35552.	3.4	41
65	Profiling placental and fetal DNA methylation in human neural tube defects. Epigenetics and Chromatin, 2016, 9, 6.	3.9	41
66	DNA methylation profiling of acute chorioamnionitis-associated placentas and fetal membranes: insights into epigenetic variation in spontaneous preterm births. Epigenetics and Chromatin, 2018, 11, 63.	3.9	41
67	DNA methylation at H19/IGF2 ICR1 in the placenta of pregnancies conceived by in vitro fertilization and intracytoplasmic sperm injection. Fertility and Sterility, 2011, 95, 2524-2526.e3.	1.0	40
68	Accurate ethnicity prediction from placental DNA methylation data. Epigenetics and Chromatin, 2019, 12, 51.	3.9	40
69	Number of Children and Telomere Length in Women: A Prospective, Longitudinal Evaluation. PLoS ONE, 2016, 11, e0146424.	2.5	40
70	Patterns of placental development evaluated by X chromosome inactivation profiling provide a basis to evaluate the origin of epigenetic variation. Human Reproduction, 2012, 27, 1745-1753.	0.9	39
71	Molecular definition of the Prader — Willi syndrome chromosome region and orientation of the SNRPN gene. Human Molecular Genetics, 1993, 2, 1991-1994.	2.9	37
72	DNA Methylation Profiling of Placental Villi from Karyotypically Normal Miscarriage and Recurrent Miscarriage. American Journal of Pathology, 2013, 182, 2276-2284.	3.8	37

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73	Recurrent triploidy due to a failure to complete maternal meiosis II: whole-exome sequencing reveals candidate variants. Molecular Human Reproduction, 2015, 21, 339-346.	2.8	37
74	Quantification of Cell-Free DNA in Normal and Complicated Pregnancies: Overcoming Biological and Technical Issues. PLoS ONE, 2014, 9, e101500.	2.5	37
75	Recurrent trisomy 21 in a couple with a child presenting trisomy 21 mosaicism and maternal uniparental disomy for chromosome 21 in the euploid cell line. American Journal of Medical Genetics Part A, 2000, 94, 35-41.	2.4	35
76	Exclusively paternal X chromosomes in a girl with short stature. Human Genetics, 1993, 92, 175-8.	3.8	34
77	Molecular and clinical correlation study of Williams-Beuren syndrome: No evidence of molecular factors in the deletion region or imprinting affecting clinical outcome. , 1999, 86, 34-43.		34
78	Placental mesenchymal dysplasia associated with fetal overgrowth and mosaic deletion of the maternal copy of 11p15.5. American Journal of Medical Genetics, Part A, 2007, 143A, 1752-1759.	1.2	34
79	Methylation of <i>ZNF261</i> as an assay for determining X chromosome inactivation patterns. American Journal of Medical Genetics, Part A, 2003, 120A, 439-441.	1.2	33
80	The association between preeclampsia and placental trisomy 16 mosaicism. Prenatal Diagnosis, 2006, 26, 956-961.	2.3	33
81	Partial tetrasomy with triplication of chromosome (5) (p14-p15.33) in a patient with severe multiple congenital anomalies. American Journal of Medical Genetics Part A, 1998, 79, 103-107.	2.4	32
82	ICSI and the transmission of X-autosomal translocation: a three-generation evaluation of X;20 translocation: Case report. Human Reproduction, 2003, 18, 1377-1382.	0.9	32
83	Parental origin of the supernumerary chromosome in trisomy 18. Clinical Genetics, 1993, 44, 57-61.	2.0	32
84	The utility of quantitative methylation assays at imprinted genes for the diagnosis of fetal and placental disorders. Clinical Genetics, 2011, 79, 169-175.	2.0	32
85	Review: placental biomarkers for assessing fetal health. Human Molecular Genetics, 2017, 26, R237-R245.	2.9	32
