

# Jeffrey C Murray

## List of Publications by Year in descending order

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Version: 2024-02-01

136  
papers

16,645  
citations

61857

43  
h-index

19136

118  
g-index

143  
all docs

143  
docs citations

143  
times ranked

22151  
citing authors

#	ARTICLE	IF	CITATIONS
1	Variant analyses of candidate genes in orofacial clefts in multi-ethnic populations. <i>Oral Diseases</i> , 2022, 28, 1921-1935.	1.5	3
2	Targeted newborn metabolomics: prediction of gestational age from cord blood. <i>Journal of Perinatology</i> , 2022, 42, 181-186.	0.9	2
3	Genome-wide association study of multiethnic nonsyndromic orofacial cleft families identifies novel loci specific to family and phenotypic subtypes. <i>Genetic Epidemiology</i> , 2022, , .	0.6	4
4	Genetic predictors of severe intraventricular hemorrhage in extremely low-birthweight infants. <i>Journal of Perinatology</i> , 2021, 41, 286-294.	0.9	3
5	Using an aquatic model, <i>Xenopus laevis</i> , to uncover the role of chromodomain 1 in craniofacial disorders. <i>Genesis</i> , 2021, 59, e23394.	0.8	10
6	Cost-effectiveness of a gestational age metabolic algorithm for preterm and small-for-gestational-age classification. <i>American Journal of Obstetrics &amp; Gynecology MFM</i> , 2021, 3, 100279.	1.3	7
7	Co-occurrence of orofacial clefts and clubfoot phenotypes in a sub-Saharan African cohort: Whole-exome sequencing implicates multiple syndromes and genes. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2021, 9, e1655.	0.6	3
8	Genome-Wide Association Study of Non-syndromic Orofacial Clefts in a Multiethnic Sample of Families and Controls Identifies Novel Regions. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 621482.	1.8	16
9	Interactions between PDA-associated polymorphisms and genetic ancestry alter ductus arteriosus gene expression. <i>Pediatric Research</i> , 2021, , .	1.1	0
10	The PAX1 locus at 20p11 is a potential genetic modifier for bilateral cleft lip. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100025.	1.0	9
11	<i>FAT4</i> identified as a potential modifier of orofacial cleft laterality. <i>Genetic Epidemiology</i> , 2021, 45, 721-735.	0.6	14
12	Pleiotropy method reveals genetic overlap between orofacial clefts at multiple novel loci from GWAS of multi-ethnic trios. <i>PLoS Genetics</i> , 2021, 17, e1009584.	1.5	18
13	Integrative genetic, genomic and transcriptomic analysis of heat shock protein and nuclear hormone receptor gene associations with spontaneous preterm birth. <i>Scientific Reports</i> , 2021, 11, 17115.	1.6	12
14	Genome-Wide Scan for Parent-of-Origin Effects in a sub-Saharan African Cohort With Nonsyndromic Cleft Lip and/or Cleft Palate (CL/P). <i>Cleft Palate-Craniofacial Journal</i> , 2021, , 105566562110363.	0.5	1
15	Association of maternal prenatal selenium concentration and preterm birth: a multicountry meta-analysis. <i>BMJ Global Health</i> , 2021, 6, e005856.	2.0	13
16	Re-evaluating surgery and re-irradiation for locally recurrent pediatric ependymoma – a multi-institutional study. <i>Neuro-Oncology Advances</i> , 2021, 3, vdab158.	0.4	5
17	Whole genome sequencing of orofacial cleft trios from the Gabriella Miller Kids First Pediatric Research Consortium identifies a new locus on chromosome 21. <i>Human Genetics</i> , 2020, 139, 215-226.	1.8	19
18	Dissecting maternal and fetal genetic effects underlying the associations between maternal phenotypes, birth outcomes, and adult phenotypes: A mendelian-randomization and haplotype-based genetic score analysis in 10,734 mother-infant pairs. <i>PLoS Medicine</i> , 2020, 17, e1003305.	3.9	37

