Terri H Beaty

List of Publications by Year in Descending Order

162 papers	10,809 citations	45 h-index	102 g-index
236 ext. papers	13,258 ext. citations	7.9 avg, IF	5.49 L-index

#	Paper	IF	Citations
162	Individual and Combined Association Between Prenatal Polysubstance Exposure and Childhood Risk of Attention-Deficit/Hyperactivity Disorder.. *JAMA Network Open*, **2022**, 5, e221957	10.4	2
161	Lung tissue shows divergent gene expression between chronic obstructive pulmonary disease and idiopathic pulmonary fibrosis.. *Respiratory Research*, **2022**, 23, 97	7.3	0
160	Evidence of the folate-mediated one-carbon metabolism pathway genes in controlling the non-syndromic oral clefts risks. *Oral Diseases*, **2021**,	3.5	1
159	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	5.7	0
158	The PAX1 locus at 20p11 is a potential genetic modifier for bilateral cleft lip. *Human Genetics and Genomics Advances*, **2021**, 2, 100025-100025	0.8	3
157	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. *American Journal of Human Genetics*, **2021**, 108, 874-893	11	5
156	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	5.3	0
155	FAT4 identified as a potential modifier of orofacial cleft laterality. *Genetic Epidemiology*, **2021**, 45, 721-735	2.6	1
154	Integrative approaches generate insights into the architecture of non-syndromic cleft lip with or without cleft palate.. *Human Genetics and Genomics Advances*, **2021**, 2, 100038	0.8	1
153	Pleiotropy method reveals genetic overlap between orofacial clefts at multiple novel loci from GWAS of multi-ethnic trios. *PLoS Genetics*, **2021**, 17, e1009584	6	4
152	Genome-Wide Gene-by-Smoking Interaction Study of Chronic Obstructive Pulmonary Disease. *American Journal of Epidemiology*, **2021**, 190, 875-885	3.8	9
151	Multiethnic genome-wide and HLA association study of total serum IgE level. *Journal of Allergy and Clinical Immunology*, **2021**, 148, 1589-1595	11.5	1
150	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	11	1
149	Interaction of Cigarette Smoking and Polygenic Risk Score on Reduced Lung Function.. *JAMA Network Open*, **2021**, 4, e2139525	10.4	3
148	Co-Morbidity Patterns Identified Using Latent Class Analysis of Medications Predict All-Cause Mortality Independent of Other Known Risk Factors: The COPDGene Study. *Clinical Epidemiology*, **2020**, 12, 1171-1181	5.9	3
147	A pseudolikelihood approach for assessing genetic association in case-control studies with unmeasured population structure. *Statistical Methods in Medical Research*, **2020**, 29, 3153-3165	2.3	
146	Genome-wide Enrichment of De Novo Coding Mutations in Orofacial Cleft Trios. *American Journal of Human Genetics*, **2020**, 107, 124-136	11	16

