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	Cleft lip and palate: understanding genetic and environmental influences. Nature Reviews Genetics, 2011, 12, 167-178.	16.3	1,435
2	Genetic Epidemiology of COPD (COPDGene) Study Design. COPD: Journal of Chronic Obstructive Pulmonary Disease, 2011, 7, 32-43.	1.6	1,007
3	Meta-analysis of genome-wide association studies of asthma in ethnically diverse North American populations. Nature Genetics, 2011, 43, 887-892.	21.4	736
4	Family history and the risk of prostate cancer. Prostate, 1990, 17, 337-347.	2.3	609
5	Hereditary Prostate Cancer: Epidemiologic and Clinical Features. Journal of Urology, 1993, 150, 797-802.	0.4	519
6	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
7	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	21.4	426
8	Pulmonary Arterial Enlargement and Acute Exacerbations of COPD. New England Journal of Medicine, 2012, 367, 913-921.	27.0	397
9	Clinical and Radiologic Disease in Smokers With Normal Spirometry. JAMA Internal Medicine, 2015, 175, 1539.	5.1	360
10	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
11	Variants in FAM13A are associated with chronic obstructive pulmonary disease. Nature Genetics, 2010, 42, 200-202.	21.4	348
12	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
13	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
14	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
15	Assembly of a pan-genome from deep sequencing of 910 humans of African descent. Nature Genetics, 2019, 51, 30-35.	21.4	276
16	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
17	Genetic landscape of chronic obstructive pulmonary disease identifies heterogeneous cell-type and phenotype associations. Nature Genetics, 2019, 51, 494-505.	21.4	257
18	The clinical and genetic features of COPD-asthma overlap syndrome. European Respiratory Journal, 2014, 44, 341-350.	6.7	249

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19	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
20	A genome-wide association study of COPD identifies a susceptibility locus on chromosome 19q13. Human Molecular Genetics, 2012, 21, 947-957.	2.9	216
21	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
22	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
23	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
24	Epidemiology, genetics, and subtyping of preserved ratio impaired spirometry (PRISm) in COPDGene. Respiratory Research, 2014, 15, 89.	3.6	196
25	Neuroanatomy of Rett syndrome: A volumetric imaging study. Annals of Neurology, 1993, 34, 227-234.	5.3	180
26	Genetic factors influencing risk to orofacial clefts: todayâ€™s challenges and tomorrowâ€™s opportunities. F1000Research, 2016, 5, 2800.	1.6	155
27	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
28	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
29	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
30	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
31	A continuum of admixture in the Western Hemisphere revealed by the African Diaspora genome. Nature Communications, 2016, 7, 12522.	12.8	136
32	Risk of Cancer in Relatives of Prostate Cancer Probands. Journal of the National Cancer Institute, 1995, 87, 991-996.	6.3	134
33	Review of the role of potential teratogens in the origin of human nonsyndromic oral clefts. Teratology, 1996, 53, 309-317.	1.6	131
34	Application of transmission disequilibrium tests to nonsyndromic oral clefts: Including candidate genes and environmental exposures in the models. , 1997, 73, 337-344.		129
35	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
36	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

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37	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	6.2	101
38	Common Genetic Polymorphisms Influence Blood Biomarker Measurements in COPD. PLoS Genetics, 2016, 12, e1006011.	3.5	88
39	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
40	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
41	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
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	Genome-wide interaction studies reveal sex-specific asthma risk alleles. Human Molecular Genetics, 2014, 23, 5251-5259.	2.9	70
44	Dissecting direct and indirect genetic effects on chronic obstructive pulmonary disease (COPD) susceptibility. Human Genetics, 2013, 132, 431-441.	3.8	69
45	Challenges and disparities in the application of personalized genomic medicine to populations with African ancestry. Nature Communications, 2016, 7, 12521.	12.8	68
46	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
47	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
48	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
49	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
50	Measuring familial aggregation by using odds-ratio regression models. Genetic Epidemiology, 1991, 8, 361-370.	1.3	55
51	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
52	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
53	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
54	Identification of common non-coding variants at 1p22 that are functional for non-syndromic orofacial clefting. Nature Communications, 2017, 8, 14759.	12.8	48