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19	Reply to "Diversity is essential for good science and Reproductive science is no different: A response to the recent formulation of the Burroughs Wellcome Fund Pregnancy Think-Tank" American Journal of Obstetrics and Gynecology, 2020, 223, 951-952.	0.7	0
20	Advancing human health in the decade ahead: pregnancy as a key window for discovery. American Journal of Obstetrics and Gynecology, 2020, 223, 312-321.	0.7	13
21	Non-random distribution of deleterious mutations in the DNA and protein-binding domains of <i>IRF6</i> are associated with Van Der Woude syndrome. Molecular Genetics & Genomic Medicine, 2020, 8, e1355.	0.6	13
22	Genome-wide Enrichment of De Novo Coding Mutations in Orofacial Cleft Trios. American Journal of Human Genetics, 2020, 107, 124-136.	2.6	48
23	SPECC1L regulates palate development downstream of IRF6. Human Molecular Genetics, 2020, 29, 845-858.	1.4	18
24	CDH1 Mutation Distribution and Type Suggests Genetic Differences between the Etiology of Orofacial Clefting and Gastric Cancer. Genes, 2020, 11, 391.	1.0	11
25	A phase 2 study of valproic acid and radiation, followed by maintenance valproic acid and bevacizumab in children with newly diagnosed diffuse intrinsic pontine glioma or high-grade glioma. Pediatric Blood and Cancer, 2020, 67, e28283.	0.8	40
26	Multimiomics Characterization of Preterm Birth in Low- and Middle-Income Countries. JAMA Network Open, 2020, 3, e2029655.	2.8	53
27	Title is missing!. , 2020, 17, e1003305.		0
28	Title is missing!. , 2020, 17, e1003305.		0
29	Title is missing!. , 2020, 17, e1003305.		0
30	Title is missing!. , 2020, 17, e1003305.		0
31	Title is missing!. , 2020, 17, e1003305.		0
32	Title is missing!. , 2020, 17, e1003305.		0
33	Detection of de novo copy number deletions from targeted sequencing of trios. Bioinformatics, 2019, 35, 571-578.	1.8	2
34	Variants in the fetal genome near pro-inflammatory cytokine genes on 2q13 associate with gestational duration. Nature Communications, 2019, 10, 3927.	5.8	49
35	Mutations in GDF11 and the extracellular antagonist, Follistatin, as a likely cause of Mendelian forms of orofacial clefting in humans. Human Mutation, 2019, 40, 1813-1825.	1.1	26
36	A systematic genetic analysis and visualization of phenotypic heterogeneity among orofacial cleft GWAS signals. Genetic Epidemiology, 2019, 43, 704-716.	0.6	36

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37	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. <i>Nature Genetics</i> , 2019, 51, 804-814.	9.4	402
38	Deletions and loss-of-function variants in TP63 associated with orofacial clefting. <i>European Journal of Human Genetics</i> , 2019, 27, 1101-1112.	1.4	16
39	Front Cover, Volume 40, Issue 10. <i>Human Mutation</i> , 2019, 40, i.	1.1	0
40	Association of low-frequency genetic variants in regulatory regions with nonsyndromic orofacial clefts. <i>American Journal of Medical Genetics, Part A</i> , 2019, 179, 467-474.	0.7	18
41	Genomic analyses in African populations identify novel risk loci for cleft palate. <i>Human Molecular Genetics</i> , 2019, 28, 1038-1051.	1.4	61
42	Genetic variants associated with patent ductus arteriosus in extremely preterm infants. <i>Journal of Perinatology</i> , 2019, 39, 401-408.	0.9	16
43	Inferring disease risk genes from sequencing data in multiplex pedigrees through sharing of rare variants. <i>Genetic Epidemiology</i> , 2019, 43, 37-49.	0.6	6
44	Genetic Variants and the Cortisol Response in Children: An Exploratory Study. <i>Biological Research for Nursing</i> , 2019, 21, 157-165.	1.0	1
45	Novel <i>GREM1</i> Variations in Sub-Saharan African Patients With Cleft Lip and/or Cleft Palate. <i>Cleft Palate-Craniofacial Journal</i> , 2018, 55, 736-742.	0.5	9
46	Genome-wide association study of offspring birth weight in 86%577 women identifies five novel loci and highlights maternal genetic effects that are independent of fetal genetics. <i>Human Molecular Genetics</i> , 2018, 27, 742-756.	1.4	156
47	Polymorphisms in urea cycle enzyme genes are associated with persistent pulmonary hypertension of the newborn. <i>Pediatric Research</i> , 2018, 83, 142-147.	1.1	22
48	Genome-wide interaction studies identify sex-specific risk alleles for nonsyndromic orofacial clefts. <i>Genetic Epidemiology</i> , 2018, 42, 664-672.	0.6	15
49	Identification of paternal uniparental disomy on chromosome 22 and a <i>de novo</i> deletion on chromosome 18 in individuals with orofacial clefts. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2018, 6, 924-932.	0.6	4
50	Mutations in the Epithelial Cadherin-p120-Catenin Complex Cause Mendelian Non-Syndromic Cleft Lip with or without Cleft Palate. <i>American Journal of Human Genetics</i> , 2018, 102, 1143-1157.	2.6	94
51	Gene-Centric Analysis of Preeclampsia Identifies Maternal Association at <i>PLEKHG1</i> . <i>Hypertension</i> , 2018, 72, 408-416.	1.3	46
52	Whole exome sequencing reveals HSPA1L as a genetic risk factor for spontaneous preterm birth. <i>PLoS Genetics</i> , 2018, 14, e1007394.	1.5	35
53	Genome-wide meta-analyses of nonsyndromic orofacial clefts identify novel associations between FOXE1 and all orofacial clefts, and TP63 and cleft lip with or without cleft palate. <i>Human Genetics</i> , 2017, 136, 275-286.	1.8	139
54	Genome-wide association study of sepsis in extremely premature infants. <i>Archives of Disease in Childhood: Fetal and Neonatal Edition</i> , 2017, 102, F439-F445.	1.4	32

