Martin D Tobin

List of Publications by Year
in descending order

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183 papers	35,508 citations	13099 68 h-index	4117 175 g-index
218 all docs	218 docs citations	218 times ranked	41648 citing authors

#	Article	IF	Citations
1	Mendelian randomisation of eosinophils and other cell types in relation to lung function and disease. Thorax, 2023, 78, 496-503.	5.6	6
2	Genome-wide gene-air pollution interaction analysis of lung function in 300,000 individuals. Environment International, 2022, 159, 107041.	10.0	8
3	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.	5.6	11
4	Genetic Associations and Architecture of Asthma-COPD Overlap. Chest, 2022, 161, 1155-1166.	0.8	15
5	Genotypic and Phenotypic Spectrum of Foveal Hypoplasia. Ophthalmology, 2022, 129, 708-718.	5.2	29
6	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. Nature Genetics, 2022, 54, 437-449.	21.4	215
7	Healthcare workersâ€™ views on mandatory SARS-CoV-2 vaccination in the UK: A cross-sectional, mixed-methods analysis from the UK-REACH study. EClinicalMedicine, 2022, 46, 101346.	7.1	27
8	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.	8.4	28
9	Genome-Wide Gene-by-Smoking Interaction Study of Chronic Obstructive Pulmonary Disease. American Journal of Epidemiology, 2021, 190, 875-885.	3.4	21
10	Pleiotropic associations of heterozygosity for the SERPINA1 Z allele in the UK Biobank. ERJ Open Research, 2021, 7, 00049-2021.	2.6	10
11	Genetic and clinical characteristics of treatment-resistant depression using primary care records in two UK cohorts. Molecular Psychiatry, 2021, 26, 3363-3373.	7.9	66
12	P_{aO₂}/F_{IO₂}ratio: the mismeasure of oxygenation in COVID-19. European Respiratory Journal, 2021, 57, 2100274.	6.7	24
13	Familial hypereosinophilia associated with eosinophilic gastrointestinal symptoms in individuals with a missense mutation in CKLFâ€like MARVEL transmembrane domain containing 3. Clinical and Experimental Allergy, 2021, 51, 1501-1504.	2.9	2
14	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.	1.9	9
15	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.	2.9	11
16	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.	5.6	116
17	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.	1.9	26
18	P040â€…Identification and functional characterisation of a rare MTTP variant underlying hereditary non-alcoholic fatty liver disease. , 2021, , .		0

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19	Rare and low-frequency exonic variants and gene-by-smoking interactions in pulmonary function. Scientific Reports, 2021, 11, 19365.	3.3	2
20	Phenotypic and functional translation of IL33 genetics in asthma. Journal of Allergy and Clinical Immunology, 2021, 147, 144-157.	2.9	29
21	Improving ethnic diversity in respiratory genomics research. European Respiratory Journal, 2021, 58, 2101615.	6.7	5
22	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.	6.4	25
23	Design and implementation of a university-based COVID-19 testing programme: an observational study. Lancet, The, 2021, 398, S24.	13.7	0
24	Interaction of Cigarette Smoking and Polygenic Risk Score on Reduced Lung Function. JAMA Network Open, 2021, 4, e2139525.	5.9	22
25	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular Psychiatry, 2020, 25, 2392-2409.	7.9	83
26	Genome-Wide Association Study of Susceptibility to Idiopathic Pulmonary Fibrosis. American Journal of Respiratory and Critical Care Medicine, 2020, 201, 564-574.	5.6	208
27	Blood eosinophil count and airway epithelial transcriptome relationships in COPD versus asthma. Allergy: European Journal of Allergy and Clinical Immunology, 2020, 75, 370-380.	5.7	37
28	Resistome analyses of sputum from COPD and healthy subjects reveals bacterial load-related prevalence of target genes. Thorax, 2020, 75, 8-16.	5.6	18
29	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. Nature Communications, 2020, 11, 5182.	12.8	32
30	The sputum microbiome is distinct between COPD and health, independent of smoking history. Respiratory Research, 2020, 21, 183.	3.6	45
31	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	21.4	91
32	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.	10.7	69
33	Identifying potential causal effects of age at menarche: a Mendelian randomization phenome-wide association study. BMC Medicine, 2020, 18, 71.	5.5	27
34	Smoking, DNA Methylation, and Lung Function: a Mendelian Randomization Analysis to Investigate Causal Pathways. American Journal of Human Genetics, 2020, 106, 315-326.	6.2	32
35	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	1.8	3
36	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