145	Association of HLA-DRB1*09:01 with tIgE levels among African-ancestry individuals with asthma. *Journal of Allergy and Clinical Immunology*, **2020**, 146, 147-155	11.5	6
144	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,	5.6	2
143	Machine Learning Characterization of COPD Subtypes: Insights From the COPDGene Study. *Chest*, **2020**, 157, 1147-1157	5.3	18
142	Mixed-model admixture mapping identifies smoking-dependent loci of lung function in African Americans. *European Journal of Human Genetics*, **2020**, 28, 656-668	5.3	3
141	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	6.3	8
140	Protective effect of club cell secretory protein (CC-16) on COPD risk and progression: a Mendelian randomisation study. *Thorax*, **2020**, 75, 934-943	7.3	7
139	Replicated methylation changes associated with eczema herpeticum and allergic response. *Clinical Epigenetics*, **2019**, 11, 122	7.7	11
138	The Evolving Field of Genetic Epidemiology: From Familial Aggregation to Genomic Sequencing. *American Journal of Epidemiology*, **2019**, 188, 2069-2077	3.8	3
137	A systematic genetic analysis and visualization of phenotypic heterogeneity among orofacial cleft GWAS signals. *Genetic Epidemiology*, **2019**, 43, 704-716	2.6	17
136	Predictors of dental care utilization in north-central Appalachia in the USA. *Community Dentistry and Oral Epidemiology*, **2019**, 47, 283-290	2.8	8
135	Exploring the interaction between FGF Genes and T-box genes among chinese nonsyndromic cleft lip with or without cleft palate case-parent trios. *Environmental and Molecular Mutagenesis*, **2019**, 60, 602-606	3.2	6
134	Genetic Advances in Chronic Obstructive Pulmonary Disease. Insights from COPDGene. *American Journal of Respiratory and Critical Care Medicine*, **2019**, 200, 677-690	10.2	31
133	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,	4.6	2
132	Assessing pleiotropy and mediation in genetic loci associated with chronic obstructive pulmonary disease. *Genetic Epidemiology*, **2019**, 43, 318-329	2.6	3
131	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. *Nature Genetics*, **2019**, 51, 481-493	36.3	156
130	Genetic landscape of chronic obstructive pulmonary disease identifies heterogeneous cell-type and phenotype associations. *Nature Genetics*, **2019**, 51, 494-505	36.3	119
129	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	4.9	7
128	Detection of de novo copy number deletions from targeted sequencing of trios. *Bioinformatics*, **2019**, 35, 571-578	7.2	1

127	Gene-gene interaction among cell adhesion genes and risk of nonsyndromic cleft lip with or without cleft palate in Chinese case-parent trios. *Molecular Genetics & Genomic Medicine*, **2019**, 7, e00872	2.3	4
126	DSP variants may be associated with longitudinal change in quantitative emphysema. *Respiratory Research*, **2019**, 20, 160	7.3	4
125	Analysis of genetically driven alternative splicing identifies FBXO38 as a novel COPD susceptibility gene. *PLoS Genetics*, **2019**, 15, e1008229	6	9
124	The pharmacogenomics of inhaled corticosteroids and lung function decline in COPD. *European Respiratory Journal*, **2019**, 54,	13.6	10
123	Subtypes of COPD Have Unique Distributions and Differential Risk of Mortality. *Chronic Obstructive Pulmonary Diseases (Miami, Fla)*, **2019**, 6, 400-413	2.7	13
122	Identifying Smoking-Related Disease on Lung Cancer Screening CT Scans: Increasing the Value. *Chronic Obstructive Pulmonary Diseases (Miami, Fla)*, **2019**, 6, 233-245	2.7	6
121	Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations. *Nature Communications*, **2019**, 10, 880	17.4	36
120	Assembly of a pan-genome from deep sequencing of 910 humans of African descent. *Nature Genetics*, **2019**, 51, 30-35	36.3	153
119	Inferring disease risk genes from sequencing data in multiplex pedigrees through sharing of rare variants. *Genetic Epidemiology*, **2019**, 43, 37-49	2.6	2
118	Genotype imputation performance of three reference panels using African ancestry individuals. *Human Genetics*, **2018**, 137, 281-292	6.3	23
117	Gene-gene interaction between MSX1 and TP63 in Asian case-parent trios with nonsyndromic cleft lip with or without cleft palate. *Birth Defects Research*, **2018**, 110, 317-324	2.9	5
116	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. *Nature Genetics*, **2018**, 50, 42-53	36.3	246
115	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	3.5	
114	Lobar Emphysema Distribution Is Associated With 5-Year Radiological Disease Progression. *Chest*, **2018**, 153, 65-76	5.3	23
113	Whole exome sequencing analysis in severe chronic obstructive pulmonary disease. *Human Molecular Genetics*, **2018**, 27, 3801-3812	5.6	19
112	The genetics of smoking in individuals with chronic obstructive pulmonary disease. *Respiratory Research*, **2018**, 19, 59	7.3	8
111	Integration of Molecular Interactome and Targeted Interaction Analysis to Identify a COPD Disease Network Module. *Scientific Reports*, **2018**, 8, 14439	4.9	21
110	Genomics and response to long-term oxygen therapy in chronic obstructive pulmonary disease. *Journal of Molecular Medicine*, **2018**, 96, 1375-1385	5.5	8