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55	Association of candidate gene polymorphisms with clinical subtypes of preterm birth in a Latin American population. <i>Pediatric Research</i> , 2017, 82, 554-559.	1.1	8
56	Association studies of low-frequency coding variants in nonsyndromic cleft lip with or without cleft palate. <i>American Journal of Medical Genetics, Part A</i> , 2017, 173, 1531-1538.	0.7	36
57	Relationship of Genetic Variants With Procedural Pain, Anxiety, and Distress in Children. <i>Biological Research for Nursing</i> , 2017, 19, 339-349.	1.0	13
58	DNA methylation of a novel PAK4 locus influences ototoxicity susceptibility following cisplatin and radiation therapy for pediatric embryonal tumors. <i>Neuro-Oncology</i> , 2017, 19, 1372-1379.	0.6	7
59	Whole exome association of rare deletions in multiplex oral cleft families. <i>Genetic Epidemiology</i> , 2017, 41, 61-69.	0.6	10
60	Evidence for SNP-SNP interaction identified through targeted sequencing of cleft case-parent trios. <i>Genetic Epidemiology</i> , 2017, 41, 244-250.	0.6	24
61	Identifying Genetic Sources of Phenotypic Heterogeneity in Orofacial Clefts by Targeted Sequencing. <i>Birth Defects Research</i> , 2017, 109, 1030-1038.	0.8	41
62	Identification of 16q21 as a modifier of nonsyndromic orofacial cleft phenotypes. <i>Genetic Epidemiology</i> , 2017, 41, 887-897.	0.6	24
63	Genome-wide analysis of parent-of-origin interaction effects with environmental exposure (PoOxE): An application to European and Asian cleft palate trios. <i>PLoS ONE</i> , 2017, 12, e0184358.	1.1	16
64	Identifying Genetic Sources of Phenotypic Heterogeneity in Orofacial Clefts by Targeted Sequencing. <i>Birth Defects Research</i> , 2017, , .	0.8	0
65	Genome-Wide Association Study Reveals Multiple Loci Influencing Normal Human Facial Morphology. <i>PLoS Genetics</i> , 2016, 12, e1006149.	1.5	140
66	A multi-ethnic genome-wide association study identifies novel loci for non-syndromic cleft lip with or without cleft palate on 2p24.2, 17q23 and 19q13. <i>Human Molecular Genetics</i> , 2016, 25, ddw104.	1.4	163
67	Maternal and neonatal epidemiological features in clinical subtypes of preterm birth. <i>Journal of Maternal-Fetal and Neonatal Medicine</i> , 2016, 29, 3153-3161.	0.7	22
68	Polymorphisms in NR5A2, gene encoding liver receptor homolog-1 are associated with preterm birth. <i>Pediatric Research</i> , 2016, 79, 776-780.	1.1	8
69	A Genome-wide Association Study of Nonsyndromic Cleft Palate Identifies an Etiologic Missense Variant in GRHL3. <i>American Journal of Human Genetics</i> , 2016, 98, 744-754.	2.6	146
70	Genetic Evidence for Causal Relationships Between Maternal Obesity-Related Traits and Birth Weight. <i>JAMA - Journal of the American Medical Association</i> , 2016, 315, 1129.	3.8	220
71	Common Genetic Variants in FOXP2 Are Not Associated with Individual Differences in Language Development. <i>PLoS ONE</i> , 2016, 11, e0152576.	1.1	18
72	Determining the prevalence of cytomegalovirus infection in a cohort of preterm infants. <i>Journal of Neonatal-Perinatal Medicine</i> , 2015, 8, 137-141.	0.4	12