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37	Phenotypic and functional translation of IL1RL1 locus polymorphisms in lung tissue and asthmatic airway epithelium. JCI Insight, 2020, 5, .	5.0	26
38	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	1.8	4
39	Cohort Profile: Extended Cohort for E-health, Environment and DNA (EXCEED). International Journal of Epidemiology, 2019, 48, 678-679j.	1.9	9
40	Epigenome-wide association study of lung function level and its change. European Respiratory Journal, 2019, 54, 1900457.	6.7	49
41	Bi-allelic Loss-of-Function CACNA1B Mutations in Progressive Epilepsy-Dyskinesia. American Journal of Human Genetics, 2019, 104, 948-956.	6.2	45
42	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
43	Genetic landscape of chronic obstructive pulmonary disease identifies heterogeneous cell-type and phenotype associations. Nature Genetics, 2019, 51, 494-505.	21.4	257
44	T76FEASIBILITY OF DEFINING TREATMENT RESISTANT DEPRESSION IN PRIMARY CARE RECORDS FOR PHARMACOGENETIC STUDIES. European Neuropsychopharmacology, 2019, 29, S256.	0.7	0
45	Moderate-to-severe asthma in individuals of European ancestry: a genome-wide association study. Lancet Respiratory Medicine,the, 2019, 7, 20-34.	10.7	183
46	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.	3.2	9
47	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.	21.4	536
48	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and AlcoholÂUse. Biological Psychiatry, 2019, 85, 946-955.	1.3	69
49	Formalising recall by genotype as an efficient approach to detailed phenotyping and causal inference. Nature Communications, 2018, 9, 711.	12.8	54
50	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.	5.6	37
51	Human CCL3L1 copy number variation, gene expression, and the role of the CCL3L1-CCR5 axis in lung function. Wellcome Open Research, 2018, 3, 13.	1.8	10
52	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.	3.6	27
53	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
54	The vitamin D binding protein axis modifies disease severity in lymphangioleiomyomatosis. European Respiratory Journal, 2018, 52, 1800951.	6.7	13

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55	Identification of susceptibility pathways for the role of chromosome 15q25.1 in modifying lung cancer risk. Nature Communications, 2018, 9, 3221.	12.8	60
56	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 2018, 3, 4.	1.8	19
57	Determinants of dayâ€“night difference in blood pressure, a comparison with determinants of daytime and night-time blood pressure. Journal of Human Hypertension, 2017, 31, 43-48.	2.2	9
58	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. International Journal of Epidemiology, 2017, 46, dyw318.	1.9	36
59	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. Nature Genetics, 2017, 49, 403-415.	21.4	492
60	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
61	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
62	Genetic variants affecting cross-sectional lung function in adults show little or no effect on longitudinal lung function decline. Thorax, 2017, 72, 400-408.	5.6	25
63	Discovery of novel heart rate-associated loci using the Exome Chip. Human Molecular Genetics, 2017, 26, 2346-2363.	2.9	29
64	Age at menarche and lung function: a Mendelian randomization study. European Journal of Epidemiology, 2017, 32, 701-710.	5.7	37
65	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. Journal of the American Heart Association, 2017, 6, .	3.7	89
66	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. American Journal of Human Genetics, 2017, 100, 865-884.	6.2	131
67	Large-scale association analysis identifies new lung cancer susceptibility loci and heterogeneity in genetic susceptibility across histological subtypes. Nature Genetics, 2017, 49, 1126-1132.	21.4	472
68	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.	10.7	233
69	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744.	12.8	64
70	Mechanical Ventilation. American Journal of Respiratory and Critical Care Medicine, 2017, 196, P3-P4.	5.6	41
71	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Hypertension, 2017, 70, .	2.7	123
72	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. Nature Communications, 2017, 8, 16015.	12.8	149

