Cynthia C Morton

List of Publications by Year
in descending order

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184	15,184	18465 62	20343 116
papers	citations	h-index	g-index

194	194	194	15008
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Experience of Low-Pass Whole-Genome Sequencing-Based Copy Number Variant Analysis: A Survey of Chinese Tertiary Hospitals. Diagnostics, 2022, 12, 1098.	1.3	4
2	Genome-wide association meta-analysis identifies 48 risk variants and highlights the role of the stria vascularis in hearing loss. American Journal of Human Genetics, 2022, 109, 1077-1091.	2.6	27
3	The Burden and Benefits of Knowledge: Ethical Considerations Surrounding Population-Based Newborn Genome Screening for Hearing. International Journal of Neonatal Screening, 2022, 8, 36.	1.2	2
4	A synonymous variant in MYO15A enriched in the Ashkenazi Jewish population causes autosomal recessive hearing loss due to abnormal splicing. European Journal of Human Genetics, 2021, 29, 988-997.	1.4	8
5	Low-pass genome sequencingâ€“based detection of absence of heterozygosity: validation in clinical cytogenetics. Genetics in Medicine, 2021, 23, 1225-1233.	1.1	16
6	Cochlin Deficiency Protects Against Noise-Induced Hearing Loss. Frontiers in Molecular Neuroscience, 2021, 14, 670013.	1.4	11
7	Disease-specific ACMG/AMP guidelines improve sequence variant interpretation for hearing loss. Genetics in Medicine, 2021, 23, 2208-2212.	1.1	18
8	Position effects of 22q13 rearrangements on candidate genes in Phelan-McDermid syndrome. PLoS ONE, 2021, 16, e0253859.	1.1	8
9	Tools for standardized data collection: Speech, Language, and Hearing measurement protocols in the PhenX Toolkit. Annals of Human Genetics, 2021, , .	0.3	2
10	First Report of Bilateral External Auditory Canal Cochlin Aggregates (â€œCochlinomasâ€) with Multifocal Amyloid-Like Deposits, Associated with Sensorineural Hearing Loss and a Novel Genetic Variant in COCH Encoding Cochlin. Head and Neck Pathology, 2020, 14, 808-816.	1.3	2
11	Low-pass genome sequencing versus chromosomal microarray analysis: implementation in prenatal diagnosis. Genetics in Medicine, 2020, 22, 500-510.	1.1	64
12	Generation of protective pneumococcal-specific nasal resident memory CD4+ T cells via parenteral immunization. Mucosal Immunology, 2020, 13, 172-182.	2.7	26
13	SYCP2 Translocation-Mediated Dysregulation and Frameshift Variants Cause Human Male Infertility. American Journal of Human Genetics, 2020, 106, 41-57.	2.6	66
14	Comprehensive clinically oriented workflow for nucleotide level resolution and interpretation in prenatal diagnosis of de novo apparently balanced chromosomal translocations in their genomic landscape. Human Genetics, 2020, 139, 531-543.	1.8	9
15	Long-range cis-regulatory elements controlling GDF6 expression are essential for ear development. Journal of Clinical Investigation, 2020, 130, 4213-4217.	3.9	9
16	Resolving Breakpoints of Chromosomal Rearrangements at the Nucleotide Level Using Sanger Sequencing. Current Protocols in Human Genetics, 2020, 108, e107.	3.5	1
17	Genome Sequencing Explores Complexity of Chromosomal Abnormalities in Recurrent Miscarriage. American Journal of Human Genetics, 2019, 105, 1102-1111.	2.6	66
18	Genome-wide association and epidemiological analyses reveal common genetic origins between uterine leiomyomata and endometriosis. Nature Communications, 2019, 10, 4857.	5.8	90

