## Dawn L Demeo

# List of Publications by Year in Descending Order

Source: https://exaly.com/author-pdf/2228380/dawn-l-demeo-publications-by-year.pdf

Version: 2024-04-10

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

168<br/>papers9,447<br/>citations51<br/>h-index94<br/>g-index183<br/>ext. papers12,425<br/>ext. citations8.9<br/>avg, IF5.54<br/>L-index

#	Paper	IF	Citations
168	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed <i>Cell Genomics</i> , <b>2022</b> , 2, 100084-100084		1
167	Optimism is associated with respiratory symptoms and functional status in chronic obstructive pulmonary disease <i>Respiratory Research</i> , <b>2022</b> , 23, 19	7.3	О
166	gpuZoo: Cost-effective estimation of gene regulatory networks using the Graphics Processing Unit <i>NAR Genomics and Bioinformatics</i> , <b>2022</b> , 4, lqac002	3.7	O
165	COPD Genetics <b>2022</b> , 503-514		
164	Protein interaction networks provide insight into fetal origins of chronic obstructive pulmonary disease <i>Respiratory Research</i> , <b>2022</b> , 23, 69	7.3	O
163	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential <i>Science Advances</i> , <b>2022</b> , 8, eabl6579	14.3	3
162	Lung tissue shows divergent gene expression between chronic obstructive pulmonary disease and idiopathic pulmonary fibrosis <i>Respiratory Research</i> , <b>2022</b> , 23, 97	7.3	O
161	Pathogenesis of chronic obstructive pulmonary disease: understanding the contributions of gene-environment interactions across the lifespan <i>Lancet Respiratory Medicine, the</i> , <b>2022</b> ,	35.1	7
160	Sex-Specific Differences in MicroRNA Expression During Human Fetal Lung Development <i>Frontiers in Genetics</i> , <b>2022</b> , 13, 762834	4.5	
159	Covariate adjustment of spirometric and smoking phenotypes: The potential of neural network models <i>PLoS ONE</i> , <b>2022</b> , 17, e0266752	3.7	
158	Constructing gene regulatory networks using epigenetic data. <i>Npj Systems Biology and Applications</i> , <b>2021</b> , 7, 45	5	3
157	DNA methylation architecture of the ACE2 gene in nasal cells of children. <i>Scientific Reports</i> , <b>2021</b> , 11, 7107	4.9	12
156	Metabolomic Profiling Reveals Sex Specific Associations with Chronic Obstructive Pulmonary Disease and Emphysema. <i>Metabolites</i> , <b>2021</b> , 11,	5.6	6
155	Soluble receptor for advanced glycation end products (sRAGE) as a biomarker of COPD. <i>Respiratory Research</i> , <b>2021</b> , 22, 127	7.3	7
154	Genome-wide association analysis of COVID-19 mortality risk in SARS-CoV-2 genomes identifies mutation in the SARS-CoV-2 spike protein that colocalizes with P.1 of the Brazilian strain. <i>Genetic Epidemiology</i> , <b>2021</b> , 45, 685-693	2.6	2
153	Secondary polycythemia in chronic obstructive pulmonary disease: prevalence and risk factors. <i>BMC Pulmonary Medicine</i> , <b>2021</b> , 21, 235	3.5	3
152	Sex and Gender Omic Biomarkers in Men and Women With COPD: Considerations for Precision Medicine. <i>Chest</i> , <b>2021</b> , 160, 104-113	5.3	4