86	Dispermyorigin of diandric triploidy: Brief Communication. Human Reproduction, 2002, 17, 3037-3038.	0.9	31
87	Methylation profiling in individuals with Russell–Silver syndrome. American Journal of Medical Genetics, Part A, 2010, 152A, 347-355.	1.2	31
88	Placental telomere length decline with gestational age differs by sex and TERT, DNMT1, and DNMT3A DNA methylation. Placenta, 2016, 48, 26-33.	1.5	31
89	Overlapping DNA methylation profile between placentas with trisomy 16 and early-onset preeclampsia. Placenta, 2014, 35, 216-222.	1.5	29
90	Characterizing the hypomethylated DNA methylation profile of nucleated red blood cells from cord blood. Epigenomics, 2016, 8, 1481-1494.	2.1	29

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91	Grandmaternal origin of an isochromosome 18p present in two maternal half-sisters. American Journal of Medical Genetics Part A, 2001, 101, 65-69.	2.4	27
92	No difference between wearing a night splint and standing on a tilt table in preventing ankle contracture early after stroke: a randomised trial. Australian Journal of Physiotherapy, 2008, 54, 33-38.	0.9	27
93	Considerations when processing and interpreting genomics data of the placenta. Placenta, 2019, 84, 57-62.	1.5	27
94	Cytogenetic investigation of fetuses and infants conceived through intracytoplasmic sperm injection. Fertility and Sterility, 2001, 76, 1272-1275.	1.0	26
95	No evidence for association of MTHFR 677C>T and 1298A>C variants with placental DNA methylation. Clinical Epigenetics, 2018, 10, 34.	4.1	25
96	Genetic variation within the hypothalamus-pituitary-ovarian axis in women with recurrent miscarriage. Human Reproduction, 2010, 25, 2664-2671.	0.9	24
97	Cord blood hematopoietic cells from preterm infants display altered DNA methylation patterns. Clinical Epigenetics, 2017, 9, 39.	4.1	24
98	Trisomy First, Translocation Second, Uniparental Disomy and Partial Trisomy Third: A New Mechanism for Complex Chromosomal Aneuploidy. European Journal of Human Genetics, 1997, 5, 308-314.	2.8	24
99	An association between skewed X-chromosome inactivation and abnormal outcome in mosaic trisomy 16 confined predominantly to the placenta. Clinical Genetics, 2008, 58, 436-446.	2.0	23
100	Activation of endocrine-related gene expression in placental choriocarcinoma cell lines following DNA methylation knock-down. Molecular Human Reproduction, 2014, 20, 677-689.	2.8	23
101	A cross-cohort analysis of autosomal DNA methylation sex differences in the term placenta. Biology of Sex Differences, 2021, 12, 38.	4.1	23
102	Sex Differences Are Here to Stay: Relevance to Prenatal Care. Journal of Clinical Medicine, 2021, 10, 3000.	2.4	23
103	Frequency of chromosomal abnormalities in spontaneous abortions derived from intracytoplasmic sperm injection compared with those from in vitro fertilization. Fertility and Sterility, 2006, 85, 236-239.	1.0	21
104	Improved reporting of DNA methylation data derived from studies of the human placenta. Epigenetics, 2014, 9, 333-337.	2.7	21
105	Noninvasive nucleic acid–based approaches to monitor placental health and predict pregnancy-related complications. American Journal of Obstetrics and Gynecology, 2015, 213, S197-S206.	1.3	21
106	Low oxygen enhances trophoblast column growth by potentiating differentiation of the extravillous lineage and promoting LOX activity. Development (Cambridge), 2020, 147, .	2.5	20
107	Defects in fatty acid amide hydrolase 2 in a male with neurologic and psychiatric symptoms. Orphanet Journal of Rare Diseases, 2015, 10, 38.	2.7	19
