Martin D Tobin

List of Publications by Citations

183 papers	27,398 citations	64 h-index	165 g-index
218 ext. papers	32,386 ext. citations	13.8 avg, IF	7.38 L-index

#	Paper	IF	Citations
183	Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. *Nature*, **2007**, 447, 661-78	50.4	7801
182	Genomewide association analysis of coronary artery disease. *New England Journal of Medicine*, **2007** , 357, 443-53	59.2	1608
181	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. *Nature* , **2011**, 478, 103-9	50.4	1564
180	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. *Nature Genetics*, **2007**, 39, 1329-37	36.3	1130
179	Genome-wide association study identifies eight loci associated with blood pressure. *Nature Genetics*, **2009**, 41, 666-76	36.3	970
178	Genome-wide association study identifies 74 loci associated with educational attainment. *Nature*, **2016**, 533, 539-42	50.4	850
177	The UK10K project identifies rare variants in health and disease. *Nature*, **2015**, 526, 82-90	50.4	776
176	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. *Nature*, **2010**, 464, 713-20	50.4	639
175	Identification of seven loci affecting mean telomere length and their association with disease. *Nature Genetics*, **2013**, 45, 422-7, 427e1-2	36.3	624
174	Adjusting for treatment effects in studies of quantitative traits: antihypertensive therapy and systolic blood pressure. *Statistics in Medicine*, **2005**, 24, 2911-35	2.3	464
173	Genome-wide association study identifies five loci associated with lung function. *Nature Genetics*, **2010**, 42, 36-44	36.3	430
172	Localization of type 1 diabetes susceptibility to the MHC class I genes HLA-B and HLA-A. *Nature*, **2007**, 450, 887-92	50.4	421
171	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. *Nature Genetics*, **2018**, 50, 1412-1425	36.3	386
170	Genome-wide association study identifies genes for biomarkers of cardiovascular disease: serum urate and dyslipidemia. *American Journal of Human Genetics*, **2008**, 82, 139-49	11	361
169	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. *Nature Genetics*, **2011**, 43, 1005-11	36.3	338
168	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. *Nature Genetics*, **2017**, 49, 403-415	36.3	313
167	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. *Nature Genetics*, **2011**, 43, 1082-90	36.3	313

166	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. *Nature Genetics*, **2019**, 51, 245-257	36.3	259
165	Common variants near TERC are associated with mean telomere length. *Nature Genetics*, **2010**, 42, 197-9	36.3	255
164	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. *Nature Genetics*, **2016**, 48, 1171-1184	36.3	251
163	Large-scale association analysis identifies new lung cancer susceptibility loci and heterogeneity in genetic susceptibility across histological subtypes. *Nature Genetics*, **2017**, 49, 1126-1132	36.3	246
162	Novel insights into the genetics of smoking behaviour, lung function, and chronic obstructive pulmonary disease (UK BiLEVE): a genetic association study in UK Biobank. *Lancet Respiratory Medicine,the*, **2015**, 3, 769-81	35.1	245
161	The impact of low-frequency and rare variants on lipid levels. *Nature Genetics*, **2015**, 47, 589-97	36.3	229
160	Mendelian randomisation and causal inference in observational epidemiology. *PLoS Medicine*, **2008**, 5, e177	11.6	219
159	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
158	Key concepts in genetic epidemiology. *Lancet, The*, **2005**, 366, 941-51	40	185
157	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. *Nature Genetics*, **2016**, 48, 1151-1161	36.3	181
156	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
155	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
154	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. *Human Molecular Genetics*, **2011**, 20, 2273-84	5.6	146
153	The role of adiposity in cardiometabolic traits: a Mendelian randomization analysis. *PLoS Medicine*, **2013**, 10, e1001474	11.6	144
152	Genomic copy number variation, human health, and disease. *Lancet, The*, **2009**, 374, 340-50	40	143
151	Genetic variants associated with susceptibility to idiopathic pulmonary fibrosis in people of European ancestry: a genome-wide association study. *Lancet Respiratory Medicine,the*, **2017**, 5, 869-880	35.1	142
150	Genome-wide association study to identify genetic determinants of severe asthma. *Thorax*, **2012**, 67, 762-8	7.3	139
149	Blood pressure loci identified with a gene-centric array. *American Journal of Human Genetics*, **2011**, 89, 688-700	11	137