## (2020-2021)

151	Epigenetics and pulmonary diseases in the horizon of precision medicine: a review. <i>European Respiratory Journal</i> , <b>2021</b> , 57,	13.6	7
150	Sex-specific associations with DNA methylation in lung tissue demonstrate smoking interactions. <i>Epigenetics</i> , <b>2021</b> , 16, 692-703	5.7	6
149	Network Medicine and Systems Biology Considerations to Understand Sex Differences in Lung Disease. <i>Physiology in Health and Disease</i> , <b>2021</b> , 345-363	0.2	
148	DNA methylation perturbations may link altered development and aging in the lung. <i>Aging</i> , <b>2021</b> , 13, 1742-1764	5.6	3
147	Maternal anxiety during pregnancy and newborn epigenome-wide DNA methylation. <i>Molecular Psychiatry</i> , <b>2021</b> , 26, 1832-1845	15.1	6
146	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. <i>Nature</i> , <b>2021</b> , 590, 290-299	50.4	268
145	Residential PM exposure and the nasal methylome in children. <i>Environment International</i> , <b>2021</b> , 153, 106505	12.9	3
144	Genetic variation in genes regulating skeletal muscle regeneration and tissue remodelling associated with weight loss in chronic obstructive pulmonary disease. <i>Journal of Cachexia, Sarcopenia and Muscle</i> , <b>2021</b> ,	10.3	1
143	Longitudinal change in blood DNA epigenetic signature after smoking cessation. <i>Epigenetics</i> , <b>2021</b> , 1-12	<del>2</del> 5.7	O
142	Significant Spirometric Transitions and Preserved Ratio Impaired Spirometry Among Ever Smokers. <i>Chest</i> , <b>2021</b> ,	5.3	2
141	Molecular markers of aging, exercise capacity, & physical activity in COPD. <i>Respiratory Medicine</i> , <b>2021</b> , 187, 106576	4.6	O
140	Co-methylation analysis in lung tissue identifies pathways for fetal origins of COPD. <i>European Respiratory Journal</i> , <b>2020</b> , 56,	13.6	10
139	Sex Differences in Gene Expression and Regulatory Networks across 29 Human Tissues. <i>Cell Reports</i> , <b>2020</b> , 31, 107795	10.6	67
138	A gene-diet interaction-based score predicts response to dietary fat in the Women's Health Initiative. <i>American Journal of Clinical Nutrition</i> , <b>2020</b> , 111, 893-902	7	2
137	Identification of Novel Alzheimer's Disease Loci Using Sex-Specific Family-Based Association Analysis of Whole-Genome Sequence Data. <i>Scientific Reports</i> , <b>2020</b> , 10, 5029	4.9	16
136	Epigenome-wide meta-analysis of blood DNA methylation in newborns and children identifies numerous loci related to gestational age. <i>Genome Medicine</i> , <b>2020</b> , 12, 25	14.4	37
135	Epigenome-wide association study reveals a molecular signature of response to phylloquinone (vitamin K1) supplementation. <i>Epigenetics</i> , <b>2020</b> , 15, 859-870	5.7	6
134	DNA Methylation Is Predictive of Mortality in Current and Former Smokers. <i>American Journal of Respiratory and Critical Care Medicine</i> , <b>2020</b> , 201, 1099-1109	10.2	6

133	The Association of Multiparity with Lung Function and Chronic Obstructive Pulmonary Disease-Related Phenotypes. <i>Chronic Obstructive Pulmonary Diseases (Miami, Fla )</i> , <b>2020</b> , 7, 86-98	2.7	3
132	A Risk Prediction Model for Mortality Among Smokers in the COPDGene Study. <i>Chronic Obstructive Pulmonary Diseases (Miami, Fla)</i> , <b>2020</b> , 7, 346-361	2.7	3
131	DNA Methylation Architecture of the ACE2 gene in Nasal Cells <b>2020</b> ,		3
130	Factors influencing decline in quality of life in smokers without airflow obstruction: The COPDGene study. <i>Respiratory Medicine</i> , <b>2020</b> , 161, 105820	4.6	3
129	Association of Neutrophil to Lymphocyte Ratio With Pulmonary Function in a 30-Year Longitudinal Study of US Veterans. <i>JAMA Network Open</i> , <b>2020</b> , 3, e2010350	10.4	9
128	Genome-Wide Sex and Gender Differences in Cancer. Frontiers in Oncology, 2020, 10, 597788	5.3	16
127	Chronic obstructive pulmonary disease and related phenotypes: polygenic risk scores in population-based and case-control cohorts. <i>Lancet Respiratory Medicine, the</i> , <b>2020</b> , 8, 696-708	35.1	29
126	Somatotypes trajectories during adulthood and their association with COPD phenotypes. <i>ERJ Open Research</i> , <b>2020</b> , 6,	3.5	3
125	Sex and gender: modifiers of health, disease, and medicine. Lancet, The, 2020, 396, 565-582	40	347
124	Maternal Gestational Diabetes Mellitus and Newborn DNA Methylation: Findings From the Pregnancy and Childhood Epigenetics Consortium. <i>Diabetes Care</i> , <b>2020</b> , 43, 98-105	14.6	45
123	Optimism is not associated with two indicators of DNA methylation aging. <i>Aging</i> , <b>2019</b> , 11, 4970-4989	5.6	5
122	Socioeconomic status and DNA methylation from birth through mid-childhood: a prospective study in Project Viva. <i>Epigenomics</i> , <b>2019</b> , 11, 1413-1427	4.4	8
121	Hypertensive Disorders of Pregnancy and DNA Methylation in Newborns. <i>Hypertension</i> , <b>2019</b> , 74, 375-3	<b>83</b> .5	40
120	Prenatal Particulate Air Pollution and DNA Methylation in Newborns: An Epigenome-Wide Meta-Analysis. <i>Environmental Health Perspectives</i> , <b>2019</b> , 127, 57012	8.4	58
119	DNA methylation is associated with inhaled corticosteroid response in persistent childhood asthmatics. <i>Clinical and Experimental Allergy</i> , <b>2019</b> , 49, 1225-1234	4.1	9
118	Meta-analysis of epigenome-wide association studies in neonates reveals widespread differential DNA methylation associated with birthweight. <i>Nature Communications</i> , <b>2019</b> , 10, 1893	17.4	79
117	Epigenome-wide association study reveals methylation pathways associated with childhood allergic sensitization. <i>Epigenetics</i> , <b>2019</b> , 14, 445-466	5.7	28
116	Genetic Advances in Chronic Obstructive Pulmonary Disease. Insights from COPDGene. <i>American Journal of Respiratory and Critical Care Medicine</i> , <b>2019</b> , 200, 677-690	10.2	31