108	Novel case of del(17)(q23.1q23.3) further highlights a recognizable phenotype involving deletions of chromosome (17)(q21q24). American Journal of Medical Genetics Part A, 1997, 71, 275-279.	2.4	18

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109	Prenatally detected trisomy 4 and 6 mosaicism?cytogenetic results and clinical phenotype. Prenatal Diagnosis, 2003, 23, 128-133.	2.3	18
110	Pseudohypoparathyroidism type 1a and the <i>GNAS</i> p.R231H mutation: Somatic mosaicism in a mother with two affected sons. American Journal of Medical Genetics, Part A, 2010, 152A, 2784-2790.	1.2	17
111	Maternal NLRP7 and C6orf221 variants are not a common risk factor for androgenetic moles, triploidy and recurrent miscarriage. Molecular Human Reproduction, 2013, 19, 539-544.	2.8	17
112	Placental DNA methylation at term reflects maternal serum levels of INHA and FN1, but not PAPPA, early in pregnancy. BMC Medical Genetics, 2015, 16, 111.	2.1	17
113	Functional consequences of copy number variants in miscarriage. Molecular Cytogenetics, 2015, 8, 6.	0.9	17
114	Exome sequencing identified a de novo mutation of PURA gene in a patient with familial Xp22.31 microduplication. European Journal of Medical Genetics, 2019, 62, 103-108.	1.3	17
115	A case of intraplacental gestational choriocarcinoma; characterised by the methylation pattern of the early placenta and an absence of driver mutations. BMC Cancer, 2019, 19, 744.	2.6	17
116	Deletion breakpoints associated with the Prader-Willi and Angelman syndromes (15q11-q13) are not sites of high homologous recombination. Human Genetics, 1993, 91, 181-4.	3.8	16
117	Recurrent trisomy 15 in a female carrier of der(15)t(Y;15)(q12;p13). American Journal of Medical Genetics Part A, 2001, 99, 320-324.	2.4	16
118	Toll-like receptor 4 polymorphisms and idiopathic chromosomally normal miscarriage. Human Reproduction, 2007, 22, 440-443.	0.9	16
119	Chorea as a side effect of gabapentin (Neurontin®) in a patient with complex regional pain syndrome Type 1. Clinical Rheumatology, 2008, 27, 389-390.	2.2	16
120	IFPA meeting 2016 workshop report II: Placental imaging, placenta and development of other organs, sexual dimorphism in placental function and trophoblast cell lines. Placenta, 2017, 60, S10-S14.	1.5	16
121	Utility of DNA methylation to assess placental health. Placenta, 2018, 64, S23-S28.	1.5	16
122	XISTExpression and X-Chromosome Inactivation in Human Preimplantation Embryos. American Journal of Human Genetics, 1997, 61, 5-8.	6.2	15
123	Placental Weight in Pregnancies With Trisomy Confined to the Placenta. Journal of Obstetrics and Gynaecology Canada, 2009, 31, 605-610.	0.7	15
124	Association of a placental Interleukin-6 genetic variant (rs1800796) with DNA methylation, gene expression and risk of acute chorioamnionitis. BMC Medical Genetics, 2019, 20, 36.	2.1	15
125	The significance of the placental genome and methylome in fetal and maternal health. Human Genetics, 2020, 139, 1183-1196.	3.8	14
126	Absence of SYCP3 mutations in women with recurrent miscarriage with at least one trisomic miscarriage. Reproductive BioMedicine Online, 2012, 24, 251-253.	2.4	13

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127	Genomic imbalances in the placenta are associated with poor fetal growth. Molecular Medicine, 2021, 27, 3.	4.4	13
128	Skewed X-chromosome inactivation is associated with primary but not secondary ovarian failure. American Journal of Medical Genetics, Part A, 2007, 143A, 945-951.	1.2	12