148	Gene-centric meta-analysis in 87,736 individuals of European ancestry identifies multiple blood-pressure-related loci. *American Journal of Human Genetics*, **2014**, 94, 349-60	11	131
147	Genome-wide association studies identify CHRNA5/3 and HTR4 in the development of airflow obstruction. *American Journal of Respiratory and Critical Care Medicine*, **2012**, 186, 622-32	10.2	131
146	Haplotype estimation for biobank-scale data sets. *Nature Genetics*, **2016**, 48, 817-20	36.3	121
145	Genetic landscape of chronic obstructive pulmonary disease identifies heterogeneous cell-type and phenotype associations. *Nature Genetics*, **2019**, 51, 494-505	36.3	119
144	Effect of five genetic variants associated with lung function on the risk of chronic obstructive lung disease, and their joint effects on lung function. *American Journal of Respiratory and Critical Care Medicine*, **2011**, 184, 786-95	10.2	112
143	Genotypes and haplotypes predisposing to myocardial infarction: a multilocus case-control study. *European Heart Journal*, **2004**, 25, 459-67	9.5	110
142	Moderate-to-severe asthma in individuals of European ancestry: a genome-wide association study. *Lancet Respiratory Medicine,the*, **2019**, 7, 20-34	35.1	109
141	Genome-wide joint meta-analysis of SNP and SNP-by-smoking interaction identifies novel loci for pulmonary function. *PLoS Genetics*, **2012**, 8, e1003098	6	108
140	Beyond "misunderstanding": written information and decisions about taking part in a genetic epidemiology study. *Social Science and Medicine*, **2007**, 65, 2212-22	5.1	108
139	Association of WNK1 gene polymorphisms and haplotypes with ambulatory blood pressure in the general population. *Circulation*, **2005**, 112, 3423-9	16.7	105
138	Genome-wide association analysis identifies six new loci associated with forced vital capacity. *Nature Genetics*, **2014**, 46, 669-77	36.3	104
137	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. *American Journal of Human Genetics*, **2011**, 88, 6-18	11	103
136	DataSHIELD: resolving a conflict in contemporary bioscience--performing a pooled analysis of individual-level data without sharing the data. *International Journal of Epidemiology*, **2010**, 39, 1372-82	7.8	102
135	Adiposity as a cause of cardiovascular disease: a Mendelian randomization study. *International Journal of Epidemiology*, **2015**, 44, 578-86	7.8	97
134	Common variants in genes underlying monogenic hypertension and hypotension and blood pressure in the general population. *Hypertension*, **2008**, 51, 1658-64	8.5	95
133	Secretory phospholipase A(2)-IIA and cardiovascular disease: a mendelian randomization study. *Journal of the American College of Cardiology*, **2013**, 62, 1966-1976	15.1	91
132	Genetic variants linked to education predict longevity. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 13366-13371	11.5	90
131	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. *Hypertension*, **2017**,	8.5	85