115	Epigenetic age acceleration is associated with allergy and asthma in children in Project Viva. <i>Journal of Allergy and Clinical Immunology</i> , <b>2019</b> , 143, 2263-2270.e14	11.5	25
114	Prenatal maternal antidepressants, anxiety, and depression and offspring DNA methylation: epigenome-wide associations at birth and persistence into early childhood. <i>Clinical Epigenetics</i> , <b>2019</b> , 11, 56	7.7	26
113	RNA-sequencing across three matched tissues reveals shared and tissue-specific gene expression and pathway signatures of COPD. <i>Respiratory Research</i> , <b>2019</b> , 20, 65	7.3	20
112	Newborn DNA-methylation, childhood lung function, and the risks of asthma and COPD across the life course. <i>European Respiratory Journal</i> , <b>2019</b> , 53,	13.6	32
111	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. <i>Nature Genetics</i> , <b>2019</b> , 51, 481-493	36.3	156
110	Genetic landscape of chronic obstructive pulmonary disease identifies heterogeneous cell-type and phenotype associations. <i>Nature Genetics</i> , <b>2019</b> , 51, 494-505	36.3	119
109	Common and Rare Variants Genetic Association Analysis of Cigarettes per Day Among Ever-Smokers in Chronic Obstructive Pulmonary Disease Cases and Controls. <i>Nicotine and Tobacco Research</i> , <b>2019</b> , 21, 714-722	4.9	7
108	The nasal methylome as a biomarker of asthma and airway inflammation in children. <i>Nature Communications</i> , <b>2019</b> , 10, 3095	17.4	72
107	Clinical Epidemiology of COPD: Insights From 10 Years of the COPDGene Study. <i>Chest</i> , <b>2019</b> , 156, 228-2	. <b>35</b> 3	29
106	DNA methylation modules associate with incident cardiovascular disease and cumulative risk factor exposure. <i>Clinical Epigenetics</i> , <b>2019</b> , 11, 142	7.7	20
105	COPDGene 2019: Redefining the Diagnosis of Chronic Obstructive Pulmonary Disease. <i>Chronic Obstructive Pulmonary Diseases (Miami, Fla)</i> , <b>2019</b> , 6, 384-399	2.7	61
104	Maternal corticotropin-releasing hormone is associated with LEP DNA methylation at birth and in childhood: an epigenome-wide study in Project Viva. <i>International Journal of Obesity</i> , <b>2019</b> , 43, 1244-12	5§·5	4
103	Smoking duration alone provides stronger risk estimates of chronic obstructive pulmonary disease than pack-years. <i>Thorax</i> , <b>2018</b> , 73, 414-421	7.3	60
102	Human Lung DNA Methylation Quantitative Trait Loci Colocalize with Chronic Obstructive Pulmonary Disease Genome-Wide Association Loci. <i>American Journal of Respiratory and Critical Care Medicine</i> , <b>2018</b> , 197, 1275-1284	10.2	29
101	Epigenome-wide association study of total serum immunoglobulin E in children: a life course approach. <i>Clinical Epigenetics</i> , <b>2018</b> , 10, 55	7.7	24
100	Lobar Emphysema Distribution Is Associated With 5-Year Radiological Disease Progression. <i>Chest</i> , <b>2018</b> , 153, 65-76	5.3	23
99	Folic Acid in Pregnancy and Childhood Asthma: A US Cohort. Clinical Pediatrics, 2018, 57, 421-427	1.2	13
98	Ensemble genomic analysis in human lung tissue identifies novel genes for chronic obstructive pulmonary disease. <i>Human Genomics</i> , <b>2018</b> , 12, 1	6.8	20