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73	Phenotypic and pharmacogenetic evaluation of patients with thiazide-induced hyponatremia. Journal of Clinical Investigation, 2017, 127, 3367-3374.	8.2	58
74	Targeted Sequencing of Lung Function Loci in Chronic Obstructive Pulmonary Disease Cases and Controls. PLoS ONE, 2017, 12, e0170222.	2.5	9
75	A Method to Exploit the Structure of Genetic Ancestry Space to Enhance Case-Control Studies. American Journal of Human Genetics, 2016, 98, 857-868.	6.2	21
76	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204
77	Analysis with the exome array identifies multiple new independent variants in lipid loci. Human Molecular Genetics, 2016, 25, 4094-4106.	2.9	19
78	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	21.4	261
79	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	21.4	362
80	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	7.1	110
81	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.	2.7	0
82	Haplotype estimation for biobank-scale data sets. Nature Genetics, 2016, 48, 817-820.	21.4	192
83	International Genome-Wide Association Study Consortium Identifies Novel Loci Associated With Blood Pressure in Children and Adolescents. Circulation: Cardiovascular Genetics, 2016, 9, 266-278.	5.1	48
84	Exome-wide analysis of rare coding variation identifies novel associations with COPD and airflow limitation inMOCS3,IFIT3andSERPINA12. Thorax, 2016, 71, 501-509.	5.6	22
85	Use of FEV1 as a measure of lung health in the UK BiLEVE study â€“ Authors' reply. Lancet Respiratory Medicine,the, 2015, 3, e42-e43.	10.7	1
86	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. PLoS Genetics, 2015, 11, e1005230.	3.5	77
87	Adiposity as a cause of cardiovascular disease: a Mendelian randomization study. International Journal of Epidemiology, 2015, 44, 578-586.	1.9	123
88	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. Nature Communications, 2015, 6, 8658.	12.8	108
89	Age- and Sex-Specific Causal Effects of Adiposity on Cardiovascular Risk Factors. Diabetes, 2015, 64, 1841-1852.	0.6	63
90	The impact of low-frequency and rare variants on lipid levels. Nature Genetics, 2015, 47, 589-597.	21.4	310

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91	Molecular mechanisms underlying variations in lung function: a systems genetics analysis. Lancet Respiratory Medicine,the, 2015, 3, 782-795.	10.7	66
92	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, 769-781.	10.7	346
93	Integrative pathway genomics of lung function and airflow obstruction. Human Molecular Genetics, 2015, 24, 6836-6848.	2.9	28
94	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	27.8	1,014
95	Large-Scale Genome-Wide Association Studies and Meta-Analyses of Longitudinal Change in Adult Lung Function. PLoS ONE, 2014, 9, e100776.	2.5	52
96	Whole Exome Re-Sequencing Implicates CCDC38 and Cilia Structure and Function in Resistance to Smoking Related Airflow Obstruction. PLoS Genetics, 2014, 10, e1004314.	3.5	29
97	Detection of mutations in KLHL3 and CUL3 in families with FHHt (familial hyperkalaemic) Tj ETQq1 1 0.784314 rgBT /Ov	4.3	49
98	APOM and high-density lipoprotein cholesterol are associated with lung function and per cent emphysema. European Respiratory Journal, 2014, 43, 1003-1017.	6.7	37
99	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, 1633-1644.	1.9	16
100	Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. American Journal of Human Genetics, 2014, 94, 349-360.	6.2	158
101	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, 2498-2510.	2.9	28
102	Genome-wide association analysis identifies six new loci associated with forced vital capacity. Nature Genetics, 2014, 46, 669-677.	21.4	131
103	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.	6.2	73
104	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.	2.5	11
105	Common Genetic Determinants of Lung Function, Subclinical Atherosclerosis and Risk of Coronary Artery Disease. PLoS ONE, 2014, 9, e104082.	2.5	36
106	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	51
107	Secretory Phospholipase A2-IIA and Cardiovascular Disease. Journal of the American College of Cardiology, 2013, 62, 1966-1976.	2.8	115
108	Identification of seven loci affecting mean telomere length and their association with disease. Nature Genetics, 2013, 45, 422-427.	21.4	808