130	Genome-Wide Association Study of Susceptibility to Idiopathic Pulmonary Fibrosis. *American Journal of Respiratory and Critical Care Medicine*, **2020**, 201, 564-574	10.2	81
129	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. *Nature Communications*, **2017**, 8, 16015	17.4	80
128	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. *Nature Communications*, **2015**, 6, 8658	17.4	79
127	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. *American Journal of Human Genetics*, **2012**, 90, 1116-1117	11	78
126	Coronary artery disease-associated locus on chromosome 9p21 and early markers of atherosclerosis. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2008**, 28, 1679-83	9.4	77
125	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. *American Journal of Human Genetics*, **2017**, 100, 865-884	11	74
124	Gene-centric meta-analyses of 108 912 individuals confirm known body mass index loci and reveal three novel signals. *Human Molecular Genetics*, **2013**, 22, 184-201	5.6	73
123	Heritability of early repolarization: a population-based study. *Circulation: Cardiovascular Genetics*, **2011**, 4, 134-8		72
122	The novel genetic variant predisposing to coronary artery disease in the region of the PSRC1 and CELSR2 genes on chromosome 1 associates with serum cholesterol. *Journal of Molecular Medicine*, **2008**, 86, 1233-41	5.5	69
121	Dense genotyping of candidate gene loci identifies variants associated with high-density lipoprotein cholesterol. *Circulation: Cardiovascular Genetics*, **2011**, 4, 145-55		66
120	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. *Journal of the American Heart Association*, **2017**, 6,	6	65
119	Meta-analysis of genetic studies using Mendelian randomization--a multivariate approach. *Statistics in Medicine*, **2005**, 24, 2241-54	2.3	61
118	Adjusting for bias and unmeasured confounding in Mendelian randomization studies with binary responses. *International Journal of Epidemiology*, **2008**, 37, 1161-8	7.8	60
117	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. *PLoS Genetics*, **2015**, 11, e1005230	6	59
116	Genetic architecture of ambulatory blood pressure in the general population: insights from cardiovascular gene-centric array. *Hypertension*, **2010**, 56, 1069-76	8.5	59
115	An integrated approach to the meta-analysis of genetic association studies using Mendelian randomization. *American Journal of Epidemiology*, **2004**, 160, 445-52	3.8	59
114	Molecular mechanisms underlying variations in lung function: a systems genetics analysis. *Lancet Respiratory Medicine,the*, **2015**, 3, 782-95	35.1	52
113	Effects of long-term averaging of quantitative blood pressure traits on the detection of genetic associations. *American Journal of Human Genetics*, **2014**, 95, 49-65	11	52

112	Age- and sex-specific causal effects of adiposity on cardiovascular risk factors. *Diabetes*, **2015**, 64, 1841-52	8.9	50
111	Common genetic variation near the phospholamban gene is associated with cardiac repolarisation: meta-analysis of three genome-wide association studies. *PLoS ONE*, **2009**, 4, e6138	3.7	50
110	Gender and effects of a common genetic variant in the NOS1 regulator NOS1AP on cardiac repolarization in 3761 individuals from two independent populations. *International Journal of Epidemiology*, **2008**, 37, 1132-41	7.8	47
109	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. *Molecular Psychiatry*, **2020**, 25, 2392-2409	15.1	45
108	Large-scale genome-wide association studies and meta-analyses of longitudinal change in adult lung function. *PLoS ONE*, **2014**, 9, e100776	3.7	42
107	Pedigree and genotyping quality analyses of over 10,000 DNA samples from the Generation Scotland: Scottish Family Health Study. *BMC Medical Genetics*, **2013**, 14, 38	2.1	41
106	A comprehensive evaluation of potential lung function associated genes in the SpiroMeta general population sample. *PLoS ONE*, **2011**, 6, e19382	3.7	41
105	A large genome scan for rare CNVs in amyotrophic lateral sclerosis. *Human Molecular Genetics*, **2010**, 19, 4091-9	5.6	40
104	Teaching and learning about human sexuality in undergraduate medical education. *Medical Education*, **2002**, 36, 432-40	3.7	40
103	Detection of mutations in KLHL3 and CUL3 in families with FHHt (familial hyperkalaemic hypertension or Gordon's syndrome). *Clinical Science*, **2014**, 126, 721-6	6.5	38
102	Opportunities and challenges in the genetics of COPD 2010: an International COPD Genetics Conference report. *COPD: Journal of Chronic Obstructive Pulmonary Disease*, **2011**, 8, 121-35	2	38
101	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. *Nature Communications*, **2017**, 8, 744	17.4	37
100	Causal and synthetic associations of variants in the SERPINA gene cluster with alpha1-antitrypsin serum levels. *PLoS Genetics*, **2013**, 9, e1003585	6	37
99	The role of copy number variation in susceptibility to amyotrophic lateral sclerosis: genome-wide association study and comparison with published loci. *PLoS ONE*, **2009**, 4, e8175	3.7	37
98	GSTCD and INTS12 regulation and expression in the human lung. *PLoS ONE*, **2013**, 8, e74630	3.7	37
97	Ethnic differences in SARS-CoV-2 vaccine hesitancy in United Kingdom healthcare workers: Results from the UK-REACH prospective nationwide cohort study. *Lancet Regional Health - Europe, The*, **2021**, 9, 100180		37
96	Formalising recall by genotype as an efficient approach to detailed phenotyping and causal inference. *Nature Communications*, **2018**, 9, 711	17.4	35
95	Phenotypic and pharmacogenetic evaluation of patients with thiazide-induced hyponatremia. *Journal of Clinical Investigation*, **2017**, 127, 3367-3374	15.9	35