97	Female Sex and Gender in Lung/Sleep Health and Disease. Increased Understanding of Basic Biological, Pathophysiological, and Behavioral Mechanisms Leading to Better Health for Female Patients with Lung Disease. <i>American Journal of Respiratory and Critical Care Medicine</i> , <b>2018</b> , 198, 850-8	10.2 358	44
96	Detecting Differentially Variable MicroRNAs via Model-Based Clustering. <i>International Journal of Genomics</i> , <b>2018</b> , 2018, 6591634	2.5	
95	Longitudinal Phenotypes and Mortality in Preserved Ratio Impaired Spirometry in the COPDGene Study. <i>American Journal of Respiratory and Critical Care Medicine</i> , <b>2018</b> , 198, 1397-1405	10.2	59
94	Maternal alcohol consumption and offspring DNA methylation: findings from six general population-based birth cohorts. <i>Epigenomics</i> , <b>2018</b> , 10, 27-42	4.4	43
93	DNA methylation in blood as a mediator of the association of mid-childhood body mass index with cardio-metabolic risk score in early adolescence. <i>Epigenetics</i> , <b>2018</b> , 13, 1072-1087	5.7	14
92	Association of low income with pulmonary disease progression in smokers with and without chronic obstructive pulmonary disease. <i>ERJ Open Research</i> , <b>2018</b> , 4,	3.5	6
91	Gene Regulatory Network Analysis Identifies Sex-Linked Differences in Colon Cancer Drug Metabolism. <i>Cancer Research</i> , <b>2018</b> , 78, 5538-5547	10.1	41
90	Residential Proximity to Major Roadways at Birth, DNA Methylation at Birth and Midchildhood, and Childhood Cognitive Test Scores: Project Viva(Massachusetts, USA). <i>Environmental Health Perspectives</i> , <b>2018</b> , 126, 97006	8.4	8
89	Women manifest more severe COPD symptoms across the life course. <i>International Journal of COPD</i> , <b>2018</b> , 13, 3021-3029	3	33
88	Metabolomic profiling in a Hedgehog Interacting Protein (Hhip) murine model of chronic obstructive pulmonary disease. <i>Scientific Reports</i> , <b>2017</b> , 7, 2504	4.9	11
87	Persistent DNA methylation changes associated with prenatal mercury exposure and cognitive performance during childhood. <i>Scientific Reports</i> , <b>2017</b> , 7, 288	4.9	71
86	Functional interactors of three genome-wide association study genes are differentially expressed in severe chronic obstructive pulmonary disease lung tissue. <i>Scientific Reports</i> , <b>2017</b> , 7, 44232	4.9	57
85	Optimism and Cause-Specific Mortality: A Prospective Cohort Study. <i>American Journal of Epidemiology</i> , <b>2017</b> , 185, 21-29	3.8	98
84	The value of blood cytokines and chemokines in assessing COPD. Respiratory Research, 2017, 18, 180	7.3	62
83	Exposure to Low Levels of Lead and Umbilical Cord Blood DNA Methylation in Project Viva: An Epigenome-Wide Association Study. <i>Environmental Health Perspectives</i> , <b>2017</b> , 125, 087019	8.4	46
82	Prenatal Exposure to Mercury: Associations with Global DNA Methylation and Hydroxymethylation in Cord Blood and in Childhood. <i>Environmental Health Perspectives</i> , <b>2017</b> , 125, 087022	8.4	43
81	Electronic Cigarette Use in US Adults at Risk for or with COPD: Analysis from Two Observational Cohorts. <i>Journal of General Internal Medicine</i> , <b>2017</b> , 32, 1315-1322	4	48
80	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