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73	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015, 11, e1005378.	1.5	331
74	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. <i>American Journal of Human Genetics</i> , 2015, 96, 487-497.	2.6	101
75	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	13.7	3,823
76	Identification of Functional Variants for Cleft Lip with or without Cleft Palate in or near PAX7, FGFR2, and NOG by Targeted Sequencing of GWAS Loci. <i>American Journal of Human Genetics</i> , 2015, 96, 397-411.	2.6	150
77	Genome-Wide Association Studies in Dogs and Humans Identify ADAMTS20 as a Risk Variant for Cleft Lip and Palate. <i>PLoS Genetics</i> , 2015, 11, e1005059.	1.5	82
78	Integrated Genomic Analyses in Bronchopulmonary Dysplasia. <i>Journal of Pediatrics</i> , 2015, 166, 531-537.e13.	0.9	93
79	Replication of 13q31.1 association in nonsyndromic cleft lip with cleft palate in Europeans. <i>American Journal of Medical Genetics, Part A</i> , 2015, 167, 1054-1060.	0.7	31
80	Antioxidant response genes sequence variants and BPD susceptibility in VLBW infants. <i>Pediatric Research</i> , 2015, 77, 477-483.	1.1	52
81	Genetic variation in CYB5R3 is associated with methemoglobin levels in preterm infants receiving nitric oxide therapy. <i>Pediatric Research</i> , 2015, 77, 472-476.	1.1	5
82	Evidence of Gene×Environment Interaction for Two Genes on Chromosome 4 and Environmental Tobacco Smoke in Controlling the Risk of Nonsyndromic Cleft Palate. <i>PLoS ONE</i> , 2014, 9, e88088.	1.1	33
83	A LINE-1 Insertion in DLX6 Is Responsible for Cleft Palate and Mandibular Abnormalities in a Canine Model of Pierre Robin Sequence. <i>PLoS Genetics</i> , 2014, 10, e1004257.	1.5	49
84	Identification of single nucleotide polymorphisms in hematopoietic cell transplant patients affecting early recognition of, and response to, endotoxin. <i>Innate Immunity</i> , 2014, 20, 697-711.	1.1	9
85	2013 Presidential Address: Just Another President's Speech (but It's All about You). <i>American Journal of Human Genetics</i> , 2014, 94, 319-323.	2.6	0
86	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	9.4	1,818
87	Whole Exome Sequencing of Distant Relatives in Multiplex Families Implicates Rare Variants in Candidate Genes for Oral Clefts. <i>Genetics</i> , 2014, 197, 1039-1044.	1.2	79
88	Dominant Mutations in GRHL3 Cause Van der Woude Syndrome and Disrupt Oral Periderm Development. <i>American Journal of Human Genetics</i> , 2014, 94, 23-32.	2.6	195
89	Search for genetic modifiers of IRF6 and genotype×phenotype correlations in Van der Woude and popliteal pterygium syndromes. <i>American Journal of Medical Genetics, Part A</i> , 2013, 161, 2535-2544.	0.7	21
90	A solution pathway for preterm birth: accelerating a priority research agenda. <i>The Lancet Global Health</i> , 2013, 1, e328-e330.	2.9	44