94	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and Alcohol Use. *Biological Psychiatry*, **2019**, 85, 946-955	7.9	35
93	Commentary: development of Mendelian randomization: from hypothesis test to Mendelian deconfounding*International Journal of Epidemiology*, **2004**, 33, 26-9	7.8	33
92	International Genome-Wide Association Study Consortium Identifies Novel Loci Associated With Blood Pressure in Children and Adolescents. *Circulation: Cardiovascular Genetics*, **2016**, 9, 266-278		32
91	Large-scale candidate gene analysis of HDL particle features. *PLoS ONE*, **2011**, 6, e14529	3.7	31
90	Common variation in the WNK1 gene and blood pressure in childhood: the Avon Longitudinal Study of Parents and Children. *Hypertension*, **2008**, 52, 974-9	8.5	31
89	Common genetic determinants of lung function, subclinical atherosclerosis and risk of coronary artery disease. *PLoS ONE*, **2014**, 9, e104082	3.7	30
88	Identification of susceptibility pathways for the role of chromosome 15q25.1 in modifying lung cancer risk. *Nature Communications*, **2018**, 9, 3221	17.4	29
87	APOM and high-density lipoprotein cholesterol are associated with lung function and per cent emphysema. *European Respiratory Journal*, **2014**, 43, 1003-17	13.6	29
86	Longitudinal data analysis in pedigree studies. *Genetic Epidemiology*, **2003**, 25 Suppl 1, S18-28	2.6	29
85	Chronic obstructive pulmonary disease and related phenotypes: polygenic risk scores in population-based and case-control cohorts. *Lancet Respiratory Medicine,the*, **2020**, 8, 696-708	35.1	29
84	A Genome-Wide Association Study in Hispanics/Latinos Identifies Novel Signals for Lung Function. The Hispanic Community Health Study/Study of Latinos. *American Journal of Respiratory and Critical Care Medicine*, **2018**, 198, 208-219	10.2	27
83	The sputum microbiome is distinct between COPD and health, independent of smoking history. *Respiratory Research*, **2020**, 21, 183	7.3	26
82	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. *Nature Genetics*, **2020**, 52, 1314-1332	36.3	26
81	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. *International Journal of Epidemiology*, **2017**, 46, 894-904	7.8	25
80	Age at menarche and lung function: a Mendelian randomization study. *European Journal of Epidemiology*, **2017**, 32, 701-710	12.1	25
79	Epigenome-wide association study of lung function level and its change. *European Respiratory Journal*, **2019**, 54,	13.6	25
78	Whole exome re-sequencing implicates CCDC38 and cilia structure and function in resistance to smoking related airflow obstruction. *PLoS Genetics*, **2014**, 10, e1004314	6	24
77	Mechanical Ventilation. *American Journal of Respiratory and Critical Care Medicine*, **2017**, 196, P3-P4	10.2	23