109	Childhood asthma is associated with COPD and known asthma variants in COPDGene: a genome-wide association study. *Respiratory Research*, **2018**, 19, 209	7.3	22
108	Optimized distributed systems achieve significant performance improvement on sorted merging of massive VCF files. *GigaScience*, **2018**, 7,	7.6	1
107	Whole-Genome Sequencing in Severe Chronic Obstructive Pulmonary Disease. *American Journal of Respiratory Cell and Molecular Biology*, **2018**, 59, 614-622	5.7	14
106	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	6.3	92
105	Association between dietary fat intake and insulin resistance in Chinese child twins. *British Journal of Nutrition*, **2017**, 117, 230-236	3.6	11
104	Genome-wide analyses of non-syndromic cleft lip with palate identify 14 novel loci and genetic heterogeneity. *Nature Communications*, **2017**, 8, 14364	17.4	131
103	Genetic loci associated with chronic obstructive pulmonary disease overlap with loci for lung function and pulmonary fibrosis. *Nature Genetics*, **2017**, 49, 426-432	36.3	201
102	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	36.3	170
101	The role of ST2 and ST2 genetic variants in schistosomiasis. *Journal of Allergy and Clinical Immunology*, **2017**, 140, 1416-1422.e6	11.5	10
100	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	5.7	37
99	Gene-based segregation method for identifying rare variants in family-based sequencing studies. *Genetic Epidemiology*, **2017**, 41, 309-319	2.6	11
98	Gene-gene interaction of single nucleotide polymorphisms in 16p13.3 may contribute to the risk of non-syndromic cleft lip with or without cleft palate in Chinese case-parent trios. *American Journal of Medical Genetics, Part A*, **2017**, 173, 1489-1494	2.5	4
97	Variable Susceptibility to Cigarette Smoke-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	5.7	13
96	Whole exome association of rare deletions in multiplex oral cleft families. *Genetic Epidemiology*, **2017**, 41, 61-69	2.6	8
95	Identifying tagging SNPs for African specific genetic variation from the African Diaspora Genome. *Scientific Reports*, **2017**, 7, 46398	4.9	17
94	Prevalence of Orofacial Clefts among Live Births in China: A Systematic Review and Meta-Analysis. *Birth Defects Research*, **2017**, 109, 1011-1019	2.9	18
93	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	4.7	39
92	Identification of common non-coding variants at 1p22 that are functional for non-syndromic orofacial clefting. *Nature Communications*, **2017**, 8, 14759	17.4	34

