Terri H Beaty

List of Publications by Year
in descending order

165 papers	14,915 citations	41344 49 h-index	21540 114 g-index
236 all docs	236 docs citations	236 times ranked	15933 citing authors

#	Article	IF	Citations
1	Evidence of the folateâ€mediated oneâ€carbon metabolism pathway genes in controlling the nonâ€syndromic oral clefts risks. Oral Diseases, 2023, 29, 1080-1088.	3.0	1
2	Development of a Blood-based Transcriptional Risk Score for Chronic Obstructive Pulmonary Disease. American Journal of Respiratory and Critical Care Medicine, 2022, 205, 161-170.	5.6	15
3	Individual and Combined Association Between Prenatal Polysubstance Exposure and Childhood Risk of Attention-Deficit/Hyperactivity Disorder. JAMA Network Open, 2022, 5, e221957.	5.9	13
4	Lung tissue shows divergent gene expression between chronic obstructive pulmonary disease and idiopathic pulmonary fibrosis. Respiratory Research, 2022, 23, 97.	3.6	7
5	Benchmarking statistical methods for analyzing parentâ€“child dyads in genetic association studies. Genetic Epidemiology, 2022, 46, 266-284.	1.3	2
6	Genome-Wide Gene-by-Smoking Interaction Study of Chronic Obstructive Pulmonary Disease. American Journal of Epidemiology, 2021, 190, 875-885.	3.4	21
7	Detecting Gene-Environment Interaction for Maternal Exposures Using Case-Parent Trios Ascertained Through a Case With Non-Syndromic Orofacial Cleft. Frontiers in Cell and Developmental Biology, 2021, 9, 621018.	3.7	2
8	The PAX1 locus at 20p11 is a potential genetic modifier for bilateral cleft lip. Human Genetics and Genomics Advances, 2021, 2, 100025.	1.7	9
9	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 874-893.	6.2	28
10	Emphysema Progression and Lung Function Decline Among Angiotensin Converting Enzyme Inhibitors and Angiotensin-Receptor Blockade Users in the COPDGene Cohort. Chest, 2021, 160, 1245-1254.	0.8	9
11	FAT4 identified as a potential modifier of orofacial cleft laterality. Genetic Epidemiology, 2021, 45, 721-735.	1.3	14
12	Integrative approaches generate insights into the architecture of non-syndromic cleft lip Â± cleft palate. Human Genetics and Genomics Advances, 2021, 2, 100038.	1.7	8
13	Pleiotropy method reveals genetic overlap between orofacial clefts at multiple novel loci from GWAS of multi-ethnic trios. PLoS Genetics, 2021, 17, e1009584.	3.5	18
14	Multiethnic genome-wide and HLA association study of total serum IgE level. Journal of Allergy and Clinical Immunology, 2021, 148, 1589-1595.	2.9	15
15	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 1836-1851.	6.2	14
16	Interaction of Cigarette Smoking and Polygenic Risk Score on Reduced Lung Function. JAMA Network Open, 2021, 4, e2139525.	5.9	22
17	Machine Learning Characterization of COPD Subtypes. Chest, 2020, 157, 1147-1157.	0.8	44
18	Mixed-model admixture mapping identifies smoking-dependent loci of lung function in African Americans. European Journal of Human Genetics, 2020, 28, 656-668.	2.8	7

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19	Whole genome sequencing of orofacial cleft trios from the Gabriella Miller Kids First Pediatric Research Consortium identifies a new locus on chromosome 21. Human Genetics, 2020, 139, 215-226.	3.8	19
20	Protective effect of club cell secretory protein (CC-16) on COPD risk and progression: a Mendelian randomisation study. Thorax, 2020, 75, 934-943.	5.6	17
21	Co-Morbidity Patterns Identified Using Latent Class Analysis of Medications Predict All-Cause Mortality Independent of Other Known Risk Factors: The COPDGene^{Â®} Study . Clinical Epidemiology, 2020, Volume 12, 1171-1181.	3.0	6
22	A pseudolikelihood approach for assessing genetic association in caseâ€“control studies with unmeasured population structure. Statistical Methods in Medical Research, 2020, 29, 3153-3165.	1.5	0