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19	GWAS Identifies 44 Independent Associated Genomic Loci for Self-Reported Adult Hearing Difficulty in UK Biobank. American Journal of Human Genetics, 2019, 105, 788-802.	2.6	101
20	A proposal for comprehensive newborn hearing screening to improve identification of deaf and hard-of-hearing children. Genetics in Medicine, 2019, 21, 2614-2630.	1.1	63
21	Nationwide population genetic screening improves outcomes of newborn screening for hearing loss in China. Genetics in Medicine, 2019, 21, 2231-2238.	1.1	40
22	The Iceberg under Water: Unexplored Complexity of Chromoanagenesis in Congenital Disorders. American Journal of Human Genetics, 2019, 104, 565-577.	2.6	46
23	Pelvic and pulmonary benign metastasizing leiomyoma: A case report. Case Reports in Women's Health, 2018, 18, e00061.	0.2	9
24	Balanced Chromosomal Rearrangement Detection by Lowâ€Pass Wholeâ€Genome Sequencing. Current Protocols in Human Genetics, 2018, 96, 8.18.1-8.18.16.	3.5	10
25	Phenotypic interpretation of complex chromosomal rearrangements informed by nucleotide-level resolution and structural organization of chromatin. European Journal of Human Genetics, 2018, 26, 374-381.	1.4	8
26	Computational Prediction of Position Effects of Human Chromosome Rearrangements. Current Protocols in Human Genetics, 2018, 97, e57.	3.5	2
27	Clinical, pathologic, cytogenetic, and molecular profiling in self-identified black women with uterine leiomyomata. Cancer Genetics, 2018, 222-223, 1-8.	0.2	12
28	Identification of balanced chromosomal rearrangements previously unknown among participants in the 1000 Genomes Project: implications for interpretation of structural variation in genomes and the future of clinical cytogenetics. Genetics in Medicine, 2018, 20, 697-707.	1.1	52
29	3C-PCR: a novel proximity ligation-based approach to phase chromosomal rearrangement breakpoints with distal allelic variants. Human Genetics, 2018, 137, 55-62.	1.8	5
30	Loss of LDAH associated with prostate cancer and hearing loss. Human Molecular Genetics, 2018, 27, 4194-4203.	1.4	14
31	Historical and Clinical Perspectives on Chromosomal Translocations. Advances in Experimental Medicine and Biology, 2018, 1044, 1-14.	0.8	50
32	Yield of additional genetic testing after chromosomal microarray for diagnosis of neurodevelopmental disability and congenital anomalies: a clinical practice resource of the American College of Medical Genetics and Genomics (ACMG). Genetics in Medicine, 2018, 20, 1105-1113.	1.1	57
33	Target-enriched massively parallel sequencing for genetic diagnosis of hereditary hearing loss in patients with normal array CGH result. Hong Kong Medical Journal, 2018, 24 Suppl 3, 11-14.	0.1	1
34	Cover Image, Volume 173A, Number 2, February 2017. American Journal of Medical Genetics, Part A, 2017, 173, i.	0.7	0
35	SMCHD1 mutations associated with a rare muscular dystrophy can also cause isolated arhinia and Bosma arhinia microphthalmia syndrome. Nature Genetics, 2017, 49, 238-248.	9.4	131
36	A multi-stage genome-wide association study of uterine fibroids in African Americans. Human Genetics, 2017, 136, 1363-1373.	1.8	39

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37	Computational Prediction of Position Effects of Apparently Balanced Human Chromosomal Rearrangements. American Journal of Human Genetics, 2017, 101, 206-217.	2.6	51
38	Hereditary leiomyomatosis and renal cell cancer: Cutaneous lesions & atypical fibroids. Case Reports in Women's Health, 2017, 15, 31-34.	0.2	3