91	Evidence for SNP-SNP interaction identified through targeted sequencing of cleft case-parent trios. *Genetic Epidemiology*, **2017**, 41, 244-250	2.6	16
90	Analysis of sequence data to identify potential risk variants for oral clefts in multiplex families. *Molecular Genetics & Genomic Medicine*, **2017**, 5, 570-579	2.3	9
89	Identifying Genetic Sources of Phenotypic Heterogeneity in Orofacial Clefts by Targeted Sequencing. *Birth Defects Research*, **2017**, 109, 1030-1038	2.9	18
88	Surfactant protein D is a causal risk factor for COPD: results of Mendelian randomisation. *European Respiratory Journal*, **2017**, 50,	13.6	18
87	Identification of 16q21 as a modifier of nonsyndromic orofacial cleft phenotypes. *Genetic Epidemiology*, **2017**, 41, 887-897	2.6	10
86	Susceptibility to Childhood Pneumonia: A Genome-Wide Analysis. *American Journal of Respiratory Cell and Molecular Biology*, **2017**, 56, 20-28	5.7	17
85	Genome-Wide Association Study of the Genetic Determinants of Emphysema Distribution. *American Journal of Respiratory and Critical Care Medicine*, **2017**, 195, 757-771	10.2	33
84	Genome-Wide Association of Copy Number Polymorphisms and Kidney Function. *PLoS ONE*, **2017**, 12, e0170815	3.7	3
83	Methods to estimate underlying blood pressure: The Atherosclerosis Risk in Communities (ARIC) Study. *PLoS ONE*, **2017**, 12, e0179234	3.7	14
82	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	3.7	13
81	A continuum of admixture in the Western Hemisphere revealed by the African Diaspora genome. *Nature Communications*, **2016**, 7, 12522	17.4	90
80	Challenges and disparities in the application of personalized genomic medicine to populations with African ancestry. *Nature Communications*, **2016**, 7, 12521	17.4	45
79	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	10.2	37
78	Exome Sequencing Analysis in Severe, Early-Onset Chronic Obstructive Pulmonary Disease. *American Journal of Respiratory and Critical Care Medicine*, **2016**, 193, 1353-63	10.2	35
77	Common Genetic Polymorphisms Influence Blood Biomarker Measurements in COPD. *PLoS Genetics* , **2016**, 12, e1006011	6	64
76	Hemizygous Deletion on Chromosome 3p26.1 Is Associated with Heavy Smoking among African American Subjects in the COPDGene Study. *PLoS ONE*, **2016**, 11, e0164134	3.7	4
75	Genetic factors influencing risk to orofacial clefts: today's challenges and tomorrow's opportunities. *F1000Research*, **2016**, 5, 2800	3.6	103
74	Identifying a Deletion Affecting Total Lung Capacity Among Subjects in the COPDGene Study Cohort. *Genetic Epidemiology*, **2016**, 40, 81-8	2.6	4

73	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	11	106
72	Clinical and Radiologic Disease in Smokers With Normal Spirometry. *JAMA Internal Medicine*, **2015**, 175, 1539-49	11.5	243
71	Gene-Gene Interaction Among WNT Genes for Oral Cleft in Trios. *Genetic Epidemiology*, **2015**, 39, 385-94	2.6	22
70	A Genome-Wide Association Study of Emphysema and Airway Quantitative Imaging Phenotypes. *American Journal of Respiratory and Critical Care Medicine*, **2015**, 192, 559-69	10.2	103
69	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, 857-62		9
68	A genome-wide association study identifies risk loci for spirometric measures among smokers of European and African ancestry. *BMC Genetics*, **2015**, 16, 138	2.6	84
67	Genome-wide site-specific differential methylation in the blood of individuals with Klinefelter syndrome. *Molecular Reproduction and Development*, **2015**, 82, 377-86	2.6	16
66	Characterization of large structural genetic mosaicism in human autosomes. *American Journal of Human Genetics*, **2015**, 96, 487-97	11	77
65	A colorectal cancer prediction model using traditional and genetic risk scores in Koreans. *BMC Genetics*, **2015**, 16, 49	2.6	18
64	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	11.5	28
63	An IL-13 promoter polymorphism associated with liver fibrosis in patients with Schistosoma japonicum. *PLoS ONE*, **2015**, 10, e0135360	3.7	23
62	Inferring rare disease risk variants based on exact probabilities of sharing by multiple affected relatives. *Bioinformatics*, **2014**, 30, 2189-96	7.2	22
61	Epidemiology, genetics, and subtyping of preserved ratio impaired spirometry (PRISm) in COPDGene. *Respiratory Research*, **2014**, 15, 89	7.3	109
60	Oesophageal squamous cell carcinoma in high-risk Chinese populations: Possible role for vascular epithelial growth factor A. *European Journal of Cancer*, **2014**, 50, 2855-65	7.5	6
59	Whole exome sequencing of distant relatives in multiplex families implicates rare variants in candidate genes for oral clefts. *Genetics*, **2014**, 197, 1039-44	4	58
58	Risk loci for chronic obstructive pulmonary disease: a genome-wide association study and meta-analysis. *Lancet Respiratory Medicine,the*, **2014**, 2, 214-25	35.1	208
57	Evidence of gene-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	3.7	27
56	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	3.7	12