## (2015-2017)

79	Examining the Effects of Age on Health Outcomes of Chronic Obstructive Pulmonary Disease: Results From the Genetic Epidemiology of Chronic Obstructive Pulmonary Disease Study and Evaluation of Chronic Obstructive Pulmonary Disease Longitudinally to Identify Predictive Surrogate Endpoints Cohorts. Journal of the American Medical Directors Association, 2017, 18, 1063-1068	5.9	5
78	Regulatory network changes between cell lines and their tissues of origin. <i>BMC Genomics</i> , <b>2017</b> , 18, 723		28
77	Reduced microRNA-503 expression augments lung fibroblast VEGF production in chronic obstructive pulmonary disease. <i>PLoS ONE</i> , <b>2017</b> , 12, e0184039	3.7	15
76	DNA methylation profiling in human lung tissue identifies genes associated with COPD. <i>Epigenetics</i> , <b>2016</b> , 11, 730-739	5.7	48
75	A whole-blood transcriptome meta-analysis identifies gene expression signatures of cigarette smoking. <i>Human Molecular Genetics</i> , <b>2016</b> , 25, 4611-4623	5.6	58
74	Epigenetic Signatures of Cigarette Smoking. <i>Circulation: Cardiovascular Genetics</i> , <b>2016</b> , 9, 436-447		442
73	Mitochondrial iron chelation ameliorates cigarette smoke-induced bronchitis and emphysema in mice. <i>Nature Medicine</i> , <b>2016</b> , 22, 163-74	50.5	136
72	Sex-specific features of emphysema among current and former smokers with COPD. <i>European Respiratory Journal</i> , <b>2016</b> , 47, 104-12	13.6	37
71	Bipartite Community Structure of eQTLs. PLoS Computational Biology, 2016, 12, e1005033	5	28
70	Common Genetic Polymorphisms Influence Blood Biomarker Measurements in COPD. <i>PLoS Genetics</i> , <b>2016</b> , 12, e1006011	6	64
69	Birth weight-for-gestational age is associated with DNA methylation at birth and in childhood. <i>Clinical Epigenetics</i> , <b>2016</b> , 8, 118	7.7	43
68	Differential DNA methylation marks and gene comethylation of COPD in African-Americans with COPD exacerbations. <i>Respiratory Research</i> , <b>2016</b> , 17, 143	7.3	42
67	DNA Methylation in Newborns and Maternal Smoking in Pregnancy: Genome-wide Consortium Meta-analysis. <i>American Journal of Human Genetics</i> , <b>2016</b> , 98, 680-96	11	489
66	Clinical and Radiologic Disease in Smokers With Normal Spirometry. <i>JAMA Internal Medicine</i> , <b>2015</b> , 175, 1539-49	11.5	243
65	A genome-wide association study identifies risk loci for spirometric measures among smokers of European and African ancestry. <i>BMC Genetics</i> , <b>2015</b> , 16, 138	2.6	84
64	Genome-wide site-specific differential methylation in the blood of individuals with Klinefelter syndrome. <i>Molecular Reproduction and Development</i> , <b>2015</b> , 82, 377-86	2.6	16
63	The impact of genetic variation and cigarette smoke on DNA methylation in current and former smokers from the COPDGene study. <i>Epigenetics</i> , <b>2015</b> , 10, 1064-73	5.7	24
62	Smoking-Associated Site-Specific Differential Methylation in Buccal Mucosa in the COPDGene Study. <i>American Journal of Respiratory Cell and Molecular Biology</i> , <b>2015</b> , 53, 246-54	5.7	41