39	The genomic landscape of balanced cytogenetic abnormalities associated with human congenital anomalies. Nature Genetics, 2017, 49, 36-45.	9.4	251
40	Commentary on the decision of the American Board of Medical Genetics and Genomics to create a 24-month specialty of Laboratory Genetics and Genomics. Genetics in Medicine, 2017, 19, 294-296.	1.1	2
41	Implication of LRRC4C and DPP6 in neurodevelopmental disorders. American Journal of Medical Genetics, Part A, 2017, 173, 395-406.	0.7	40
42	Screening of deafness-causing DNA variants that are common in patients of European ancestry using a microarray-based approach. PLoS ONE, 2017, 12, e0169219.	1.1	26
43	Uterine Leiomyoma. , 2017, , 4751-4755.		0
44	Training the Future Leaders in Personalized Medicine. Journal of Personalized Medicine, 2016, 6, 1.	1.1	21
45	Estrogen-related receptor gamma implicated in a phenotype including hearing loss and mild developmental delay. European Journal of Human Genetics, 2016, 24, 1622-1626.	1.4	12
46	Histopathology of the Human Inner Ear in the p.L114P COCH Mutation (DFNA9). Audiology and Neuro-Otology, 2016, 21, 88-97.	0.6	18
47	Next-Generation Newborn Hearing Screening. Monographs in Human Genetics, 2016, , 30-39.	0.5	6
48	Recommendations for the integration of genomics into clinical practice. Genetics in Medicine, 2016, 18, 1075-1084.	1.1	125
49	Section E6.5â€“6.8 of the ACMG technical standards and guidelines: chromosome studies of lymph node and solid tumorâ€“acquired chromosomal abnormalities. Genetics in Medicine, 2016, 18, 643-648.	1.1	17
50	Genetic Association Studies in Uterine Fibroids: Risk Alleles Presage the Path to Personalized Therapies. Seminars in Reproductive Medicine, 2016, 34, 235-241.	0.5	13
51	Structural Chromosomal Rearrangements Require Nucleotide-Level Resolution: Lessons from Next-Generation Sequencing in Prenatal Diagnosis. American Journal of Human Genetics, 2016, 99, 1015-1033.	2.6	53
52	Intravenous leiomyomatosis: an unusual intermediate between benign and malignant uterine smooth muscle tumors. Modern Pathology, 2016, 29, 500-510.	2.9	65
53	Actin capping protein CAPZB regulates cell morphology, differentiation, and neural crest migration in craniofacial morphogenesis. Human Molecular Genetics, 2016, 25, 1255-1270.	1.4	30
54	MATR3 disruption in human and mouse associated with bicuspid aortic valve, aortic coarctation and patent ductus arteriosus. Human Molecular Genetics, 2015, 24, 2375-2389.	1.4	90

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55	Cutaneous and Uterine Leiomyomas. Mayo Clinic Proceedings, 2015, 90, 990.	1.4	1
56	Prenatal diagnosis of chromothripsis, with nine breaks characterized by karyotyping, FISH, microarray and wholeâ€genome sequencing. Prenatal Diagnosis, 2015, 35, 299-301.	1.1	30
57	From GWAS to Therapy: Fatty Acid Synthase in Uterine Leiomyomata. FASEB Journal, 2015, 29, 147.5.	0.2	1
58	Cochlin in Normal Middle Ear and Abnormal Middle Ear Deposits in DFNA9 and Coch G88E/G88E Mice. JARO - Journal of the Association for Research in Otolaryngology, 2014, 15, 961-974.	0.9	17
59	Disruption of MBD5 contributes to a spectrum of psychopathology and neurodevelopmental abnormalities. Molecular Psychiatry, 2014, 19, 368-379.	4.1	54
60	Describing Sequencing Results of Structural Chromosome Rearrangements with a Suggested Next-Generation Cytogenetic Nomenclature. American Journal of Human Genetics, 2014, 94, 695-709.	2.6	42