23	Genome-wide Enrichment of De Novo Coding Mutations in Orofacial Cleft Trios. American Journal of Human Genetics, 2020, 107, 124-136.	6.2	48
24	Association of HLA-DRB1âˆ—09:01 with tIgE levels among African-ancestry individuals with asthma. Journal of Allergy and Clinical Immunology, 2020, 146, 147-155.	2.9	14
25	Relative contributions of family history and a polygenic risk score on COPD and related outcomes: COPDGene and ECLIPSE studies. BMJ Open Respiratory Research, 2020, 7, e000755.	3.0	14
26	Common and Rare Variants Genetic Association Analysis of Cigarettes per Day Among Ever-Smokers in Chronic Obstructive Pulmonary Disease Cases and Controls. Nicotine and Tobacco Research, 2019, 21, 714-722.	2.6	7
27	Detection of de novo copy number deletions from targeted sequencing of trios. Bioinformatics, 2019, 35, 571-578.	4.1	2
28	Geneâ€“gene interaction among cell adhesion genes and risk of nonsyndromic cleft lip with or without cleft palate in Chinese caseâ€parent trios. Molecular Genetics & Genomic Medicine, 2019, 7, e00872.	1.2	11
29	DSP variants may be associated with longitudinal change in quantitative emphysema. Respiratory Research, 2019, 20, 160.	3.6	7
30	Analysis of genetically driven alternative splicing identifies FBXO38 as a novel COPD susceptibility gene. PLoS Genetics, 2019, 15, e1008229.	3.5	17
31	The pharmacogenomics of inhaled corticosteroids and lung function decline in COPD. European Respiratory Journal, 2019, 54, 1900521.	6.7	14
32	Replicated methylation changes associated with eczema herpeticum and allergic response. Clinical Epigenetics, 2019, 11, 122.	4.1	22
33	The Evolving Field of Genetic Epidemiology: From Familial Aggregation to Genomic Sequencing. American Journal of Epidemiology, 2019, 188, 2069-2077.	3.4	6
34	A systematic genetic analysis and visualization of phenotypic heterogeneity among orofacial cleft GWAS signals. Genetic Epidemiology, 2019, 43, 704-716.	1.3	36
35	Predictors of dental care utilization in northâ€central Appalachia in the USA. Community Dentistry and Oral Epidemiology, 2019, 47, 283-290.	1.9	17
36	Exploring the interaction between FGF Genes and Tâ€box genes among chinese nonsyndromic cleft lip with or without cleft palate caseâ€parent trios. Environmental and Molecular Mutagenesis, 2019, 60, 602-606.	2.2	12

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37	Genetic Advances in Chronic Obstructive Pulmonary Disease. Insights from COPDGene. American Journal of Respiratory and Critical Care Medicine, 2019, 200, 677-690.	5.6	66
38	Haplotype and Haplotype-Environment Interaction Analysis Revealed Roles of SPRY2 for NSCL/P among Chinese Populations. International Journal of Environmental Research and Public Health, 2019, 16, 557.	2.6	4
39	Assessing pleiotropy and mediation in genetic loci associated with chronic obstructive pulmonary disease. Genetic Epidemiology, 2019, 43, 318-329.	1.3	5
40	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. Nature Genetics, 2019, 51, 481-493.	21.4	350
41	Genetic landscape of chronic obstructive pulmonary disease identifies heterogeneous cell-type and phenotype associations. Nature Genetics, 2019, 51, 494-505.	21.4	257
42	Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations. Nature Communications, 2019, 10, 880.	12.8	71
43	Assembly of a pan-genome from deep sequencing of 910 humans of African descent. Nature Genetics, 2019, 51, 30-35.	21.4	276
44	Inferring disease risk genes from sequencing data in multiplex pedigrees through sharing of rare variants. Genetic Epidemiology, 2019, 43, 37-49.	1.3	6
45	Subtypes of COPD Have Unique Distributions and Differential Risk of Mortality. Chronic Obstructive Pulmonary Diseases (Miami, Fla), 2019, 6, 400-413.	0.7	24
46	Identifying Smoking-Related Disease on Lung Cancer Screening CT Scans: Increasing the Value. Chronic Obstructive Pulmonary Diseases (Miami, Fla), 2019, 6, 233-245.	0.7	11
