Wendy P Robinson

List of Publications by Year
in descending order

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181	8,959	38742 50	51608 86
papers	citations	h-index	g-index

212	212	212	10213
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Are sex differences in cognitive impairment reflected in epigenetic age acceleration metrics?. Neurobiology of Aging, 2022, 109, 192-194.	3.1	6
2	Small Non-Coding RNAs in the Human Placenta: Regulatory Roles and Clinical Utility. Frontiers in Genetics, 2022, 13, 868598.	2.3	6
3	Genetic and Epigenetic Mechanisms Deregulate the CRL2pVHL Complex in Hepatocellular Carcinoma. Frontiers in Genetics, 2022, 13, .	2.3	1
4	Genomic imbalances in the placenta are associated with poor fetal growth. Molecular Medicine, 2021, 27, 3.	4.4	13
5	Cell-specific characterization of the placental methylome. BMC Genomics, 2021, 22, 6.	2.8	62
6	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
7	A cross-cohort analysis of autosomal DNA methylation sex differences in the term placenta. Biology of Sex Differences, 2021, 12, 38.	4.1	23
8	Reactivation of Multiple Fetal miRNAs in Lung Adenocarcinoma. Cancers, 2021, 13, 2686.	3.7	0
9	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
10	Human placental piwi-interacting RNA transcriptome is characterized by expression from the DLK1-DIO3 imprinted region. Scientific Reports, 2021, 11, 14981.	3.3	4
11	Sex Differences Are Here to Stay: Relevance to Prenatal Care. Journal of Clinical Medicine, 2021, 10, 3000.	2.4	23
12	Profiling the small non-coding RNA transcriptome of the human placenta. Scientific Data, 2021, 8, 166.	5.3	7
13	Mistakes Are Common; Should We Worry about Them?. Trends in Molecular Medicine, 2021, 27, 721-722.	6.7	3
14	Low oxygen enhances trophoblast column growth by potentiating differentiation of the extravillous lineage and promoting LOX activity. Development (Cambridge), 2020, 147, .	2.5	20
15	The significance of the placental genome and methylome in fetal and maternal health. Human Genetics, 2020, 139, 1183-1196.	3.8	14
16	Renpenning syndrome in a female. American Journal of Medical Genetics, Part A, 2020, 182, 498-503.	1.2	4
17	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
18	Accurate ethnicity prediction from placental DNA methylation data. Epigenetics and Chromatin, 2019, 12, 51.	3.9	40

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19	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
20	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
21	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
22	Considerations when processing and interpreting genomics data of the placenta. Placenta, 2019, 84, 57-62.	1.5	27
23	Epigenetic Modifications in the Human Placenta. , 2019, , 293-311.		3
24	Placental epigenetic clocks: estimating gestational age using placental DNA methylation levels. Aging, 2019, 11, 4238-4253.	3.1	79
25	Mining DNA methylation alterations towards a classification of placental pathologies. Human Molecular Genetics, 2018, 27, 135-146.	2.9	50
26	Utility of DNA methylation to assess placental health. Placenta, 2018, 64, S23-S28.	1.5	16
27	Epigenetic regulation of placental gene expression in transcriptional subtypes of preeclampsia. Clinical Epigenetics, 2018, 10, 28.	4.1	63
28	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
29	CHIPS-Child: Testing the developmental programming hypothesis in the offspring of the CHIPS trial. Pregnancy Hypertension, 2018, 14, 15-22.	1.4	4
30	Adjusting for Batch Effects in DNA Methylation Microarray Data, a Lesson Learned. Frontiers in Genetics, 2018, 9, 83.	2.3	66
31	No evidence for association of MTHFR 677C>T and 1298A>C variants with placental DNA methylation. Clinical Epigenetics, 2018, 10, 34.	4.1	25
32	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
33	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
34	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
35	Placentation and Genomic Imprinting. , 2017, , 159-184.		0
36	Review: placental biomarkers for assessing fetal health. Human Molecular Genetics, 2017, 26, R237-R245.	2.9	32