61	Identification of Pathogenic Mechanisms ofCOCHMutations, Abolished Cochlin Secretion, and Intracellular Aggregate Formation: Genotype-Phenotype Correlations in DFNA9 Deafness and Vestibular Disorder. Human Mutation, 2014, 35, 1506-1513.	1.1	48
62	Haploinsufficiency of KDM6A is associated with severe psychomotor retardation, global growth restriction, seizures and cleft palate. Human Genetics, 2013, 132, 537-552.	1.8	60
63	Mechanisms for Structural Variation in the Human Genome. Current Genetic Medicine Reports, 2013, 1, 81-90.	1.9	29
64	Complex cytogenetic rearrangements at the DURS 1 locus in syndromic Duane retraction syndrome. Clinical Case Reports (discontinued), 2013, 1, 30-37.	0.2	3
65	Clinical Diagnosis by Whole-Genome Sequencing of a Prenatal Sample. New England Journal of Medicine, 2012, 367, 2226-2232.	13.9	174
66	Complex reorganization and predominant non-homologous repair following chromosomal breakage in karyotypically balanced germline rearrangements and transgenic integration. Nature Genetics, 2012, 44, 390-397.	9.4	229
67	A novel COCH mutation associated with autosomal dominant nonsyndromic hearing loss disrupts the structural stability of the vWFA2 domain. Journal of Molecular Medicine, 2012, 90, 1321-1331.	1.7	20
68	Expression profiling of uterine leiomyomata cytogenetic subgroups reveals distinct signatures in matched myometrium: transcriptional profiling of the t(12;14) and evidence in support of predisposing genetic heterogeneity. Human Molecular Genetics, 2012, 21, 2312-2329.	1.4	44
69	Sequencing Chromosomal Abnormalities Reveals Neurodevelopmental Loci that Confer Risk across Diagnostic Boundaries. Cell, 2012, 149, 525-537.	13.5	534
70	Genome-wide Linkage and Association Analyses Implicate FASN in Predisposition to Uterine Leiomyomata. American Journal of Human Genetics, 2012, 91, 621-628.	2.6	83
71	Disruption of a Large Intergenic Noncoding RNA in Subjects with Neurodevelopmental Disabilities. American Journal of Human Genetics, 2012, 91, 1128-1134.	2.6	61
72	Uterine Leiomyoma. , 2012, , 1-6.		0

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73	Hearing and vestibular deficits in the Coch null mouse model: Comparison to the Coch mouse and to DFNA9 hearing and balance disorder. Hearing Research, 2011, 272, 42-48.	0.9	37
74	Next-Generation Sequencing Strategies Enable Routine Detection of Balanced Chromosome Rearrangements for Clinical Diagnostics and Genetic Research. American Journal of Human Genetics, 2011, 88, 469-481.	2.6	154
75	Assessment of 2q23.1 Microdeletion Syndrome Implicates MBD5 as a Single Causal Locus of Intellectual Disability, Epilepsy, and Autism Spectrum Disorder. American Journal of Human Genetics, 2011, 89, 551-563.	2.6	195
76	Uterine Leiomyoma. , 2011, , 3859-3862.		0
77	Deletion of an enhancer near DLX5 and DLX6 in a family with hearing loss, craniofacial defects, and an inv(7)(q21.3q35). Human Genetics, 2010, 127, 19-31.	1.8	32
78	Disseminated peritoneal leiomyomatosis after laparoscopic supracervical hysterectomy with characteristic molecular cytogenetic findings of uterine leiomyoma. Genes Chromosomes and Cancer, 2010, 49, 1152-1160.	1.5	67
79	NR2F1 deletion in a patient with a de novo paracentric inversion, inv(5)(q15q33.2), and syndromic deafness. American Journal of Medical Genetics, Part A, 2009, 149A, 931-938.	0.7	41
80	Identifying the molecular signature of the interstitial deletion 7q subgroup of uterine leiomyomata using a paired analysis. Genes Chromosomes and Cancer, 2009, 48, 865-885.	1.5	29