55	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, 408-18	10.2	77
54	Beyond GWAS in COPD: probing the landscape between gene-set associations, genome-wide associations and protein-protein interaction networks. *Human Heredity*, **2014**, 78, 131-9	1.1	15
53	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	10.2	62
52	Genome-wide interaction studies reveal sex-specific asthma risk alleles. *Human Molecular Genetics*, **2014**, 23, 5251-9	5.6	50
51	Detecting disease variants in case-parent trio studies using the bioconductor software package trio. *Genetic Epidemiology*, **2014**, 38, 516-22	2.6	16
50	The clinical and genetic features of COPD-asthma overlap syndrome. *European Respiratory Journal*, **2014**, 44, 341-50	13.6	205
49	Susceptibility to chronic mucus hypersecretion, a genome wide association study. *PLoS ONE*, **2014**, 9, e91621	3.7	19
48	Comorbidities of COPD have a major impact on clinical outcomes, particularly in African Americans. *Chronic Obstructive Pulmonary Diseases (Miami, Fla)*, **2014**, 1, 105-114	2.7	32
47	Dissecting direct and indirect genetic effects on chronic obstructive pulmonary disease (COPD) susceptibility. *Human Genetics*, **2013**, 132, 431-41	6.3	59
46	The FGF and FGFR Gene Family and Risk of Cleft Lip With or Without Cleft Palate. *Cleft Palate-Craniofacial Journal*, **2013**, 50, 96-103	1.9	29
45	Rapid testing of SNPs and gene-environment interactions in case-parent trio data based on exact analytic parameter estimation. *Biometrics*, **2012**, 68, 766-73	1.8	28
44	A genome-wide association study of COPD identifies a susceptibility locus on chromosome 19q13. *Human Molecular Genetics*, **2012**, 21, 947-57	5.6	181
43	Genome-wide meta-analyses of nonsyndromic cleft lip with or without cleft palate identify six new risk loci. *Nature Genetics*, **2012**, 44, 968-71	36.3	246
42	Incorporating genotype uncertainties into the genotypic TDT for main effects and gene-environment interactions. *Genetic Epidemiology*, **2012**, 36, 225-34	2.6	11
41	Examining markers in 8q24 to explain differences in evidence for association with cleft lip with/without cleft palate between Asians and Europeans. *Genetic Epidemiology*, **2012**, 36, 392-9	2.6	22
40	Evidence of gene-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		23
39	Pulmonary arterial enlargement and acute exacerbations of COPD. *New England Journal of Medicine*, **2012**, 367, 913-21	59.2	316
38	Meta-analysis of genome-wide association studies of asthma in ethnically diverse North American populations. *Nature Genetics*, **2011**, 43, 887-92	36.3	605