61	Characterising the association of latency with (1)-antitrypsin polymerisation using a novel monoclonal antibody. <i>International Journal of Biochemistry and Cell Biology</i> , <b>2015</b> , 58, 81-91	5.6	22
60	A Comparative Study of Tests for Homogeneity of Variances with Application to DNA Methylation Data. <i>PLoS ONE</i> , <b>2015</b> , 10, e0145295	3.7	11
59	Phenotypic and genetic heterogeneity among subjects with mild airflow obstruction in COPDGene. <i>Respiratory Medicine</i> , <b>2014</b> , 108, 1469-80	4.6	22
58	Risk loci for chronic obstructive pulmonary disease: a genome-wide association study and meta-analysis. <i>Lancet Respiratory Medicine,the</i> , <b>2014</b> , 2, 214-25	35.1	208
57	Prediction of acute respiratory disease in current and former smokers with and without COPD. <i>Chest</i> , <b>2014</b> , 146, 941-950	5.3	61
56	A simplified score to quantify comorbidity in COPD. <i>PLoS ONE</i> , <b>2014</b> , 9, e114438	3.7	44
55	Sexually-dimorphic targeting of functionally-related genes in COPD. <i>BMC Systems Biology</i> , <b>2014</b> , 8, 118	3.5	38
54	Fetal lung and placental methylation is associated with in utero nicotine exposure. <i>Epigenetics</i> , <b>2014</b> , 9, 1473-84	5.7	72
53	Circulating polymers in 🛘 -antitrypsin deficiency. European Respiratory Journal, 2014, 43, 1501-4	13.6	50
52	Interstitial pneumonitis and the risk of chronic allograft rejection in lung transplant recipients. <i>Chest</i> , <b>2013</b> , 143, 1430-1435	5.3	2
51	Association of IREB2 and CHRNA3 polymorphisms with airflow obstruction in severe alpha-1 antitrypsin deficiency. <i>Respiratory Research</i> , <b>2012</b> , 13, 16	7.3	39
50	Association of cigarette smoking and CRP levels with DNA methylation in El antitrypsin deficiency. <i>Epigenetics</i> , <b>2012</b> , 7, 720-8	5.7	19
49	A genome-wide association study of COPD identifies a susceptibility locus on chromosome 19q13. Human Molecular Genetics, <b>2012</b> , 21, 947-57	5.6	181
48	Cigarette smoking behaviors and time since quitting are associated with differential DNA methylation across the human genome. <i>Human Molecular Genetics</i> , <b>2012</b> , 21, 3073-82	5.6	228
47	Variable DNA methylation is associated with chronic obstructive pulmonary disease and lung function. <i>American Journal of Respiratory and Critical Care Medicine</i> , <b>2012</b> , 185, 373-81	10.2	163
46	Gene-environment interaction testing in family-based association studies with phenotypically ascertained samples: a causal inference approach. <i>Biostatistics</i> , <b>2012</b> , 13, 468-81	3.7	3
45	Alu and LINE-1 methylation and lung function in the normative ageing study. BMJ Open, 2012, 2,	3	30
44	Systemic steroid exposure is associated with differential methylation in chronic obstructive pulmonary disease. <i>American Journal of Respiratory and Critical Care Medicine</i> , <b>2012</b> , 186, 1248-55	10.2	52