81	Uterine leiomyomata and decreased height: a common HMGA2 predisposition allele. Human Genetics, 2009, 125, 257-263.	1.8	40
82	Novel SSBP2â€JAK2 fusion gene resulting from a t(5;9)(q14.1;p24.1) in preâ€B acute lymphocytic leukemia. Genes Chromosomes and Cancer, 2008, 47, 884-889.	1.5	63
83	Characterization of Apparently Balanced Chromosomal Rearrangements from the Developmental Genome Anatomy Project. American Journal of Human Genetics, 2008, 82, 712-722.	2.6	95
84	The impact of race as a risk factor for symptom severity and age at diagnosis of uterine leiomyomata among affected sisters. American Journal of Obstetrics and Gynecology, 2008, 198, 168.e1-168.e9.	0.7	81
85	Expression studies of osteoglycin/mimecan (OGN) in the cochlea and auditory phenotype of Ogn-deficient mice. Hearing Research, 2008, 237, 57-65.	0.9	18
86	Disruption of Neurexin 1 Associated with Autism Spectrum Disorder. American Journal of Human Genetics, 2008, 82, 199-207.	2.6	545
87	Molecular and Cytogenetic Characterization of Plexiform Leiomyomata Provide Further Evidence for Genetic Heterogeneity Underlying Uterine Fibroids. American Journal of Pathology, 2008, 172, 1403-1410.	1.9	24
88	A targeted Coch missense mutation: a knock-in mouse model for DFNA9 late-onset hearing loss and vestibular dysfunction. Human Molecular Genetics, 2008, 17, 3426-3434.	1.4	44
89	Genetic heterogeneity among uterine leiomyomata: insights into malignant progression. Human Molecular Genetics, 2007, 16, R7-R13.	1.4	69
90	NFIA Haploinsufficiency Is Associated with a CNS Malformation Syndrome and Urinary Tract Defects. PLoS Genetics, 2007, 3, e80.	1.5	100

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91	Disruption of ROBO2 Is Associated with Urinary Tract Anomalies and Confers Risk of Vesicoureteral Reflux. American Journal of Human Genetics, 2007, 80, 616-632.	2.6	189
92	Methylthioadenosine phosphorylase (MTAP) in hearing: Gene disruption by chromosomal rearrangement in a hearing impaired individual and model organism analysis. American Journal of Medical Genetics, Part A, 2007, 143A, 1630-1639.	0.7	12
93	Cochlin in the eye: Functional implications. Progress in Retinal and Eye Research, 2007, 26, 453-469.	7.3	29
94	Ion Channel Gene Expression in the Inner Ear. JARO - Journal of the Association for Research in Otolaryngology, 2007, 8, 305-328.	0.9	56
95	The Genetic Heterogeneity of Uterine Leiomyomata. Obstetrics and Gynecology Clinics of North America, 2006, 33, 13-39.	0.7	38
96	SUMO1 Haploinsufficiency Leads to Cleft Lip and Palate. Science, 2006, 313, 1751-1751.	6.0	165
97	Newborn Hearing Screening â€" A Silent Revolution. New England Journal of Medicine, 2006, 354, 2151-2164.	13.9	1,267
98	The Genetics of Uterine Leiomyomata. Obstetrics and Gynecology, 2006, 107, 917-921.	1.2	58
99	Characterization of an Abundant COL9A1 Transcript in the Cochlea with a Novel 3â€² UTR: Expression Studies and Detection of miRNA Target Sequence. JARO - Journal of the Association for Research in Otolaryngology, 2006, 7, 160-172.	0.9	13
100	Uterine leiomyomata with deletions of Ip represent a distinct cytogenetic subgroup associated with unusual histologic features. Genes Chromosomes and Cancer, 2006, 45, 304-312.	1.5	62
101	Cochlin immunostaining of inner ear pathologic deposits and proteomic analysis in DFNA9 deafness and vestibular dysfunction. Human Molecular Genetics, 2006, 15, 1071-1085.	1.4	100