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55	Genome-wide Enrichment of De Novo Coding Mutations in Orofacial Cleft Trios. American Journal of Human Genetics, 2020, 107, 124-136.	6.2	48
56	Genetics of total serum IgE levels: A regressive model approach to segregation analysis. Genetic Epidemiology, 1991, 8, 351-359.	1.3	47
57	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
58	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
59	Surfactant protein D is a causal risk factor for COPD: results of Mendelian randomisation. European Respiratory Journal, 2017, 50, 1700657.	6.7	45
60	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
61	Machine Learning Characterization of COPD Subtypes. Chest, 2020, 157, 1147-1157.	0.8	44
62	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
63	Identifying Genetic Sources of Phenotypic Heterogeneity in Orofacial Clefts by Targeted Sequencing. Birth Defects Research, 2017, 109, 1030-1038.	1.5	41
64	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
65	Integration of Molecular Interactome and Targeted Interaction Analysis to Identify a COPD Disease Network Module. Scientific Reports, 2018, 8, 14439.	3.3	40
66	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
67	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
68	Association between homeobox-containing geneMSX1 and the occurrence of limb deficiency. , 1998, 75, 419-423.		38
69	Genotype imputation performance of three reference panels using African ancestry individuals. Human Genetics, 2018, 137, 281-292.	3.8	38
70	Lobar Emphysema Distribution Is Associated With 5-Year Radiological Disease Progression. Chest, 2018, 153, 65-76.	0.8	36
71	A systematic genetic analysis and visualization of phenotypic heterogeneity among orofacial cleft GWAS signals. Genetic Epidemiology, 2019, 43, 704-716.	1.3	36
72	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

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73	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
74	Comparative epidemiology of selected midline congenital abnormalities. Genetic Epidemiology, 1994, 11, 141-154.	1.3	32
75	Whole exome sequencing analysis in severe chronic obstructive pulmonary disease. Human Molecular Genetics, 2018, 27, 3801-3812.	2.9	32
76	Inferring rare disease risk variants based on exact probabilities of sharing by multiple affected relatives. Bioinformatics, 2014, 30, 2189-2196.	4.1	30
77	Geneâ€Gene Interaction Among WNT Genes for Oral Cleft in Trios. Genetic Epidemiology, 2015, 39, 385-394.	1.3	30
78	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
79	An IL-13 Promoter Polymorphism Associated with Liver Fibrosis in Patients with Schistosoma japonicum. PLoS ONE, 2015, 10, e0135360.	2.5	29
80	Interface of Genetics and Epidemiology. Epidemiologic Reviews, 2000, 22, 120-125.	3.5	28
81	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
82	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
83	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
84	A colorectal cancer prediction model using traditional and genetic risk scores in Koreans. BMC Genetics, 2015, 16, 49.	2.7	26
85	Identifying tagging SNPs for African specific genetic variation from the African Diaspora Genome. Scientific Reports, 2017, 7, 46398.	3.3	26
86	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
87	Methods to estimate underlying blood pressure: The Atherosclerosis Risk in Communities (ARIC) Study. PLoS ONE, 2017, 12, e0179234.	2.5	26
88	Susceptibility to Chronic Mucus Hypersecretion, a Genome Wide Association Study. PLoS ONE, 2014, 9, e91621.	2.5	25
89	Evidence for SNP-SNP interaction identified through targeted sequencing of cleft case-parent trios. Genetic Epidemiology, 2017, 41, 244-250.	1.3	24
90	Identification of 16q21 as a modifier of nonsyndromic orofacial cleft phenotypes. Genetic Epidemiology, 2017, 41, 887-897.	1.3	24

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91	Susceptibility to Childhood Pneumonia: A Genome-Wide Analysis. American Journal of Respiratory Cell and Molecular Biology, 2017, 56, 20-28.	2.9	24
92	Subtypes of COPD Have Unique Distributions and Differential Risk of Mortality. Chronic Obstructive Pulmonary Diseases (Miami, Fla), 2019, 6, 400-413.	0.7	24
93	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
94	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
95	Whole-Genome Sequencing in Severe Chronic Obstructive Pulmonary Disease. American Journal of Respiratory Cell and Molecular Biology, 2018, 59, 614-622.	2.9	22
96	Replicated methylation changes associated with eczema herpeticum and allergic response. Clinical Epigenetics, 2019, 11, 122.	4.1	22
97	Interaction of Cigarette Smoking and Polygenic Risk Score on Reduced Lung Function. JAMA Network Open, 2021, 4, e2139525.	5.9	22
98	Multipoint analysis using affected sib pairs: Incorporating linkage evidence from unlinked regions. Genetic Epidemiology, 2001, 21, 105-122.	1.3	21
99	Genome-Wide Gene-by-Smoking Interaction Study of Chronic Obstructive Pulmonary Disease. American Journal of Epidemiology, 2021, 190, 875-885.	3.4	21
100	EPIDEMIOLOGIC APPROACHES TO THE USE OF DNA MARKERS IN THE SEARCH FOR DISEASE SUSCEPTIBILITY GENES. Epidemiologic Reviews, 1990, 12, 41-55.	3.5	19
101	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
102	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
103	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
104	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
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	Genomics and response to long-term oxygen therapy in chronic obstructive pulmonary disease. Journal of Molecular Medicine, 2018, 96, 1375-1385.	3.9	17
107	Analysis of genetically driven alternative splicing identifies FBXO38 as a novel COPD susceptibility gene. PLoS Genetics, 2019, 15, e1008229.	3.5	17
108	Predictors of dental care utilization in northâ€central Appalachia in the USA. Community Dentistry and Oral Epidemiology, 2019, 47, 283-290.	1.9	17