47	Genotype imputation performance of three reference panels using African ancestry individuals. Human Genetics, 2018, 137, 281-292.	3.8	38
48	Geneâ€“gene interaction between MSX1 and TP63 in Asian caseâ€parent trios with nonsyndromic cleft lip with or without cleft palate. Birth Defects Research, 2018, 110, 317-324.	1.5	8
49	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	21.4	426
50	Evaluating the effect of nicotinic cholinergic receptor genes on the risk of nonsyndromic cleft lip with or without cleft palate. Oral Diseases, 2018, 24, 1068-1072.	3.0	0
51	Lobar Emphysema Distribution Is Associated With 5-Year Radiological Disease Progression. Chest, 2018, 153, 65-76.	0.8	36
52	Integration of Molecular Interactome and Targeted Interaction Analysis to Identify a COPD Disease Network Module. Scientific Reports, 2018, 8, 14439.	3.3	40
53	Genomics and response to long-term oxygen therapy in chronic obstructive pulmonary disease. Journal of Molecular Medicine, 2018, 96, 1375-1385.	3.9	17
54	Childhood asthma is associated with COPD and known asthma variants in COPDGene: a genome-wide association study. Respiratory Research, 2018, 19, 209.	3.6	41

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55	Optimized distributed systems achieve significant performance improvement on sorted merging of massive VCF files. GigaScience, 2018, 7, .	6.4	4
56	Whole-Genome Sequencing in Severe Chronic Obstructive Pulmonary Disease. American Journal of Respiratory Cell and Molecular Biology, 2018, 59, 614-622.	2.9	22
57	Whole exome sequencing analysis in severe chronic obstructive pulmonary disease. Human Molecular Genetics, 2018, 27, 3801-3812.	2.9	32
58	The genetics of smoking in individuals with chronic obstructive pulmonary disease. Respiratory Research, 2018, 19, 59.	3.6	11
59	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. Human Genetics, 2017, 136, 275-286.	3.8	139
60	Association between dietary fat intake and insulin resistance in Chinese child twins. British Journal of Nutrition, 2017, 117, 230-236.	2.3	15
61	Genome-wide analyses of non-syndromic cleft lip with palate identify 14 novel loci and genetic heterogeneity. Nature Communications, 2017, 8, 14364.	12.8	207
62	Genetic loci associated with chronic obstructive pulmonary disease overlap with loci for lung function and pulmonary fibrosis. Nature Genetics, 2017, 49, 426-432.	21.4	306
63	Genome-wide association analyses for lung function and chronic obstructive pulmonary disease identify new loci and potential druggable targets. Nature Genetics, 2017, 49, 416-425.	21.4	257
64	The role of ST2 and ST2 genetic variants in schistosomiasis. Journal of Allergy and Clinical Immunology, 2017, 140, 1416-1422.e6.	2.9	15
65	Genetic Association and Risk Scores in a Chronic Obstructive Pulmonary Disease Meta-analysis of 16,707 Subjects. American Journal of Respiratory Cell and Molecular Biology, 2017, 57, 35-46.	2.9	55
66	Geneâ€based segregation method for identifying rare variants in familyâ€based sequencing studies. Genetic Epidemiology, 2017, 41, 309-319.	1.3	14
67	Geneâ€gene interaction of single nucleotide polymorphisms in 16p13.3 may contribute to the risk of nonâ€syndromic cleft lip with or without cleft palate in Chinese caseâ€parent trios. American Journal of Medical Genetics, Part A, 2017, 173, 1489-1494.	1.2	4
68	Variable Susceptibility to Cigarette Smokeâ€“Induced Emphysema in 34 Inbred Strains of Mice Implicates Abi3bp in Emphysema Susceptibility. American Journal of Respiratory Cell and Molecular Biology, 2017, 57, 367-375.	2.9	22
69	Whole exome association of rare deletions in multiplex oral cleft families. Genetic Epidemiology, 2017, 41, 61-69.	1.3	10
70	Identifying tagging SNPs for African specific genetic variation from the African Diaspora Genome. Scientific Reports, 2017, 7, 46398.	3.3	26