76	Covariance components models for longitudinal family data. *International Journal of Epidemiology*, **2005**, 34, 1063-77; discussion 1077-9	7.8	23
75	Gene-centric meta-analyses for central adiposity traits in up to 57 412 individuals of European descent confirm known loci and reveal several novel associations. *Human Molecular Genetics*, **2014**, 23, 2498-510	5.6	22
74	Four genetic loci influencing electrocardiographic indices of left ventricular hypertrophy. *Circulation: Cardiovascular Genetics*, **2011**, 4, 626-35		22
73	Genetic variants affecting cross-sectional lung function in adults show little or no effect on longitudinal lung function decline. *Thorax*, **2017**, 72, 400-408	7.3	20
72	Integrative pathway genomics of lung function and airflow obstruction. *Human Molecular Genetics*, **2015**, 24, 6836-48	5.6	20
71	Tumour necrosis factor gene complex polymorphisms in chronic obstructive pulmonary disease. *Respiratory Medicine*, **2007**, 101, 340-4	4.6	20
70	Genetic and clinical characteristics of treatment-resistant depression using primary care records in two UK cohorts. *Molecular Psychiatry*, **2021**, 26, 3363-3373	15.1	20
69	Exome-wide analysis of rare coding variation identifies novel associations with COPD and airflow limitation in MOCS3, IFIT3 and SERPINA12. *Thorax*, **2016**, 71, 501-9	7.3	18
68	Discovery of novel heart rate-associated loci using the Exome Chip. *Human Molecular Genetics*, **2017** , 26, 2346-2363	5.6	17
67	Bi-allelic Loss-of-Function CACNA1B Mutations in Progressive Epilepsy-Dyskinesia. *American Journal of Human Genetics*, **2019**, 104, 948-956	11	17
66	Leukotriene B4 production in healthy subjects carrying variants of the arachidonate 5-lipoxygenase-activating protein gene associated with a risk of myocardial infarction. *Clinical Science*, **2007**, 112, 411-6	6.5	16
65	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*, **2018**, 3, 4	4.8	16
64	Blood eosinophil count and airway epithelial transcriptome relationships in COPD versus asthma. *Allergy: European Journal of Allergy and Clinical Immunology*, **2020**, 75, 370-380	9.3	16
63	A Method to Exploit the Structure of Genetic Ancestry Space to Enhance Case-Control Studies. *American Journal of Human Genetics*, **2016**, 98, 857-868	11	14
62	Analysis with the exome array identifies multiple new independent variants in lipid loci. *Human Molecular Genetics*, **2016**, 25, 4094-4106	5.6	14
61	ExomeChip-Wide Analysis of 95 626 Individuals Identifies 10 Novel Loci Associated With QT and JT Intervals. *Circulation Genomic and Precision Medicine*, **2018**, 11, e001758	5.2	14
60	Understanding the impact of pre-analytic variation in haematological and clinical chemistry analytes on the power of association studies. *International Journal of Epidemiology*, **2014**, 43, 1633-44	7.8	13
59	Smoking, DNA Methylation, and Lung Function: a Mendelian Randomization Analysis to Investigate Causal Pathways. *American Journal of Human Genetics*, **2020**, 106, 315-326	11	12