129	A de novo mosaic mutation in SPAST with two novel alternative alleles and chromosomal copy number variant in a boy with spastic paraplegia and autism spectrum disorder. European Journal of Medical Genetics, 2017, 60, 548-552.	1.3	12
130	Genome-wide DNA methylation identifies trophoblast invasion-related genes: Claudin-4 and Fucosyltransferase IV control mobility via altering matrix metalloproteinase activity. Molecular Human Reproduction, 2015, 21, 452-465.	2.8	11
131	A cryptic familial rearrangement of 11p15.5, involving both imprinting centers, in a family with a history of short stature. American Journal of Medical Genetics, Part A, 2014, 164, 1587-1594.	1.2	10
132	The English «Teaching Excellence Framework» and Professionalising Teaching and Learning in Research-Intensive Universities: An Exploration of Opportunities, Challenges, Rewards and Values from a Recent Empirical Study. Foro De Educacion, 2016, 14, 151.	0.1	10
133	Phenotype of maternal UPD(14). , 1996, 66, 89-89.		9
134	Multipoint Genetic Mapping with Uniparental Disomy Data. American Journal of Human Genetics, 2000, 67, 851-861.	6.2	9
135	Recurrent trisomy 21: four cases in three generations. Clinical Genetics, 2005, 68, 430-435.	2.0	8
136	Pregnancy and postnatal outcome of mosaic isochromosome 20q. Prenatal Diagnosis, 2007, 27, 143-145.	2.3	8
137	Cell-Free Placental DNA in Maternal Plasma in Relation to Placental Health and Function. Fetal Diagnosis and Therapy, 2017, 41, 258-264.	1.4	8
138	Mosaicism most likely accounts for extended survival of trisomy 22. , 1996, 62, 100-100.		7
139	Variant ATRX Syndrome with Dysfunction of ATRX and MAGT1 Genes. Human Mutation, 2014, 35, 58-62.	2.5	7
140	Biallelic mutations in huntington disease: A new case with just one affected parent, review of the literature and terminology. American Journal of Medical Genetics, Part A, 2015, 167, 1152-1160.	1.2	7
141	Whole exome sequencing of families with 1q21.1 microdeletion or microduplication. American Journal of Medical Genetics, Part A, 2017, 173, 1782-1791.	1.2	7
142	Profiling the small non-coding RNA transcriptome of the human placenta. Scientific Data, 2021, 8, 166.	5.3	7
143	Developmental Origin of Chorionic Villus Cultures From Spontaneous Abortion and Chorionic Villus Sampling. Journal of Obstetrics and Gynaecology Canada, 2011, 33, 449-452.	0.7	6
144	Beckwith–Wiedemann syndrome in sibs discordant for IC2 methylation. American Journal of Medical Genetics, Part A, 2012, 158A, 1662-1669.	1.2	6

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145	Child mortality, hypothalamic-pituitary-adrenal axis activity and cellular aging in mothers. PLoS ONE, 2017, 12, e0177869.	2.5	6
146	Confined placental mosaicism involving multiple de novo copy number variants associated with fetal growth restriction: A case report. American Journal of Medical Genetics, Part A, 2021, 185, 1908-1912.	1.2	6
147	Are sex differences in cognitive impairment reflected in epigenetic age acceleration metrics?. Neurobiology of Aging, 2022, 109, 192-194.	3.1	6
148	Small Non-Coding RNAs in the Human Placenta: Regulatory Roles and Clinical Utility. Frontiers in Genetics, 2022, 13, 868598.	2.3	6
149	Are we ready for DNA methylation-based prenatal testing?. Epigenomics, 2011, 3, 387-390.	2.1	5
150	Protein Kinase Profiling in Miscarriage: Implications for the Pathogenesis of Trisomic Pregnancy. Journal of Obstetrics and Gynaecology Canada, 2012, 34, 1141-1148.	0.7	5
151	"Willing enthusiasts―or "lame ducks� Issues in teacher professional development policy in England and Wales 1910–1975. Paedagogica Historica, 2013, 49, 345-360.	0.1	5