71	Prevalence of Orofacial Clefts among Live Births in China: A Systematic Review and Metaâ€Analysis. Birth Defects Research, 2017, 109, 1011-1019.	1.5	26
72	Alpha-1 Antitrypsin PiMZ Genotype Is Associated with Chronic Obstructive Pulmonary Disease in Two Racial Groups. Annals of the American Thoracic Society, 2017, 14, 1280-1287.	3.2	60

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73	Identification of common non-coding variants at 1p22 that are functional for non-syndromic orofacial clefting. Nature Communications, 2017, 8, 14759.	12.8	48
74	Evidence for SNP-SNP interaction identified through targeted sequencing of cleft case-parent trios. Genetic Epidemiology, 2017, 41, 244-250.	1.3	24
75	Analysis of sequence data to identify potential risk variants for oral clefts in multiplex families. Molecular Genetics & Genomic Medicine, 2017, 5, 570-579.	1.2	13
76	Identifying Genetic Sources of Phenotypic Heterogeneity in Orofacial Clefts by Targeted Sequencing. Birth Defects Research, 2017, 109, 1030-1038.	1.5	41
77	Surfactant protein D is a causal risk factor for COPD: results of Mendelian randomisation. European Respiratory Journal, 2017, 50, 1700657.	6.7	45
78	Identification of 16q21 as a modifier of nonsyndromic orofacial cleft phenotypes. Genetic Epidemiology, 2017, 41, 887-897.	1.3	24
79	Susceptibility to Childhood Pneumonia: A Genome-Wide Analysis. American Journal of Respiratory Cell and Molecular Biology, 2017, 56, 20-28.	2.9	24
80	Genome-Wide Association Study of the Genetic Determinants of Emphysema Distribution. American Journal of Respiratory and Critical Care Medicine, 2017, 195, 757-771.	5.6	45
81	Genome-Wide Association of Copy Number Polymorphisms and Kidney Function. PLoS ONE, 2017, 12, e0170815.	2.5	3
82	Methods to estimate underlying blood pressure: The Atherosclerosis Risk in Communities (ARIC) Study. PLoS ONE, 2017, 12, e0179234.	2.5	26
83	Genome-wide analysis of parent-of-origin interaction effects with environmental exposure (PoOxE): An application to European and Asian cleft palate trios. PLoS ONE, 2017, 12, e0184358.	2.5	16
84	Identifying Genetic Sources of Phenotypic Heterogeneity in Orofacial Clefts by Targeted Sequencing. Birth Defects Research, 2017, , .	1.5	0
85	Genetic factors influencing risk to orofacial clefts: todayâ€™s challenges and tomorrowâ€™s opportunities. F1000Research, 2016, 5, 2800.	1.6	155
86	Identifying a Deletion Affecting Total Lung Capacity Among Subjects in the COPDGene Study Cohort. Genetic Epidemiology, 2016, 40, 81-88.	1.3	5
87	A continuum of admixture in the Western Hemisphere revealed by the African Diaspora genome. Nature Communications, 2016, 7, 12522.	12.8	136
88	Challenges and disparities in the application of personalized genomic medicine to populations with African ancestry. Nature Communications, 2016, 7, 12521.	12.8	68
89	Exome Array Analysis Identifies a Common Variant in IL27 Associated with Chronic Obstructive Pulmonary Disease. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 48-57.	5.6	52
90	Exome Sequencing Analysis in Severe, Early-Onset Chronic Obstructive Pulmonary Disease. American Journal of Respiratory and Critical Care Medicine, 2016, 193, 1353-1363.	5.6	46

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91	Common Genetic Polymorphisms Influence Blood Biomarker Measurements in COPD. PLoS Genetics, 2016, 12, e1006011.	3.5	88
92	Hemizygous Deletion on Chromosome 3p26.1 Is Associated with Heavy Smoking among African American Subjects in the COPDGene Study. PLoS ONE, 2016, 11, e0164134.	2.5	4
93	Novel evidence of association with nonsyndromic cleft lip with or without cleft palate was shown for single nucleotide polymorphisms in FOXF2 gene in an Asian population. Birth Defects Research Part A: Clinical and Molecular Teratology, 2015, 103, 857-862.	1.6	11