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109	Body mass index, asthma, and genetic variation. Clinical and Experimental Allergy, 2013, 43, 383-384.	2.9	1
110	Bed Occupancy Rates and Hospital-Acquired Clostridium difficile Infection: A Cohort Study. Infection Control and Hospital Epidemiology, 2013, 34, 1062-1069.	1.8	15
111	Causal and Synthetic Associations of Variants in the SERPINA Gene Cluster with Alpha1-antitrypsin Serum Levels. PLoS Genetics, 2013, 9, e1003585.	3.5	43
112	The Role of Adiposity in Cardiometabolic Traits: A Mendelian Randomization Analysis. PLoS Medicine, 2013, 10, e1001474.	8.4	178
113	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.	2.9	82
114	GSTCD and INTS12 Regulation and Expression in the Human Lung. PLoS ONE, 2013, 8, e74630.	2.5	46
115	Genome-Wide Joint Meta-Analysis of SNP and SNP-by-Smoking Interaction Identifies Novel Loci for Pulmonary Function. PLoS Genetics, 2012, 8, e1003098.	3.5	130
116	Genome-wide association studies in lung disease: Figure 1. Thorax, 2012, 67, 271-273.	5.6	16
117	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, 622-632.	5.6	164
118	Integration of Genetics into a Systems Model of Electrocardiographic Traits Using HumanCVD BeadChip. Circulation: Cardiovascular Genetics, 2012, 5, 630-638.	5.1	12
119	Allelic variant ofNOS1APeffects on cardiac alternans of repolarization during exercise testing. Scandinavian Journal of Clinical and Laboratory Investigation, 2012, 72, 100-107.	1.2	3
120	Genome-wide association study to identify genetic determinants of severe asthma. Thorax, 2012, 67, 762-768.	5.6	169
121	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2012, 90, 1116-1117.	6.2	0
122	What can genetics tell us about the cause of fixed airflow obstruction?. Clinical and Experimental Allergy, 2012, 42, 1176-1182.	2.9	7
123	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	27.8	1,855
124	Large-Scale Candidate Gene Analysis of HDL Particle Features. PLoS ONE, 2011, 6, e14529.	2.5	32
125	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2011, 88, 6-18.	6.2	122
126	Blood Pressure Loci Identified with a Gene-Centric Array. American Journal of Human Genetics, 2011, 89, 688-700.	6.2	159

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127	Pharmacogenetic interactions and their potential effects on genetic analyses of blood pressure. Statistics in Medicine, 2011, 30, 769-783.	1.6	4
128	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, 786-795.	5.6	128
129	Dense Genotyping of Candidate Gene Loci Identifies Variants Associated With High-Density Lipoprotein Cholesterol. Circulation: Cardiovascular Genetics, 2011, 4, 145-155.	5.1	71
130	Reply to the Letter by Hayashi et al. Circulation: Cardiovascular Genetics, 2011, 4, .	5.1	0
131	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. Human Molecular Genetics, 2011, 20, 2273-2284.	2.9	168
132	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	21.4	403
133	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. Nature Genetics, 2011, 43, 1082-1090.	21.4	367
134	Four Genetic Loci Influencing Electrocardiographic Indices of Left Ventricular Hypertrophy. Circulation: Cardiovascular Genetics, 2011, 4, 626-635.	5.1	28
135	Heritability of Early Repolarization. Circulation: Cardiovascular Genetics, 2011, 4, 134-138.	5.1	89
136	Opportunities and Challenges in the Genetics of COPD 2010: An International COPD Genetics Conference Report. COPD: Journal of Chronic Obstructive Pulmonary Disease, 2011, 8, 121-135.	1.6	43
137	Copy Number Variation. Methods in Molecular Biology, 2011, 713, 167-183.	0.9	3
138	A Comprehensive Evaluation of Potential Lung Function Associated Genes in the SpiroMeta General Population Sample. PLoS ONE, 2011, 6, e19382.	2.5	56
139	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. Nature, 2010, 464, 713-720.	27.8	737
140	Genome-wide association study identifies five loci associated with lung function. Nature Genetics, 2010, 42, 36-44.	21.4	518
141	A large genome scan for rare CNVs in amyotrophic lateral sclerosis. Human Molecular Genetics, 2010, 19, 4091-4099.	2.9	51
142	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, 1372-1382.	1.9	150
143	Genetic Architecture of Ambulatory Blood Pressure in the General Population. Hypertension, 2010, 56, 1069-1076.	2.7	64
144	Common variants near TERC are associated with mean telomere length. Nature Genetics, 2010, 42, 197-199.	21.4	296