102	Increased Frequencies of Cochlin-Specific T Cells in Patients with Autoimmune Sensorineural Hearing Loss. Journal of Immunology, 2006, 177, 4203-4210.	0.4	88
103	Audiometric, Vestibular, and Genetic Aspects of a DFNA9 Family with a G88E COCH Mutation. Otology and Neurotology, 2005, 26, 926-933.	0.7	38
104	OC10.04: Predicting outcomes for fibroid therapies: clinical research and genetics. Ultrasound in Obstetrics and Gynecology, 2005, 26, 325-325.	0.9	0
105	A novelDFNA9mutation in the vWFA2 domain ofCOCHalters a conserved cysteine residue and intrachain disulfide bond formation resulting in progressive hearing loss and site-specific vestibular and central oculomotor dysfunction. American Journal of Medical Genetics, Part A, 2005, 139A, 86-95.	0.7	58
106	Targeted disruption of mouse Coch provides functional evidence that DFNA9 hearing loss is not a COCH haploinsufficiency disorder. Human Genetics, 2005, 118, 29-34.	1.8	33
107	Hypogonadotropic hypogonadism and cleft lip and palate caused by a balanced translocation producing haploinsufficiency for FGFR1. Journal of Medical Genetics, 2005, 42, 666-672.	1.5	55
108	Proteomics Reveal Cochlin Deposits Associated with Glaucomatous Trabecular Meshwork. Journal of Biological Chemistry, 2005, 280, 6080-6084.	1.6	140

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109	Constitutional Rearrangement of the Architectural Factor HMGA2: A Novel Human Phenotype Including Overgrowth and Lipomas. American Journal of Human Genetics, 2005, 76, 340-348.	2.6	116
110	Uterine Leiomyomata with t(10;17) Disrupt the Histone Acetyltransferase MORF. Cancer Research, 2004, 64, 5570-5577.	0.4	106
111	Isolation from Cochlea of a Novel Human Intronless Gene with Predominant Fetal Expression. JARO - Journal of the Association for Research in Otolaryngology, 2004, 5, 185-202.	0.9	48
112	Gene discovery in the auditory system using a tissue specific approach. American Journal of Medical Genetics Part A, 2004, 130A, 26-28.	2.4	6
113	Molecular pathogenesis of uterine smooth muscle tumors from transcriptional profiling. Genes Chromosomes and Cancer, 2004, 40, 97-108.	1.5	145
114	Involvement of fumarate hydratase in nonsyndromic uterine leiomyomas: Genetic linkage analysis and FISH studies. Genes Chromosomes and Cancer, 2004, 41, 183-190.	1.5	64
115	Intravenous leiomyomatosis is characterized by a der(14)t(12;14)(q15;q24). Genes Chromosomes and Cancer, 2003, 36, 205-206.	1.5	69
116	HMGA2 expression in uterine leiomyomata and myometrium: Quantitative analysis and tissue culture studies. Genes Chromosomes and Cancer, 2003, 38, 68-79.	1.5	65
117	Subcellular localisation, secretion, and post-translational processing of normal cochlin, and of mutants causing the sensorineural deafness and vestibular disorder, DFNA9. Journal of Medical Genetics, 2003, 40, 479-486.	1.5	76
118	Fusion transcripts involving HMGA2 are not a common molecular mechanism in uterine leiomyomata with rearrangements in 12q15. Cancer Research, 2003, 63, 1351-8.	0.4	79
119	Genetics, genomics and gene discovery in the auditory system. Human Molecular Genetics, 2002, 11, 1229-1240.	1.4	110
120	Continuing to break the sound barrier: genes in hearing. Current Opinion in Genetics and Development, 2002, 12, 343-348.	1.5	8
121	1q42â^¼q44 is rarely cytogenetically involved in sporadic uterine leiomyomata. Cancer Genetics and Cytogenetics, 2002, 138, 92-93.	1.0	9