94	A genome-wide association study identifies risk loci for spirometric measures among smokers of European and African ancestry. BMC Genetics, 2015, 16, 138.	2.7	119
95	Genome-wide site-specific differential methylation in the blood of individuals with Klinefelter syndrome. Molecular Reproduction and Development, 2015, 82, 377-386.	2.0	29
96	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	6.2	101
97	A colorectal cancer prediction model using traditional and genetic risk scores in Koreans. BMC Genetics, 2015, 16, 49.	2.7	26
98	Targeted deep sequencing identifies rare loss-of-function variants in IFNGR1 for risk of atopic dermatitis complicated by eczema herpeticum. Journal of Allergy and Clinical Immunology, 2015, 136, 1591-1600.	2.9	42
99	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. American Journal of Human Genetics, 2015, 96, 397-411.	6.2	150
100	Clinical and Radiologic Disease in Smokers With Normal Spirometry. JAMA Internal Medicine, 2015, 175, 1539.	5.1	360
101	Geneâ€Gene Interaction Among WNT Genes for Oral Cleft in Trios. Genetic Epidemiology, 2015, 39, 385-394.	1.3	30
102	A Genome-Wide Association Study of Emphysema and Airway Quantitative Imaging Phenotypes. American Journal of Respiratory and Critical Care Medicine, 2015, 192, 559-569.	5.6	128
103	An IL-13 Promoter Polymorphism Associated with Liver Fibrosis in Patients with Schistosoma japonicum. PLoS ONE, 2015, 10, e0135360.	2.5	29
104	Evidence of Geneâ^'Environment Interaction for Two Genes on Chromosome 4 and Environmental Tobacco Smoke in Controlling the Risk of Nonsyndromic Cleft Palate. PLoS ONE, 2014, 9, e88088.	2.5	33
105	Joint Testing of Genotypic and Gene-Environment Interaction Identified Novel Association for BMP4 with Non-Syndromic CL/P in an Asian Population Using Data from an International Cleft Consortium. PLoS ONE, 2014, 9, e109038.	2.5	17
106	Genome-Wide Study of Percent Emphysema on Computed Tomography in the General Population. The Multi-Ethnic Study of Atherosclerosis Lung/SNP Health Association Resource Study. American Journal of Respiratory and Critical Care Medicine, 2014, 189, 408-418.	5.6	87
107	Beyond GWAS in COPD: Probing the Landscape between Gene-Set Associations, Genome-Wide Associations and Protein-Protein Interaction Networks. Human Heredity, 2014, 78, 131-139.	0.8	18
108	Genome-Wide Association Identifies Regulatory Loci Associated with Distinct Local Histogram Emphysema Patterns. American Journal of Respiratory and Critical Care Medicine, 2014, 190, 399-409.	5.6	77

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109	Genome-wide interaction studies reveal sex-specific asthma risk alleles. Human Molecular Genetics, 2014, 23, 5251-5259.	2.9	70
110	Detecting Disease Variants in Case-Parent Trio Studies Using the Bioconductor Software Package<tt>trio</tt>. Genetic Epidemiology, 2014, 38, 516-522.	1.3	19
111	The clinical and genetic features of COPD-asthma overlap syndrome. European Respiratory Journal, 2014, 44, 341-350.	6.7	249
112	Inferring rare disease risk variants based on exact probabilities of sharing by multiple affected relatives. Bioinformatics, 2014, 30, 2189-2196.	4.1	30
113	Epidemiology, genetics, and subtyping of preserved ratio impaired spirometry (PRISm) in COPDGene. Respiratory Research, 2014, 15, 89.	3.6	196
114	Oesophageal squamous cell carcinoma in high-risk Chinese populations: Possible role for vascular epithelial growth factor A. European Journal of Cancer, 2014, 50, 2855-2865.	2.8	9
115	Whole Exome Sequencing of Distant Relatives in Multiplex Families Implicates Rare Variants in Candidate Genes for Oral Clefts. Genetics, 2014, 197, 1039-1044.	2.9	79
116	Risk loci for chronic obstructive pulmonary disease: a genome-wide association study and meta-analysis. Lancet Respiratory Medicine,the, 2014, 2, 214-225.	10.7	291