43	Racial differences in quality of life in patients with COPD. <i>Chest</i> , <b>2011</b> , 140, 1169-1176	5.3	42
42	Combining disease models to test for gene-environment interaction in nuclear families. <i>Biometrics</i> , <b>2011</b> , 67, 1260-70	1.8	4
41	Early-onset chronic obstructive pulmonary disease is associated with female sex, maternal factors, and African American race in the COPDGene Study. <i>American Journal of Respiratory and Critical Care Medicine</i> , <b>2011</b> , 184, 414-20	10.2	135
40	Genome-wide association analysis of body mass in chronic obstructive pulmonary disease. <i>American Journal of Respiratory Cell and Molecular Biology</i> , <b>2011</b> , 45, 304-10	5.7	43
39	Association of SERPINE2 with asthma. <i>Chest</i> , <b>2011</b> , 140, 667-674	5.3	14
38	Polymorphisms in surfactant protein-D are associated with chronic obstructive pulmonary disease. <i>American Journal of Respiratory Cell and Molecular Biology</i> , <b>2011</b> , 44, 316-22	5.7	61
37	Opportunities and challenges in the genetics of COPD 2010: an International COPD Genetics Conference report. <i>COPD: Journal of Chronic Obstructive Pulmonary Disease</i> , <b>2011</b> , 8, 121-35	2	38
36	Variants in FAM13A are associated with chronic obstructive pulmonary disease. <i>Nature Genetics</i> , <b>2010</b> , 42, 200-2	36.3	295
35	Multistudy fine mapping of chromosome 2q identifies XRCC5 as a chronic obstructive pulmonary disease susceptibility gene. <i>American Journal of Respiratory and Critical Care Medicine</i> , <b>2010</b> , 182, 605-1	3 <sup>10.2</sup>	28
34	Gender differences in COPD: are women more susceptible to smoking effects than men?. <i>Thorax</i> , <b>2010</b> , 65, 480-5	7.3	192
33	MMP12, lung function, and COPD in high-risk populations. <i>New England Journal of Medicine</i> , <b>2009</b> , 361, 2599-608	59.2	257
32	Molecular biomarkers for quantitative and discrete COPD phenotypes. <i>American Journal of Respiratory Cell and Molecular Biology</i> , <b>2009</b> , 40, 359-67	5.7	84
31	Integration of genomic and genetic approaches implicates IREB2 as a COPD susceptibility gene. <i>American Journal of Human Genetics</i> , <b>2009</b> , 85, 493-502	11	118
30	Genetic association analysis of COPD candidate genes with bronchodilator responsiveness. <i>Respiratory Medicine</i> , <b>2009</b> , 103, 552-7	4.6	31
29	IL10 polymorphisms are associated with airflow obstruction in severe alpha1-antitrypsin deficiency. <i>American Journal of Respiratory Cell and Molecular Biology</i> , <b>2008</b> , 38, 114-20	5.7	63
28	National Emphysema Treatment Trial state of the art: genetics of emphysema. <i>Proceedings of the American Thoracic Society</i> , <b>2008</b> , 5, 486-93		24
27	Testing and estimating gene-environment interactions in family-based association studies. <i>Biometrics</i> , <b>2008</b> , 64, 458-67	1.8	34
26	Xenobiotic metabolizing enzyme gene polymorphisms predict response to lung volume reduction surgery. <i>Respiratory Research</i> , <b>2007</b> , 8, 59	7.3	14