58	Genome-wide association studies in lung disease. *Thorax*, **2012**, 67, 271-3, 280	7.3	12
57	Integration of genetics into a systems model of electrocardiographic traits using HumanCVD BeadChip. *Circulation: Cardiovascular Genetics*, **2012**, 5, 630-8		12
56	Phenotypic and functional translation of IL1RL1 locus polymorphisms in lung tissue and asthmatic airway epithelium. *JCI Insight*, **2020**, 5,	9.9	11
55	Bed occupancy rates and hospital-acquired Clostridium difficile infection: a cohort study. *Infection Control and Hospital Epidemiology*, **2013**, 34, 1062-9	2	10
54	Copy number variation of the beta-defensin genes in europeans: no supporting evidence for association with lung function, chronic obstructive pulmonary disease or asthma. *PLoS ONE*, **2014**, 9, e84192	3.7	10
53	Phenotypic and functional translation of IL33 genetics in asthma. *Journal of Allergy and Clinical Immunology*, **2021**, 147, 144-157	11.5	10
52	South Asian ethnicity and risk of childhood accidents: an ecological study at enumeration district level in Leicester. *Journal of Public Health*, **2002**, 24, 313-8	3.5	9
51	Resistome analyses of sputum from COPD and healthy subjects reveals bacterial load-related prevalence of target genes. *Thorax*, **2020**, 75, 8-16	7.3	9
50	Genome-Wide Gene-by-Smoking Interaction Study of Chronic Obstructive Pulmonary Disease. *American Journal of Epidemiology*, **2021**, 190, 875-885	3.8	9
49	The vitamin D binding protein axis modifies disease severity in lymphangioleiomyomatosis. *European Respiratory Journal*, **2018**, 52,	13.6	8
48	Seeking consent to tissue banking: a survey of health professionals in childhood cancer. *European Journal of Cancer Care*, **2009**, 18, 391-400	2.4	8
47	Meta-analysis of Mendelian randomization studies incorporating all three genotypes. *Statistics in Medicine*, **2008**, 27, 6570-82	2.3	8
46	Longitudinal variance components models for systolic blood pressure, fitted using Gibbs sampling. *BMC Genetics*, **2003**, 4 Suppl 1, S25	2.6	8
45	The United Kingdom Research study into Ethnicity And COVID-19 outcomes in Healthcare workers (UK-REACH): protocol for a prospective longitudinal cohort study of healthcare and ancillary workers in UK healthcare settings. *BMJ Open*, **2021**, 11, e050647	3	8
44	Identifying potential causal effects of age at menarche: a Mendelian randomization phenome-wide association study. *BMC Medicine*, **2020**, 18, 71	11.4	7
43	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals.. *Nature Genetics*, **2022**,	36.3	7
42	Determinants of day-night difference in blood pressure, a comparison with determinants of daytime and night-time blood pressure. *Journal of Human Hypertension*, **2017**, 31, 43-48	2.6	6
41	What can genetics tell us about the cause of fixed airflow obstruction?. *Clinical and Experimental Allergy*, **2012**, 42, 1176-82	4.1	6

40	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*,3, 4	4.8	6
39	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. *Nature Communications*, **2020**, 11, 5182	17.4	6
38	/ ratio: the mismeasure of oxygenation in COVID-19. *European Respiratory Journal*, **2021**, 57,	13.6	6
37	Healthcare workersQviews on mandatory SARS-CoV-2 vaccination in the UK: A cross-sectional, mixed-methods analysis from the UK-REACH study.. *EClinicalMedicine*, **2022**, 101346	11.3	6
36	Targeted Sequencing of Lung Function Loci in Chronic Obstructive Pulmonary Disease Cases and Controls. *PLoS ONE*, **2017**, 12, e0170222	3.7	5
35	New genetic signals for lung function highlight pathways and pleiotropy, and chronic obstructive pulmonary disease associations across multiple ancestries		5
34	High-Throughput Sequencing in Respiratory, Critical Care, and Sleep Medicine Research. An Official American Thoracic Society Workshop Report. *Annals of the American Thoracic Society*, **2019**, 16, 1-16	4.7	5
33	Persistent hesitancy for SARS-CoV-2 vaccines among healthcare workers in the United Kingdom: analysis of longitudinal data from the UK-REACH cohort study.. *Lancet Regional Health - Europe, The* , **2022**, 13, 100299		4
32	Genetic analysis of over one million people identifies 535 novel loci for blood pressure		4
31	Ethnic differences in SARS-CoV-2 vaccine hesitancy in United Kingdom healthcare workers: Results from the UK-REACH prospective nationwide cohort study		4
30	Access to personal protective equipment in healthcare workers during the COVID-19 pandemic in the United Kingdom: results from a nationwide cohort study (UK-REACH)		4
29	Cohort Profile: Extended Cohort for E-health, Environment and DNA (EXCEED). *International Journal of Epidemiology*, **2019**, 48, 678-679j	7.8	3
28	Allelic variant of NOS1AP effects on cardiac alternans of repolarization during exercise testing. *Scandinavian Journal of Clinical and Laboratory Investigation*, **2012**, 72, 100-7	2	3
27	Public health professionalsQperceptions toward provision of health protection in England: a survey of expectations of Primary Care Trusts and Health Protection Units in the delivery of health protection. *BMC Public Health*, **2006**, 6, 297	4.1	3
26	Copy number variation. *Methods in Molecular Biology*, **2011**, 713, 167-83	1.4	3
25	Genetic and clinical characteristics of treatment-resistant depression using primary care records in two UK cohorts		3
24	Pleiotropic associations of heterozygosity for the Z allele in the UK Biobank. *ERJ Open Research*, **2021**, 7,	3.5	3
23	United Kingdom Research study into Ethnicity And COVID-19 outcomes in Healthcare workers (UK-REACH): a retrospective cohort study using linked routinely collected data, study protocol. *BMJ Open*, **2021**, 11, e046392	3	3