122	Gene Discovery in the Auditory System: Characterization of Additional Cochlear-Expressed Sequences. JARO - Journal of the Association for Research in Otolaryngology, 2002, 3, 45-53.	0.9	26
123	Genetics and the Development of Fibroids. Clinical Obstetrics and Gynecology, 2001, 44, 335-349.	0.6	55
124	Genomic structure, functional comparison, and tissue distribution of mouse Cd59a and Cd59b. Mammalian Genome, 2001, 12, 582-589.	1.0	43
125	Fluorescencein situ hybridization (FISH) for rapid detection of aneuploidy: experience in 911 prenatal cases. Prenatal Diagnosis, 2001, 21, 262-269.	1.1	55
126	Prenatal diagnosis and molecular cytogenetics in a case of partial trisomy 14 and monosomy 21. American Journal of Medical Genetics Part A, 2001, 100, 246-250.	2.4	4

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127	Chromosomal translocation t(8;12) induces aberrantHMGIC expression in aggressive angiomyxoma of the vulva. Genes Chromosomes and Cancer, 2001, 32, 172-176.	1.5	109
128	Amplification ofAML1 in childhood acute lymphoblastic leukemias. Genes Chromosomes and Cancer, 2001, 30, 407-409.	1.5	49
129	Mutations in the transcriptional activator EYA4 cause late-onset deafness at the DFNA10 locus. Human Molecular Genetics, 2001, 10, 195-200.	1.4	210
130	Mutations in the novel protocadherin PCDH15 cause Usher syndrome type 1F. Human Molecular Genetics, 2001, 10, 1709-1718.	1.4	257
131	Integration of cytogenetic landmarks into the draft sequence of the human genome. Nature, 2001, 409, 953-958.	13.7	302
132	Dysregulation ofHMGIC in a uterine lipoleiomyoma with a complex rearrangement including chromosomes 7, 12, and 14. , 2000, 27, 209-215.		28
133	A t(2;19)(p13;p13.2) in a giant invasive cardiac lipoma from a patient with multiple lipomatosis. , 2000, 28, 133-137.		22
134	Genetics of uterine leiomyomata. Genes Chromosomes and Cancer, 2000, 28, 235-245.	1.5	111
135	A Novel Conserved Cochlear Gene, OTOR: Identification, Expression Analysis, and Chromosomal Mapping. Genomics, 2000, 66, 242-248.	1.3	42
136	Genetics of uterine leiomyomata. Genes Chromosomes and Cancer, 2000, 28, 235-245.	1.5	1
137	Genetic Approaches to the Study of Uterine Leiomyomata. Environmental Health Perspectives, 2000, 108, 775-778.	2.8	17
138	Human cochlear expressed sequence tags provide insight into cochlear gene expression and identify candidate genes for deafness. Human Molecular Genetics, 1999, 8, 439-452.	1.4	70
139	High Prevalence of Symptoms of Meniere's Disease in three Families With a Mutation in the COCH Gene. Human Molecular Genetics, 1999, 8, 1425-1429.	1.4	144
140	A Pro51Ser mutation in the COCH gene is associated with late onset autosomal dominant progressive sensorineural hearing loss with vestibular defects. Human Molecular Genetics, 1999, 8, 361-366.	1.4	124
141	Beginning of a molecular era in hearing and deafness. Clinical Genetics, 1999, 55, 149-159.	1.0	16
142	Beginning of a molecular era in hearing and deafness. Clinical Genetics, 1999, 57, 39-49.	1.0	0
143	Mutations in the gene encoding B1 subunit of H+-ATPase cause renal tubular acidosis with sensorineural deafness. Nature Genetics, 1999, 21, 84-90.	9.4	633
144	Expression of HMGIY in Three Uterine Leiomyomata with Complex Rearrangements of Chromosome 6. Cancer Genetics and Cytogenetics, 1999, 114, 9-16.	1.0	48

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145	HMGIC expression in human adult and fetal tissues and in uterine leiomyomata. Genes Chromosomes and Cancer, 1999, 25, 316-322.	1.5	125