25	Polymorphisms in IL13, total IgE, eosinophilia, and asthma exacerbations in childhood. <i>Journal of Allergy and Clinical Immunology</i> , <b>2007</b> , 120, 84-90	11.5	93
24	Determinants of airflow obstruction in severe alpha-1-antitrypsin deficiency. <i>Thorax</i> , <b>2007</b> , 62, 806-13	7.3	78
23	Genetic determinants of emphysema distribution in the national emphysema treatment trial. <i>American Journal of Respiratory and Critical Care Medicine</i> , <b>2007</b> , 176, 42-8	10.2	116
22	The Yin and Yang of COPD: sex/gender differences in the National Emphysema Treatment Trial. <i>American Journal of Respiratory and Critical Care Medicine</i> , <b>2007</b> , 176, 222-3	10.2	5
21	The SERPINE2 gene is associated with chronic obstructive pulmonary disease. <i>Proceedings of the American Thoracic Society</i> , <b>2006</b> , 3, 502		14
20	Genetic association analysis of functional impairment in chronic obstructive pulmonary disease. <i>American Journal of Respiratory and Critical Care Medicine</i> , <b>2006</b> , 173, 977-84	10.2	100
19	Transmission of lymphocytic choriomeningitis virus by organ transplantation. <i>New England Journal of Medicine</i> , <b>2006</b> , 354, 2235-49	59.2	418
18	Genetic linkage and association analysis of COPD-related traits on chromosome 8p. <i>COPD: Journal of Chronic Obstructive Pulmonary Disease</i> , <b>2006</b> , 3, 189-94	2	28
17	The SERPINE2 gene is associated with chronic obstructive pulmonary disease. <i>American Journal of Human Genetics</i> , <b>2006</b> , 78, 253-64	11	143
16	Reply to Chappell et al American Journal of Human Genetics, 2006, 79, 186-187	11	12
16 15	Reply to Chappell et al <i>American Journal of Human Genetics</i> , <b>2006</b> , 79, 186-187  Genomic screening and replication using the same data set in family-based association testing. <i>Nature Genetics</i> , <b>2005</b> , 37, 683-91	36.3	12
	Genomic screening and replication using the same data set in family-based association testing.		
15	Genomic screening and replication using the same data set in family-based association testing.  Nature Genetics, 2005, 37, 683-91  Concordance of genotypes in pre- and post-lung transplantation DNA samples. American Journal of	36.3	
15 14	Genomic screening and replication using the same data set in family-based association testing.  Nature Genetics, 2005, 37, 683-91  Concordance of genotypes in pre- and post-lung transplantation DNA samples. American Journal of Respiratory Cell and Molecular Biology, 2005, 33, 402-5  Attempted replication of reported chronic obstructive pulmonary disease candidate gene	36.3 5·7	160
15 14 13	Genomic screening and replication using the same data set in family-based association testing. Nature Genetics, 2005, 37, 683-91  Concordance of genotypes in pre- and post-lung transplantation DNA samples. American Journal of Respiratory Cell and Molecular Biology, 2005, 33, 402-5  Attempted replication of reported chronic obstructive pulmonary disease candidate gene associations. American Journal of Respiratory Cell and Molecular Biology, 2005, 33, 71-8  Genome-wide linkage of forced mid-expiratory flow in chronic obstructive pulmonary disease.	36.3 5.7 5.7	160 155
15 14 13	Genomic screening and replication using the same data set in family-based association testing.  Nature Genetics, 2005, 37, 683-91  Concordance of genotypes in pre- and post-lung transplantation DNA samples. American Journal of Respiratory Cell and Molecular Biology, 2005, 33, 402-5  Attempted replication of reported chronic obstructive pulmonary disease candidate gene associations. American Journal of Respiratory Cell and Molecular Biology, 2005, 33, 71-8  Genome-wide linkage of forced mid-expiratory flow in chronic obstructive pulmonary disease.  American Journal of Respiratory and Critical Care Medicine, 2004, 170, 1294-301  Ambient air pollution and oxygen saturation. American Journal of Respiratory and Critical Care	36.3 5.7 5.7	160 155 54
15 14 13 12	Genomic screening and replication using the same data set in family-based association testing.  Nature Genetics, 2005, 37, 683-91  Concordance of genotypes in pre- and post-lung transplantation DNA samples. American Journal of Respiratory Cell and Molecular Biology, 2005, 33, 402-5  Attempted replication of reported chronic obstructive pulmonary disease candidate gene associations. American Journal of Respiratory Cell and Molecular Biology, 2005, 33, 71-8  Genome-wide linkage of forced mid-expiratory flow in chronic obstructive pulmonary disease.  American Journal of Respiratory and Critical Care Medicine, 2004, 170, 1294-301  Ambient air pollution and oxygen saturation. American Journal of Respiratory and Critical Care Medicine, 2004, 170, 383-7  The transforming growth factor-beta1 (TGFB1) gene is associated with chronic obstructive	36·3 5·7 5·7 10·2	160 155 54 49

#### LIST OF PUBLICATIONS

7	Genetics of chronic obstructive pulmonary disease. <i>Seminars in Respiratory and Critical Care Medicine</i> , <b>2003</b> , 24, 151-60	3.9	21	
6	A new powerful non-parametric two-stage approach for testing multiple phenotypes in family-based association studies. <i>Human Heredity</i> , <b>2003</b> , 56, 10-7	1.1	51	
5	Using the noninformative families in family-based association tests: a powerful new testing strategy. <i>American Journal of Human Genetics</i> , <b>2003</b> , 73, 801-11	11	77	
4	Power and design considerations for a general class of family-based association tests: quantitative traits. <i>American Journal of Human Genetics</i> , <b>2002</b> , 71, 1330-41	11	124	
3	Lung transplantation at the turn of the century. Annual Review of Medicine, 2001, 52, 185-201	17.4	33	
2	Integrative genomics analysis identifies ACVR1B as a candidate causal gene of emphysema distribution in non-alpha 1-antitrypsin deficient smokers		1	
1	gpuZoo: Cost-effective estimation of gene regulatory networks using the Graphics Processing Unit		1	