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109	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
110	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
111	â€œPower comparisons for genotypic vs. allelic TDT methods with >2 Allelesâ€• Genetic Epidemiology, 2002, 23, 458-461.	1.3	15
112	Association between dietary fat intake and insulin resistance in Chinese child twins. British Journal of Nutrition, 2017, 117, 230-236.	2.3	15
113	The role of ST2 and ST2 genetic variants in schistosomiasis. Journal of Allergy and Clinical Immunology, 2017, 140, 1416-1422.e6.	2.9	15
114	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
115	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
116	Geneâ€‐based segregation method for identifying rare variants in familyâ€‐based sequencing studies. Genetic Epidemiology, 2017, 41, 309-319.	1.3	14
117	The pharmacogenomics of inhaled corticosteroids and lung function decline in COPD. European Respiratory Journal, 2019, 54, 1900521.	6.7	14
118	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
119	FAT4 identified as a potential modifier of orofacial cleft laterality. Genetic Epidemiology, 2021, 45, 721-735.	1.3	14
120	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
121	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
122	Incorporating Genotype Uncertainties Into the Genotypic TDT for Main Effects and Geneâ€‐Environment Interactions. Genetic Epidemiology, 2012, 36, 225-234.	1.3	13
123	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
124	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
125	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
126	Segregation analysis of hypospadias: A reanalysis of published pedigree data. American Journal of Medical Genetics Part A, 1993, 45, 420-425.	2.4	11

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127	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
128	The genetics of smoking in individuals with chronic obstructive pulmonary disease. Respiratory Research, 2018, 19, 59.	3.6	11
129	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
130	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
131	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
132	Whole exome association of rare deletions in multiplex oral cleft families. Genetic Epidemiology, 2017, 41, 61-69.	1.3	10
133	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
134	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
135	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
136	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
137	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
138	Phenotypic discordance in a family with monozygotic twins and non-syndromic cleft lip and palate. , 1996, 66, 468-470.		7
139	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
140	DSP variants may be associated with longitudinal change in quantitative emphysema. Respiratory Research, 2019, 20, 160.	3.6	7
141	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
142	Lung tissue shows divergent gene expression between chronic obstructive pulmonary disease and idiopathic pulmonary fibrosis. Respiratory Research, 2022, 23, 97.	3.6	7
143	The Evolving Field of Genetic Epidemiology: From Familial Aggregation to Genomic Sequencing. American Journal of Epidemiology, 2019, 188, 2069-2077.	3.4	6
144	Inferring disease risk genes from sequencing data in multiplex pedigrees through sharing of rare variants. Genetic Epidemiology, 2019, 43, 37-49.	1.3	6

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145	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
146	Predicting intrauterine growth reterdation in sibships while considering maternal and infant covariates. Genetic Epidemiology, 1989, 6, 525-535.	1.3	5
147	Identifying a Deletion Affecting Total Lung Capacity Among Subjects in the COPDGene Study Cohort. Genetic Epidemiology, 2016, 40, 81-88.	1.3	5
148	Assessing pleiotropy and mediation in genetic loci associated with chronic obstructive pulmonary disease. Genetic Epidemiology, 2019, 43, 318-329.	1.3	5
149	Review of the role of potential teratogens in the origin of human nonsyndromic oral clefts. Teratology, 1996, 53, 309-317.	1.6	5
150	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
151	Optimized distributed systems achieve significant performance improvement on sorted merging of massive VCF files. GigaScience, 2018, 7, .	6.4	4
152	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
153	Mild association between the A/G polymorphism in the promoter of the apolipoprotein Aâ€‰gene and apolipoprotein Aâ€‰levels: A metaâ€analysis. American Journal of Medical Genetics Part A, 1999, 82, 235-241.	2.4	4
154	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
155	Genome-Wide Association of Copy Number Polymorphisms and Kidney Function. PLoS ONE, 2017, 12, e0170815.	2.5	3
156	Detection of de novo copy number deletions from targeted sequencing of trios. Bioinformatics, 2019, 35, 571-578.	4.1	2
157	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
158	Benchmarking statistical methods for analyzing parentâ€“child dyads in genetic association studies. Genetic Epidemiology, 2022, 46, 266-284.	1.3	2
159	Determining linkage and mode of inheritance: Mod scores and other methods. Genetic Epidemiology, 1996, 13, 575-593.	1.3	1
160	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
161	Reply to Dr. Hook. American Journal of Medical Genetics Part A, 1993, 47, 436-436.	2.4	0
162	Multipoint Linkage Analysis Under Heterogeneity: Incorporation of Parametric and Nonparametric Approaches. Genetic Epidemiology, 2001, 21, S55-60.	1.3	0

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163	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
164	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
165	Identifying Genetic Sources of Phenotypic Heterogeneity in Orofacial Clefts by Targeted Sequencing. Birth Defects Research, 2017, , .	1.5	0