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37	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
38	Genetic and epigenetic changes in the placenta in intrauterine growth restriction (IUGR). Placenta, 2017, 57, 242.	1.5	2
39	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
40	Cord blood hematopoietic cells from preterm infants display altered DNA methylation patterns. Clinical Epigenetics, 2017, 9, 39.	4.1	24
41	Child mortality, hypothalamic-pituitary-adrenal axis activity and cellular aging in mothers. PLoS ONE, 2017, 12, e0177869.	2.5	6
42	Using DNA methylation signatures in placental tissue and cells to gain insight into chorioamnionitis. Placenta, 2016, 45, 113.	1.5	1
43	Placental MTHFR 677C>T genotypes in pregnancy pathologies. Placenta, 2016, 45, 112.	1.5	0
44	Epigenetic regulation of placental gene expression in transcriptional subclasses of preeclampsia. Placenta, 2016, 45, 122-123.	1.5	1
45	Characterizing the hypomethylated DNA methylation profile of nucleated red blood cells from cord blood. Epigenomics, 2016, 8, 1481-1494.	2.1	29
46	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
47	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
48	Profiling placental and fetal DNA methylation in human neural tube defects. Epigenetics and Chromatin, 2016, 9, 6.	3.9	41
49	Pervasive polymorphic imprinted methylation in the human placenta. Genome Research, 2016, 26, 756-767.	5.5	107
50	Number of Children and Telomere Length in Women: A Prospective, Longitudinal Evaluation. PLoS ONE, 2016, 11, e0146424.	2.5	40
51	The English Â«Teaching Excellence FrameworkÂ» 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
52	MG-123â€...Genomics of early pregnancy loss. Journal of Medical Genetics, 2015, 52, A6.1-A6.	3.2	0
53	Nucleated red blood cells impact DNA methylation and expression analyses of cord blood hematopoietic cells. Clinical Epigenetics, 2015, 7, 95.	4.1	47
54	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

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55	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
56	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
57	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
58	ADAM12-directed ectodomain shedding of E-cadherin potentiates trophoblast fusion. Cell Death and Differentiation, 2015, 22, 1970-1984.	11.2	51
59	The genotypic and phenotypic spectrum of PIGA deficiency. Orphanet Journal of Rare Diseases, 2015, 10, 23.	2.7	70
60	Functional consequences of copy number variants in miscarriage. Molecular Cytogenetics, 2015, 8, 6.	0.9	17
61	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
62	The Human Placental Methylome. Cold Spring Harbor Perspectives in Medicine, 2015, 5, a023044-a023044.	6.2	77
63	Noninvasive nucleic acidâ€“based approaches to monitor placental health and predict pregnancy-related complications. American Journal of Obstetrics and Gynecology, 2015, 213, S197-S206.	1.3	21
64	An integrated transcriptional, epigenetic, and clinical analysis of preeclamptic placentas. Placenta, 2015, 36, A7.	1.5	0
65	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
66	Improved reporting of DNA methylation data derived from studies of the human placenta. Epigenetics, 2014, 9, 333-337.	2.7	21
67	Overlapping DNA methylation profile between placentas with trisomy 16 and early-onset preeclampsia. Placenta, 2014, 35, 216-222.	1.5	29
68	Variant ATRX Syndrome with Dysfunction ofATRXandMAGT1Genes. Human Mutation, 2014, 35, 58-62.	2.5	7
69	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
70	Politics, professionals and practitioners. History of Education, 2014, 43, 719-723.	0.4	0
71	Quantification of Cell-Free DNA in Normal and Complicated Pregnancies: Overcoming Biological and Technical Issues. PLoS ONE, 2014, 9, e101500.	2.5	37
72	Additional annotation enhances potential for biologically-relevant analysis of the Illumina Infinium HumanMethylation450 BeadChip array. Epigenetics and Chromatin, 2013, 6, 4.	3.9	412

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73	miRNA expression in human lung cancer and fetal lung: a comparative study. BMC Proceedings, 2013, 7, .	1.6	0
74	Beckwithâ€“Wiedemann and Silverâ€“Russell syndromes: opposite developmental imbalances in imprinted regulators of placental function and embryonic growth. Clinical Genetics, 2013, 84, 326-334.	2.0	42
75	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
76	Decidual natural killer cells regulate FUT4 expression in EVT through DNA enhancer methylation. Placenta, 2013, 34, A68-A69.	1.5	0
77	Global analysis of DNA methylation changes during progression of oral cancer. Oral Oncology, 2013, 49, 1033-1042.	1.5	64
78	Hypoxia alters the epigenetic profile in cultured human placental trophoblasts. Epigenetics, 2013, 8, 192-202.	2.7	80
79	DNA Methylation Profiling of Placental Villi from Karyotypically Normal Miscarriage and Recurrent Miscarriage. American Journal of Pathology, 2013, 182, 2276-2284.	3.8	37
80	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
81	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
82	X-Chromosome Inactivation. , 2013, , 63-88.		1
83	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
84	â€œWilling enthusiastsâ€•or â€œlame ducksâ€? Issues in teacher professional development policy in England and Wales 1910â€“1975. Paedagogica Historica, 2013, 49, 345-360.	0.1	5
85	The human placenta methylome. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6037-6042.	7.1	256
86	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
87	Response to. Epigenetics, 2012, 7, 965-965.	2.7	2
88	Different measures of â€œgenome-wideâ€•DNA methylation exhibit unique properties in placental and somatic tissues. Epigenetics, 2012, 7, 652-663.	2.7	85
89	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
90	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