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91	Clinical and environmental influences on metabolic biomarkers collected for newborn screening. <i>Clinical Biochemistry</i> , 2013, 46, 133-138.	0.8	62
92	Polymorphisms of CYP51A1 from Cholesterol Synthesis: Associations with Birth Weight and Maternal Lipid Levels and Impact on CYP51 Protein Structure. <i>PLoS ONE</i> , 2013, 8, e82554.	1.1	24
93	Genetics of Nonsyndromic Orofacial Clefts. <i>Cleft Palate-Craniofacial Journal</i> , 2012, 49, 73-91.	0.5	212
94	Assessing the impact of nicotine dependence genes on the risk of facial clefts: An example of the use of national registry and biobank data. <i>Norsk Epidemiologi</i> , 2012, 21, 241-250.	0.2	5
95	Cleft lip and palate: understanding genetic and environmental influences. <i>Nature Reviews Genetics</i> , 2011, 12, 167-178.	7.7	1,435
96	Temporal lobe pleomorphic xanthoastrocytoma and acquired BRAF mutation in an adolescent with the constitutional 22q11.2 deletion syndrome. <i>Journal of Neuro-Oncology</i> , 2011, 102, 509-514.	1.4	16
97	Evidence for gene-environment interaction in a genome wide study of nonsyndromic cleft palate. <i>Genetic Epidemiology</i> , 2011, 35, n/a-n/a.	0.6	145
98	Mapping a New Spontaneous Preterm Birth Susceptibility Gene, IGF1R, Using Linkage, Haplotype Sharing, and Association Analysis. <i>PLoS Genetics</i> , 2011, 7, e1001293.	1.5	61
99	Recurrence risk for offspring of twins discordant for oral cleft: A population-based cohort study of the Danish 1936-2004 cleft twin cohort. <i>American Journal of Medical Genetics, Part A</i> , 2010, 152A, 2468-2474.	0.7	28
100	A genome-wide association study of cleft lip with and without cleft palate identifies risk variants near MAFB and ABCA4. <i>Nature Genetics</i> , 2010, 42, 525-529.	9.4	518
101	A cohort study of recurrence patterns among more than 54 000 relatives of oral cleft cases in Denmark: support for the multifactorial threshold model of inheritance. <i>Journal of Medical Genetics</i> , 2010, 47, 162-168.	1.5	188
102	Genome Scan, Fine-Mapping, and Candidate Gene Analysis of Non-Syndromic Cleft Lip with or without Cleft Palate Reveals Phenotype-Specific Differences in Linkage and Association Results. <i>Human Heredity</i> , 2009, 68, 151-170.	0.4	113
103	Maternal Contributions to Preterm Delivery. <i>American Journal of Epidemiology</i> , 2009, 170, 1358-1364.	1.6	133
104	FOXE1 association with both isolated cleft lip with or without cleft palate, and isolated cleft palate. <i>Human Molecular Genetics</i> , 2009, 18, 4879-4896.	1.4	136
105	Disruption of an AP-2 binding site in an IRF6 enhancer is associated with cleft lip. <i>Nature Genetics</i> , 2008, 40, 1341-1347.	9.4	382
106	Cancer Risk in Persons with Oral Clefts: A Population-based Study of 8,093 Cases. <i>American Journal of Epidemiology</i> , 2005, 161, 1047-1055.	1.6	111
107	Direct Sequencing of Candidate Genes for Nonsyndromic Cleft Lip and Palate. <i>PLoS Genetics</i> , 2005, preprint, e64.	1.5	1
108	Long term follow up study of survival associated with cleft lip and palate at birth. <i>BMJ: British Medical Journal</i> , 2004, 328, 1405.	2.4	205