146	Primary Parauterine Leiomyoma With a t(6;14). , 1999, 26, 385-386.		6
147	HMGIC expression in human adult and fetal tissues and in uterine leiomyomata. , 1999, 25, 316.		1
148	HMGIC expression in human adult and fetal tissues and in uterine leiomyomata. Genes Chromosomes and Cancer, 1999, 25, 316-322.	1.5	1
149	HMGIC expression in human adult and fetal tissues and in uterine leiomyomata. Genes Chromosomes and Cancer, 1999, 25, 316-22.	1.5	47
150	Mutations in a novel cochlear gene cause DFNA9, a human nonsyndromic deafness with vestibular dysfunction. Nature Genetics, 1998, 20, 299-303.	9.4	317
151	Localization and expression of the human estrogen receptor beta gene in uterine leiomyomata. , 1998, 23, 361-366.		45
152	The human ortholog of rhesus mannose-binding protein-A gene is an expressed pseudogene that localizes to Chromosome 10. Mammalian Genome, 1998, 9, 246-249.	1.0	71
153	Many Tumors and Many Genes. American Journal of Pathology, 1998, 153, 1015-1020.	1.9	15
154	Mutation in Transcription Factor POU4F3 Associated with Inherited Progressive Hearing Loss in Humans. Science, 1998, 279, 1950-1954.	6.0	322
155	Association of Unconventional Myosin MYO15 Mutations with Human Nonsyndromic Deafness DFNB3. Science, 1998, 280, 1447-1451.	6.0	419
156	Mutation of a Gene Encoding a Protein with Extracellular Matrix Motifs in Usher Syndrome Type IIa. Science, 1998, 280, 1753-1757.	6.0	366
157	Cytogenetic abnormalities in uterine myomas are associated with myoma size. Molecular Human Reproduction, 1998, 4, 83-86.	1.3	85
158	ORC5L, a New Member of the Human Origin Recognition Complex, Is Deleted in Uterine Leiomyomas and Malignant Myeloid Diseases. Journal of Biological Chemistry, 1998, 273, 27137-27145.	1.6	67
159	An Ancient Conserved Gene Expressed in the Human Inner Ear: Identification, Expression Analysis, and Chromosomal Mapping of Human and Mouse Antiquitin (ATQ1). Genomics, 1997, 46, 191-199.	1.3	38
160	Mapping and Characterization of a Novel Cochlear Gene in Human and in Mouse: A Positional Candidate Gene for a Deafness Disorder, DFNA9. Genomics, 1997, 46, 345-354.	1.3	139
161	The del(7q) subgroup in uterine leiomyomata: Genetic and biologic characteristics. Cancer Genetics and Cytogenetics, 1997, 98, 69-74.	1.0	54
162	Norrie disease gene mutation in a large Costa Rican kindred with a novel phenotype including venous insufficiency. Human Mutation, 1997, 9, 402-408.	1.1	33

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163	RARE TRISOMY MOSAICISM DIAGNOSED IN AMNIOCYTES, INVOLVING AN AUTOSOME OTHER THAN CHROMOSOMES 13, 18, 20, AND 21: KARYOTYPE/PHENOTYPE CORRELATIONS. , 1997, 17, 201-242.		185
164	HMGI(Y) expression in human uterine leiomyomata. Involvement of another high-mobility group architectural factor in a benign neoplasm. American Journal of Pathology, 1997, 150, 911-8.	1.9	67
165	Disseminated peritoneal leiomyomatosis. Clonality analysis by X chromosome inactivation and cytogenetics of a clinically benign smooth muscle proliferation. American Journal of Pathology, 1997, 150, 2153-66.	1.9	71
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167	Identification of a YAC spanning the translocation breakpoints in uterine leiomyomata, pulmonary chondroid hamartoma, and lipoma: physical mapping of the 12q14â€“q15 breakpoint region in uterine leiomyomata. Genomics, 1995, 26, 265-271.	1.3	50
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