152	Clues to IDDM pathogenesis from genetic and serological traits in multiply affected families. Genetic Epidemiology, 1989, 6, 117-122.	1.3	4
153	†That great educational experiment': the City of London Vacation Course in Education 1922–1938: a forgotten story in the history of teacher professional development. History of Education, 2011, 40, 557-575.	0.4	4
154	CHIPS-Child: Testing the developmental programming hypothesis in the offspring of the CHIPS trial. Pregnancy Hypertension, 2018, 14, 15-22.	1.4	4
155	Renpenning syndrome in a female. American Journal of Medical Genetics, Part A, 2020, 182, 498-503.	1.2	4
156	Human placental piwi-interacting RNA transcriptome is characterized by expression from the DLK1-DIO3 imprinted region. Scientific Reports, 2021, 11, 14981.	3.3	4
157	Epigenetic Modifications in the Human Placenta. , 2019, , 293-311.		3
158	Mistakes Are Common; Should We Worry about Them?. Trends in Molecular Medicine, 2021, 27, 721-722.	6.7	3
159	Mechanisms leading to uniparental disomy and their clinical consequences. BioEssays, 2000, 22, 452.	2.5	3
160	Response to. Epigenetics, 2012, 7, 965-965.	2.7	2
161	Cenetic and epigenetic changes in the placenta in intrauterine growth restriction (IUGR). Placenta, 2017, 57, 242.	1.5	2
162	Altered levels of placental miR-338-3p and miR-518b are associated with acute chorioamnionitis and IL6 genotype. Placenta, 2019, 82, 42-45.	1.5	2

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163	Partial tetrasomy with triplication of chromosome (5) (p14â€p15.33) in a patient with severe multiple congenital anomalies. American Journal of Medical Genetics Part A, 1998, 79, 103-107.	2.4	2
164	Molecular Detection of Uniparental Disomy. , 2002, 204, 291-298.		1
165	X-Chromosome Inactivation. , 2013, , 63-88.		1
166	Using DNA methylation signatures in placental tissue and cells to gain insight into chorioamnionitis. Placenta, 2016, 45, 113.	1.5	1
167	Epigenetic regulation of placental gene expression in transcriptional subclasses of preeclampsia. Placenta, 2016, 45, 122-123.	1.5	1
168	Examining the Vanishing Twin Hypothesis of Neural Tube Defects: Application of an Epigenetic Predictor for Monozygotic Twinning. Twin Research and Human Genetics, 2021, 24, 155-159.	0.6	1
169	Genetic and Epigenetic Mechanisms Deregulate the CRL2pVHL Complex in Hepatocellular Carcinoma. Frontiers in Genetics, 2022, 13, .	2.3	1
170	X-Chromosome inactivation (XCI) patterns in placental tissues of a paternally derived bal t(X;20) case. Fertility and Sterility, 2002, 78, S255-S256.	1.0	0
171	P-159. Fertility and Sterility, 2006, 86, S191.	1.0	0
172	Telomere Length and Reproductive Aging. Obstetrical and Gynecological Survey, 2009, 64, 663-664.	0.4	0
173	miRNA expression in human lung cancer and fetal lung: a comparative study. BMC Proceedings, 2013, 7, .	1.6	0
174	Decidual natural killer cells regulate FUT4 expression in EVT through DNA enhancer methylation. Placenta, 2013, 34, A68-A69.	1.5	0
175	Politics, professionals and practitioners. History of Education, 2014, 43, 719-723.	0.4	0
176	MG-123â€Genomics of early pregnancy loss. Journal of Medical Genetics, 2015, 52, A6.1-A6.	3.2	0
177	An integrated transcriptional, epigenetic, and clinical analysis of preeclamptic placentas. Placenta, 2015, 36, A7.	1.5	0
178	Placental MTHFR 677C>T genotypes in pregnancy pathologies. Placenta, 2016, 45, 112.	1.5	0
179	Placentation and Genomic Imprinting. , 2017, , 159-184.		0
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