117	Susceptibility to Chronic Mucus Hypersecretion, a Genome Wide Association Study. PLoS ONE, 2014, 9, e91621.	2.5	25
118	Comorbidities of COPD Have a Major Impact on Clinical Outcomes, Particularly in African Americans. Chronic Obstructive Pulmonary Diseases (Miami, Fla), 2014, 1, 105-114.	0.7	40
119	Dissecting direct and indirect genetic effects on chronic obstructive pulmonary disease (COPD) susceptibility. Human Genetics, 2013, 132, 431-441.	3.8	69
120	The FGF and FGFR Gene Family and Risk of Cleft Lip with or Without Cleft Palate. Cleft Palate-Craniofacial Journal, 2013, 50, 96-103.	0.9	39
121	Pulmonary Arterial Enlargement and Acute Exacerbations of COPD. New England Journal of Medicine, 2012, 367, 913-921.	27.0	397
122	A genome-wide association study of COPD identifies a susceptibility locus on chromosome 19q13. Human Molecular Genetics, 2012, 21, 947-957.	2.9	216
123	Genome-wide meta-analyses of nonsyndromic cleft lip with or without cleft palate identify six new risk loci. Nature Genetics, 2012, 44, 968-971.	21.4	311
124	Incorporating Genotype Uncertainties Into the Genotypic TDT for Main Effects and Geneâ€Environment Interactions. Genetic Epidemiology, 2012, 36, 225-234.	1.3	13
125	Examining Markers in 8q24 to Explain Differences in Evidence for Association With Cleft Lip With/Without Cleft Palate Between <scp>A</scp>sians and <scp>E</scp>uropeans. Genetic Epidemiology, 2012, 36, 392-399.	1.3	28
126	Evidence of geneâ€environment interaction for the RUNX2 gene and environmental tobacco smoke in controlling the risk of cleft lip with/without cleft palate. Birth Defects Research Part A: Clinical and Molecular Teratology, 2012, 94, 76-83.	1.6	28

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127	Rapid Testing of SNPs and Geneâ€“Environment Interactions in Caseâ€“Parent Trio Data Based on Exact Analytic Parameter Estimation. Biometrics, 2012, 68, 766-773.	1.4	34
128	Meta-analysis of genome-wide association studies of asthma in ethnically diverse North American populations. Nature Genetics, 2011, 43, 887-892.	21.4	736
129	Cleft lip and palate: understanding genetic and environmental influences. Nature Reviews Genetics, 2011, 12, 167-178.	16.3	1,435
130	Evidence for gene-environment interaction in a genome wide study of nonsyndromic cleft palate. Genetic Epidemiology, 2011, 35, n/a-n/a.	1.3	145
131	Genetic Epidemiology of COPD (COPDGene) Study Design. COPD: Journal of Chronic Obstructive Pulmonary Disease, 2011, 7, 32-43.	1.6	1,007
132	Evidence of geneâ€“environment interaction for the IRF6 gene and maternal multivitamin supplementation in controlling the risk of cleft lip with/without cleft palate. Human Genetics, 2010, 128, 401-410.	3.8	65
133	The gene, environment association studies consortium (GENEVA): maximizing the knowledge obtained from GWAS by collaboration across studies of multiple conditions. Genetic Epidemiology, 2010, 34, 364-372.	1.3	139
134	Variants in FAM13A are associated with chronic obstructive pulmonary disease. Nature Genetics, 2010, 42, 200-202.	21.4	348
135	A genome-wide association study of cleft lip with and without cleft palate identifies risk variants near MAFB and ABCA4. Nature Genetics, 2010, 42, 525-529.	21.4	518
136	A genome-wide association study on African-ancestry populations for asthma. Journal of Allergy and Clinical Immunology, 2010, 125, 336-346.e4.	2.9	213
137	Meta-Analysis of 13 Genome Scans Reveals Multiple Cleft Lip/Palate Genes with Novel Loci on 9q21 and 2q32-35. American Journal of Human Genetics, 2004, 75, 161-173.	6.2	200
138	A genomeâ€wide scan for loci predisposing to nonâ€syndromic cleft lip with or without cleft palate in two large Syrian families. American Journal of Medical Genetics Part A, 2003, 123A, 140-147.	2.4	46
139	â€œPower comparisons for genotypic vs. allelic TDT methods with >2 Allelesâ€. Genetic Epidemiology, 2002, 23, 458-461.	1.3	15