22	Human copy number variation, gene expression, and the role of the CCL3L1-CCR5 axis in lung function. *Wellcome Open Research*, **2018**, 3, 13	4.8	3
21	Interaction of Cigarette Smoking and Polygenic Risk Score on Reduced Lung Function.. *JAMA Network Open*, **2021**, 4, e2139525	10.4	3
20	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
19	SARS-CoV-2 susceptibility and COVID-19 disease severity are associated with genetic variants affecting gene expression in a variety of tissues. *Cell Reports*, **2021**, 37, 110020	10.6	2
18	A systematic analysis of protein-altering exonic variants in chronic obstructive pulmonary disease. *American Journal of Physiology - Lung Cellular and Molecular Physiology*, **2021**, 321, L130-L143	5.8	2
17	Risk factors associated with SARS-CoV-2 infection in a multiethnic cohort of United Kingdom healthcare workers (UK-REACH): A cross-sectional analysis. *PLoS Medicine*, **2022**, 19, e1004015	11.6	2
16	Use of FEV1 as a measure of lung health in the UK BiLEVE study - AuthorsQreply. *Lancet Respiratory Medicine,the*, **2015**, 3, e42-3	35.1	1
15	Pharmacogenetic interactions and their potential effects on genetic analyses of blood pressure. *Statistics in Medicine*, **2011**, 30, 769-83	2.3	1
14	Predictors of SARS-CoV-2 infection in a multi-ethnic cohort of United Kingdom healthcare workers: a prospective nationwide cohort study (UK-REACH)		1
13	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*,3, 4	4.8	1
12	Human CCL3L1 copy number variation, gene expression, and the role of the CCL3L1-CCR5 axis in lung function. *Wellcome Open Research*,3, 13	4.8	1
11	Genome-wide gene-air pollution interaction analysis of lung function in 300,000 individuals.. *Environment International*, **2021**, 159, 107041	12.9	1
10	Mendelian randomisation analyses of eosinophils and other blood cell types in relation to lung function and disease		1
9	Novel blood pressure locus and gene discovery using GWAS and expression datasets from blood and the kidney		1
8	The United Kingdom Research study into Ethnicity And COVID-19 outcomes in Healthcare workers (UK-REACH): Protocol for a prospective longitudinal cohort study of healthcare and ancillary workers in UK healthcare settings		1
7	Variants associated with HHIP expression have sex-differential effects on lung function. *Wellcome Open Research*, **2020**, 5, 111	4.8	0
6	Genome-wide association study of susceptibility to hospitalised respiratory infections. *Wellcome Open Research*,6, 290	4.8	0
5	Variants associated with expression have sex-differential effects on lung function. *Wellcome Open Research*, **2020**, 5, 111	4.8	0

4	Rare and low-frequency exonic variants and gene-by-smoking interactions in pulmonary function. *Scientific Reports*, **2021**, 11, 19365	4.9	0
3	Extended Cohort for E-health, Environment and DNA (EXCEED) COVID-19 focus. *Wellcome Open Research*,6, 349	4.8	0
2	Genome-wide association study of copy number variation with lung function identifies a novel signal of association near BANP for forced vital capacity. *BMC Genetics*, **2016**, 17, 116	2.6	
1	Familial hypereosinophilia associated with eosinophilic gastrointestinal symptoms in individuals with a missense mutation in CKLF-like MARVEL transmembrane domain containing 3. *Clinical and Experimental Allergy*, **2021**, 51, 1501-1504	4.1	