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91	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
92	Prenatal and Perinatal Environmental Influences on the Human Fetal and Placental Epigenome. Clinical Pharmacology and Therapeutics, 2012, 92, 716-726.	4.7	84
93	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
94	Beckwithâ€“Wiedemann syndrome in sibs discordant for IC2 methylation. American Journal of Medical Genetics, Part A, 2012, 158A, 1662-1669.	1.2	6
95	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
96	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
97	â€˜That great educational experimentâ€™: the City of London Vacation Course in Education 1922â€“1938: a forgotten story in the history of teacher professional development. History of Education, 2011, 40, 557-575.	0.4	4
98	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
99	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
100	Chromosome-wide DNA methylation analysis predicts human tissue-specific X inactivation. Human Genetics, 2011, 130, 187-201.	3.8	111
101	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
102	Extensive epigenetic reprogramming in human somatic tissues between fetus and adult. Epigenetics and Chromatin, 2011, 4, 7.	3.9	57
103	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
104	Are we ready for DNA methylation-based prenatal testing?. Epigenomics, 2011, 3, 387-390.	2.1	5
105	Placenta-specific Expression of the Interleukin-2 (IL-2) Receptor Î² Subunit from an Endogenous Retroviral Promoter. Journal of Biological Chemistry, 2011, 286, 35543-35552.	3.4	41
106	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
107	Evaluating DNA methylation and gene expression variability in the human term placenta. Placenta, 2010, 31, 1070-1077.	1.5	75
108	Pseudohypoparathyroidism type 1a and the GNAS 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

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109	Methylation profiling in individuals with Russellâ€“Silver syndrome. American Journal of Medical Genetics, Part A, 2010, 152A, 347-355.	1.2	31
110	Assessing the role of placental trisomy in preeclampsia and intrauterine growth restriction. Prenatal Diagnosis, 2010, 30, 1-8.	2.3	50
111	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
112	Genetic variation within the hypothalamus-pituitary-ovarian axis in women with recurrent miscarriage. Human Reproduction, 2010, 25, 2664-2671.	0.9	24
113	Identification of copy number variants in miscarriages from couples with idiopathic recurrent pregnancy loss. Human Reproduction, 2010, 25, 2913-2922.	0.9	95
114	Fertility and aging: do reproductive-aged Canadian women know what they need to know?. Fertility and Sterility, 2010, 93, 2162-2168.	1.0	162
115	Inactive X chromosome-specific reduction in placental DNA methylation. Human Molecular Genetics, 2009, 18, 3544-3552.	2.9	66
116	Telomere length and reproductive aging. Human Reproduction, 2009, 24, 1206-1211.	0.9	101
117	Telomere Length and Reproductive Aging. Obstetrical and Gynecological Survey, 2009, 64, 663-664.	0.4	0
118	Placental Weight in Pregnancies With Trisomy Confined to the Placenta. Journal of Obstetrics and Gynaecology Canada, 2009, 31, 605-610.	0.7	15
119	Human Placental-Specific Epipolymorphism and its Association with Adverse Pregnancy Outcomes. PLoS ONE, 2009, 4, e7389.	2.5	71
120	Chorea as a side effect of gabapentin (NeurontinÂ®) in a patient with complex regional pain syndrome Type 1. Clinical Rheumatology, 2008, 27, 389-390.	2.2	16
121	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
122	MECP2 promoter methylation and X chromosome inactivation in autism. Autism Research, 2008, 1, 169-178.	3.8	107
123	Estrogen receptor Î± gene polymorphisms are associated with idiopathic premature ovarian failure. Fertility and Sterility, 2008, 89, 318-324.	1.0	62
124	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
125	A skewed view of X chromosome inactivation. Journal of Clinical Investigation, 2008, 118, 20-23.	8.2	94
126	EPIGENETIC ALTERATIONS ASSOCIATED WITH PREMATURE OVARIAN FAILURE. Clinical and Investigative Medicine, 2008, 31, 11.	0.6	0