140	Multipoint Linkage Analysis Under Heterogeneity: Incorporation of Parametric and Nonparametric Approaches. Genetic Epidemiology, 2001, 21, S55-60.	1.3	0
141	Multipoint analysis using affected sib pairs: Incorporating linkage evidence from unlinked regions. Genetic Epidemiology, 2001, 21, 105-122.	1.3	21
142	Interface of Genetics and Epidemiology. Epidemiologic Reviews, 2000, 22, 120-125.	3.5	28
143	Mild association between the A/G polymorphism in the promoter of the apolipoprotein A-I gene and apolipoprotein A-I levels: A meta-analysis. , 1999, 82, 235-241.		60
144	Mild association between the A/G polymorphism in the promoter of the apolipoprotein Aâ€I gene and apolipoprotein Aâ€I levels: A metaâ€analysis. American Journal of Medical Genetics Part A, 1999, 82, 235-241.	2.4	4

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145	Association between homeobox-containing geneMSX1 and the occurrence of limb deficiency. , 1998, 75, 419-423.		38
146	Survey of genetic counselors and clinical geneticists regarding recurrence risks for families with nonsyndromic cleft lip with or without cleft palate. , 1998, 79, 184-190.		10
147	Application of transmission disequilibrium tests to nonsyndromic oral clefts: Including candidate genes and environmental exposures in the models. , 1997, 73, 337-344.		129
148	Linkage of Asthma and Total Serum IgE Concentration to Markers on Chromosome 12q: Evidence from Afro-Caribbean and Caucasian Populations. Genomics, 1996, 37, 41-50.	2.9	226
149	Evidence for an association between markers on chromosome 19q and non-syndromic cleft lip with or without cleft palate in two groups of multiplex families. Human Genetics, 1996, 99, 22-26.	3.8	51
150	Phenotypic discordance in a family with monozygotic twins and non-syndromic cleft lip and palate. , 1996, 66, 468-470.		7
151	Review of the role of potential teratogens in the origin of human nonsyndromic oral clefts. Teratology, 1996, 53, 309-317.	1.6	131
152	Review of the role of potential teratogens in the origin of human nonsyndromic oral clefts. Teratology, 1996, 53, 309-317.	1.6	5
153	Determining linkage and mode of inheritance: Mod scores and other methods. Genetic Epidemiology, 1996, 13, 575-593.	1.3	1
154	Risk of Cancer in Relatives of Prostate Cancer Probands. Journal of the National Cancer Institute, 1995, 87, 991-996.	6.3	134
155	Comparative epidemiology of selected midline congenital abnormalities. Genetic Epidemiology, 1994, 11, 141-154.	1.3	32
156	Segregation analysis of hypospadias: A reanalysis of published pedigree data. American Journal of Medical Genetics Part A, 1993, 45, 420-425.	2.4	11
157	Reply to Dr. Hook. American Journal of Medical Genetics Part A, 1993, 47, 436-436.	2.4	0
158	Neuroanatomy of Rett syndrome: A volumetric imaging study. Annals of Neurology, 1993, 34, 227-234.	5.3	180
159	Genotype at a major locus with large effects on apolipoprotein B levels predicts familial combined hyperlipidemia. Genetic Epidemiology, 1993, 10, 257-270.	1.3	23
160	Hereditary Prostate Cancer: Epidemiologic and Clinical Features. Journal of Urology, 1993, 150, 797-802.	0.4	519
161	Genetics of total serum IgE levels: A regressive model approach to segregation analysis. Genetic Epidemiology, 1991, 8, 351-359.	1.3	47
162	Measuring familial aggregation by using odds-ratio regression models. Genetic Epidemiology, 1991, 8, 361-370.	1.3	55

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163	EPIDEMIOLOGIC APPROACHES TO THE USE OF DNA MARKERS IN THE SEARCH FOR DISEASE SUSCEPTIBILITY GENES. Epidemiologic Reviews, 1990, 12, 41-55.	3.5	19
164	Family history and the risk of prostate cancer. Prostate, 1990, 17, 337-347.	2.3	609
165	Predicting intrauterine growth reterdation in sibships while considering maternal and infant covariates. Genetic Epidemiology, 1989, 6, 525-535.	1.3	5