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109	Cleft palate: players, pathways, and pursuits. <i>Journal of Clinical Investigation</i> , 2004, 113, 1676-1678.	3.9	93
110	Novel IRF6 mutations in Japanese patients with Van der Woude Syndrome: two missense mutations (R45Q and P396S) and a 17-kb deletion. <i>Journal of Human Genetics</i> , 2003, 48, 622-628.	1.1	31
111	Mutations in IRF6 cause Van der Woude and popliteal pterygium syndromes. <i>Nature Genetics</i> , 2002, 32, 285-289.	9.4	784
112	Clinical Pathology Case: Hyperimmunoglobulin E Syndrome (Job's Syndrome). <i>Fetal and Pediatric Pathology</i> , 2001, 20, 223-226.	0.3	0
113	Matroshka and ectopic polymorphisms: Two new classes of DNA sequence variation identified at the Van der Woude syndrome locus on 1q32-q41. <i>Human Mutation</i> , 2001, 18, 422-434.	1.1	2
114	Time for T. <i>Nature Genetics</i> , 2001, 29, 107-109.	9.4	8
115	Pitx2 Regulates Procollagen Lysyl Hydroxylase (Plod) Gene Expression. <i>Journal of Cell Biology</i> , 2001, 152, 545-552.	2.3	78
116	Mutations in the human forkhead transcription factor FOXE3 associated with anterior segment ocular dysgenesis and cataracts. <i>Human Molecular Genetics</i> , 2001, 10, 231-236.	1.4	184
117	CLINICAL PATHOLOGY CASE: HYPERIMMUNOGLOBULIN E SYNDROME (JOB'S SYNDROME). <i>Fetal and Pediatric Pathology</i> , 2001, 20, 223-226.	0.3	0
118	The Pitx2 protein in mouse development. <i>Developmental Dynamics</i> , 2000, 218, 195-200.	0.8	126
119	Exclusion of the branchio-oto-renal syndrome locus (EYA1) from patients with branchio-oculo-facial syndrome. , 2000, 91, 387-390.		19
120	Domain-specific mutations in TGFB1 result in Camurati-Engelmann disease. <i>Nature Genetics</i> , 2000, 26, 19-20.	9.4	239
121	Genomic structure of the human retinoic acid receptor-alpha1 gene. <i>Mammalian Genome</i> , 1999, 10, 528-529.	1.0	8
122	Microdeletions at chromosome bands 1q32-q41 as a cause of Van der Woude syndrome. , 1999, 84, 145-150.		65
123	Candidate genes for nonsyndromic cleft lip and palate and maternal cigarette smoking and alcohol consumption: Evaluation of genotype-environment interactions from a population-based case-control study of orofacial clefts. , 1999, 59, 39-50.		198
124	Analysis of select folate pathway genes, PAX3, and human T in a midwestern neural tube defect population. <i>Teratology</i> , 1999, 59, 331-341.	1.8	88
125	Analysis of select folate pathway genes, PAX3, and human T in a midwestern neural tube defect population. , 1999, 59, 331.		3
126	The effect of follow-up on limiting non-participation bias in genetic epidemiologic investigations. <i>European Journal of Epidemiology</i> , 1998, 14, 129-138.	2.5	23



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127	Cloning and chromosomal localization of two novel human genes encoding LIM-domain binding factors CLIM1 and CLIM2/LDB1/NLI. <i>Mammalian Genome</i> , 1998, 9, 921-924.	1.0	10
128	Assignment of gene responsible for progressive pseudorheumatoid dysplasia to chromosome 6 and examination of COL10A1 as candidate gene. <i>European Journal of Human Genetics</i> , 1998, 6, 251-256.	1.4	22
129	A novel homeobox gene PITX3 is mutated in families with autosomal-dominant cataracts and ASMD. <i>Nature Genetics</i> , 1998, 19, 167-170.	9.4	371
130	A new human homeobox gene OGI2X is a member of the most conserved homeobox gene family and is expressed during heart development in mouse. <i>Human Molecular Genetics</i> , 1998, 7, 415-422.	1.4	40
131	Exclusion of lfa and lfb as the Lps gene and mapping of three markers near the Lps locus. <i>Mammalian Genome</i> , 1997, 8, 785-786.	1.0	3
132	Genomic structure, sequence, and mapping of humanFGF8 with no evidence for its role in craniosynostosis/limb defect syndromes. , 1997, 72, 354-362.		16
133	Cloning and characterization of a novel bicoid-related homeobox transcription factor gene, RIEG, involved in Rieger syndrome. <i>Nature Genetics</i> , 1996, 14, 392-399.	9.4	852
134	Integrated human genome-wide maps constructed using the CEPH reference panel. <i>Nature Genetics</i> , 1994, 6, 391-393.	9.4	216
135	The chromosome 4 workshop report. <i>Genomics</i> , 1992, 12, 857-858.	1.3	0
136	Characterization of the calcitonin/CGRP gene in Williams syndrome. <i>American Journal of Medical Genetics Part A</i> , 1991, 39, 28-33.	2.4	6