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127	Origin and outcome of pregnancies affected by androgenetic/biparental chimerism. Human Reproduction, 2007, 22, 1114-1122.	0.9	75
128	Toll-like receptor 4 polymorphisms and idiopathic chromosomally normal miscarriage. Human Reproduction, 2007, 22, 440-443.	0.9	16
129	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
130	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
131	Pregnancy and postnatal outcome of mosaic isochromosome 20q. Prenatal Diagnosis, 2007, 27, 143-145.	2.3	8
132	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
133	P-159. Fertility and Sterility, 2006, 86, S191.	1.0	0
134	Postnatal followâ€up of prenatally diagnosed trisomy 16 mosaicism. Prenatal Diagnosis, 2006, 26, 548-558.	2.3	52
135	The association between preeclampsia and placental trisomy 16 mosaicism. Prenatal Diagnosis, 2006, 26, 956-961.	2.3	33
136	Recurrent trisomy 21: four cases in three generations. Clinical Genetics, 2005, 68, 430-435.	2.0	8
137	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
138	Androgenetic/biparental mosaicism causes placental mesenchymal dysplasia. Journal of Medical Genetics, 2005, 43, 187-192.	3.2	161
139	Methylation of ZNF261 as an assay for determining X chromosome inactivation patterns. American Journal of Medical Genetics, Part A, 2003, 120A, 439-441.	1.2	33
140	Prenatally detected trisomy 4 and 6 mosaicism?cytogenetic results and clinical phenotype. Prenatal Diagnosis, 2003, 23, 128-133.	2.3	18
141	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
142	Dispermy--origin of diandric triploidy: Brief Communication. Human Reproduction, 2002, 17, 3037-3038.	0.9	31
143	Cytogenetic analysis of miscarriages from couples with recurrent miscarriage: a case-control study. Human Reproduction, 2002, 17, 446-451.	0.9	381
144	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

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145	Molecular Detection of Uniparental Disomy. , 2002, 204, 291-298.		1
146	Origin of amnion and implications for evaluation of the fetal genotype in cases of mosaicism. Prenatal Diagnosis, 2002, 22, 1076-1085.	2.3	51
147	Cytogenetic investigation of fetuses and infants conceived through intracytoplasmic sperm injection. Fertility and Sterility, 2001, 76, 1272-1275.	1.0	26
148	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
149	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
150	Mechanisms leading to uniparental disomy and their clinical consequences. BioEssays, 2000, 22, 452-459.	2.5	296
151	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
152	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
153	Multipoint Genetic Mapping with Uniparental Disomy Data. American Journal of Human Genetics, 2000, 67, 851-861.	6.2	9
154	Mechanisms leading to uniparental disomy and their clinical consequences. BioEssays, 2000, 22, 452.	2.5	3
155	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
156	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
157	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
158	Maternal Uniparental Disomy of Chromosome 1 with No Apparent Phenotypic Effects. American Journal of Human Genetics, 1998, 63, 1216-1220.	6.2	56
159	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
160	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
161	XISTExpression and X-Chromosome Inactivation in Human Preimplantation Embryos. American Journal of Human Genetics, 1997, 61, 5-8.	6.2	15
162	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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163	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
164	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
165	Mosaicism most likely accounts for extended survival of trisomy 22. , 1996, 62, 100-100.		7
166	Comparison of phenotype in uniparental disomy and deletion Prader-Willi syndrome: Sex specific differences. , 1996, 65, 133-136.		63
167	Phenotype of maternal UPD(14). , 1996, 66, 89-89.		9
168	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
169	Sex-specific meiotic recombination in the Prader--Willi/Angelman syndrome imprinted region. Human Molecular Genetics, 1995, 4, 801-806.	2.9	105
170	Uniparental disomy 7 in Silverâ€"Russell syndrome and primordial growth retardation. Human Molecular Genetics, 1995, 4, 583-587.	2.9	289
171	Detection of aberrant DNA methylation in unique Prader â€" Willi syndrome patients and its diagnostic implications. Human Molecular Genetics, 1994, 3, 893-895.	2.9	47
172	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
173	Exclusively paternal X chromosomes in a girl with short stature. Human Genetics, 1993, 92, 175-8.	3.8	34
174	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
175	Molecular definition of the Prader â€" Willi syndrome chromosome region and orientation of the SNRPN gene. Human Molecular Genetics, 1993, 2, 1991-1994.	2.9	37
176	Modification of 15q11 â€" q13 DNA methylation imprints in unique Angelman and Prader â€" Willi patients. Human Molecular Genetics, 1993, 2, 1377-1382.	2.9	144
177	Parental origin of the supernumerary chromosome in trisomy 18. Clinical Genetics, 1993, 44, 57-61.	2.0	32
178	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
179	Small nuclear ribonucleoprotein polypeptide N (SNRPN), an expressed gene in the Praderâ€"Willi syndrome critical region. Nature Genetics, 1992, 2, 265-269.	21.4	271
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