37	Cleft lip and palate: understanding genetic and environmental influences. *Nature Reviews Genetics*, **2011**, 12, 167-78	30.1	1042
36	Evidence for gene-environment interaction in a genome wide study of nonsyndromic cleft palate. *Genetic Epidemiology*, **2011**, 35, 469-78	2.6	115
35	Variants in FAM13A are associated with chronic obstructive pulmonary disease. *Nature Genetics*, **2010**, 42, 200-2	36.3	295
34	A genome-wide association study of cleft lip with and without cleft palate identifies risk variants near MAFB and ABCA4. *Nature Genetics*, **2010**, 42, 525-9	36.3	419
33	A genome-wide association study on African-ancestry populations for asthma. *Journal of Allergy and Clinical Immunology*, **2010**, 125, 336-346.e4	11.5	179
32	Genetic epidemiology of COPD (COPDGene) study design. *COPD: Journal of Chronic Obstructive Pulmonary Disease*, **2010**, 7, 32-43	2	749
31	Evidence of gene-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, 401-10	6.3	53
30	The Gene, Environment Association Studies consortium (GENEVA): maximizing the knowledge obtained from GWAS by collaboration across studies of multiple conditions. *Genetic Epidemiology*, **2010**, 34, 364-72	2.6	126
29	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, 161-73	11	178
28	A genome-wide scan for loci predisposing to non-syndromic cleft lip with or without cleft palate in two large Syrian families. *American Journal of Medical Genetics Part A*, **2003**, 123A, 140-7		38
27	"Power comparisons for genotypic vs. allelic TDT methods with >2 alleles". *Genetic Epidemiology*, **2002**, 23, 458-61; author reply 462-4	2.6	11
26	Multipoint linkage analysis under heterogeneity: incorporation of parametric and nonparametric approaches. *Genetic Epidemiology*, **2001**, 21 Suppl 1, S55-60	2.6	
25	Multipoint analysis using affected sib pairs: incorporating linkage evidence from unlinked regions. *Genetic Epidemiology*, **2001**, 21, 105-22	2.6	19
24	Interface of genetics and epidemiology. *Epidemiologic Reviews*, **2000**, 22, 120-5	4.1	22
23	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		41
22	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		4
21	Association between homeobox-containing gene MSX1 and the occurrence of limb deficiency **1998**, 75, 419-423		33
20	Survey of genetic counselors and clinical geneticists regarding recurrence risks for families with nonsyndromic cleft lip with or without cleft palate. *American Journal of Medical Genetics Part A*, **1998**, 79, 184-90		9

19	Application of transmission disequilibrium tests to nonsyndromic oral clefts: including candidate genes and environmental exposures in the models. *American Journal of Medical Genetics Part A*, **1997**, 73, 337-44		108
18	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*, **1997**, 99, 22-6	6.3	46
17	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	4.3	208
16	Phenotypic discordance in a family with monozygotic twins and non-syndromic cleft lip and palate. *American Journal of Medical Genetics Part A*, **1996**, 66, 468-70		7
15	Review of the role of potential teratogens in the origin of human nonsyndromic oral clefts. *Teratology*, **1996**, 53, 309-17		115
14	Review of the role of potential teratogens in the origin of human nonsyndromic oral clefts **1996**, 53, 309		5
13	Determining linkage and mode of inheritance: Mod scores and other methods **1996**, 13, 575		1
12	Risk of cancer in relatives of prostate cancer probands. *Journal of the National Cancer Institute*, **1995**, 87, 991-6	9.7	123
11	Comparative epidemiology of selected midline congenital abnormalities. *Genetic Epidemiology*, **1994**, 11, 141-54	2.6	27
10	Hereditary prostate cancer: epidemiologic and clinical features. *Journal of Urology*, **1993**, 150, 797-802	2.5	437
9	Segregation analysis of hypospadias: a reanalysis of published pedigree data. *American Journal of Medical Genetics Part A*, **1993**, 45, 420-5		10
8	Reply to Dr. Hook. *American Journal of Medical Genetics Part A*, **1993**, 47, 436-436		
7	Neuroanatomy of Rett syndrome: a volumetric imaging study. *Annals of Neurology*, **1993**, 34, 227-34	9.4	157
6	Genotype at a major locus with large effects on apolipoprotein B levels predicts familial combined hyperlipidemia. *Genetic Epidemiology*, **1993**, 10, 257-70	2.6	22
5	Genetics of total serum IgE levels: a regressive model approach to segregation analysis. *Genetic Epidemiology*, **1991**, 8, 351-9	2.6	36
4	Measuring familial aggregation by using odds-ratio regression models. *Genetic Epidemiology*, **1991**, 8, 361-70	2.6	45
3	Epidemiologic approaches to the use of DNA markers in the search for disease susceptibility genes. *Epidemiologic Reviews*, **1990**, 12, 41-55	4.1	17
2	Family history and the risk of prostate cancer. *Prostate*, **1990**, 17, 337-47	4.2	518

1	Predicting intrauterine growth retardation in sibships while considering maternal and infant covariates. *Genetic Epidemiology*, **1989**, 6, 525-35	2.6	5