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145	Seeking consent to tissue banking: a survey of health professionals in childhood cancer. European Journal of Cancer Care, 2009, 18, 391-400.	1.5	10
146	Genome-wide association study identifies eight loci associated with blood pressure. Nature Genetics, 2009, 41, 666-676.	21.4	1,104
147	Genomic copy number variation, human health, and disease. Lancet, The, 2009, 374, 340-350.	13.7	172
148	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.	2.5	53
149	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.	2.5	39
150	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, 1233-1241.	3.9	80
151	Metaâ€analysis of Mendelian randomization studies incorporating all three genotypes. Statistics in Medicine, 2008, 27, 6570-6582.	1.6	10
152	Coronary Artery Diseaseâ€“Associated Locus on Chromosome 9p21 and Early Markers of Atherosclerosis. Arteriosclerosis, Thrombosis, and Vascular Biology, 2008, 28, 1679-1683.	2.4	80
153	Genome-wide Association Study Identifies Genes for Biomarkers of Cardiovascular Disease: Serum Urate and Dyslipidemia. American Journal of Human Genetics, 2008, 82, 139-149.	6.2	397
154	Mendelian Randomisation and Causal Inference in Observational Epidemiology. PLoS Medicine, 2008, 5, e177.	8.4	296
155	Common Variation in the WNK1 Gene and Blood Pressure in Childhood. Hypertension, 2008, 52, 974-979.	2.7	32
156	Common Variants in Genes Underlying Monogenic Hypertension and Hypotension and Blood Pressure in the General Population. Hypertension, 2008, 51, 1658-1664.	2.7	104
157	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, 1132-1141.	1.9	51
158	Adjusting for bias and unmeasured confounding in Mendelian randomization studies with binary responses. International Journal of Epidemiology, 2008, 37, 1161-1168.	1.9	75
159	Genomewide Association Analysis of Coronary Artery Disease. New England Journal of Medicine, 2007, 357, 443-453.	27.0	1,865
160	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, 411-416.	4.3	17
161	Tumour necrosis factor gene complex polymorphisms in chronic obstructive pulmonary disease. Respiratory Medicine, 2007, 101, 340-344.	2.9	23
162	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. Nature Genetics, 2007, 39, 1329-1337.	21.4	1,298

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163	Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. Nature, 2007, 447, 661-678.	27.8	8,895
164	Localization of type 1 diabetes susceptibility to the MHC class I genes HLA-B and HLA-A. Nature, 2007, 450, 887-892.	27.8	493
165	Beyond â€œmisunderstandingâ€: Written information and decisions about taking part in a genetic epidemiology study. Social Science and Medicine, 2007, 65, 2212-2222.	3.8	120
166	Public health professionals' perceptions 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.	2.9	3
167	Meta-analysis of genetic studies using Mendelian randomizationâ€”a multivariate approach. Statistics in Medicine, 2005, 24, 2241-2254.	1.6	74
168	Adjusting for treatment effects in studies of quantitative traits: antihypertensive therapy and systolic blood pressure. Statistics in Medicine, 2005, 24, 2911-2935.	1.6	571
169	Association of WNK1 Gene Polymorphisms and Haplotypes With Ambulatory Blood Pressure in the General Population. Circulation, 2005, 112, 3423-3429.	1.6	124
170	Key concepts in genetic epidemiology. Lancet, The, 2005, 366, 941-951.	13.7	223
171	Covariance components models for longitudinal family data. International Journal of Epidemiology, 2005, 34, 1063-1077.	1.9	28
172	An Integrated Approach to the Meta-Analysis of Genetic Association Studies using Mendelian Randomization. American Journal of Epidemiology, 2004, 160, 445-452.	3.4	66
173	Genotypes and haplotypes predisposing to myocardial infarction: a multilocus case-control study. European Heart Journal, 2004, 25, 459-467.	2.2	133
174	Commentary: Development of Mendelian randomization: from hypothesis test to 'Mendelian deconfounding'. International Journal of Epidemiology, 2004, 33, 26-29.	1.9	48
175	Longitudinal data analysis in pedigree studies. Genetic Epidemiology, 2003, 25, S18-S28.	1.3	32
176	Longitudinal variance components models for systolic blood pressure, fitted using Gibbs sampling. BMC Genetics, 2003, 4, S25.	2.7	10
177	South Asian ethnicity and risk of childhood accidents: an ecological study at enumeration district level in Leicester. Journal of Public Health, 2002, 24, 313-318.	1.8	11
178	Teaching and learning about human sexuality in undergraduate medical education. Medical Education, 2002, 36, 432-440.	2.1	51
179	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	1.8	11
180	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	1.8	1

#	Article	IF	Citations
181	Human CCL3L1 copy number variation, gene expression, and the role of the CCL3L1-CCR5 axis in lung function. Wellcome Open Research, 0, 3, 13.	1.8	1
182	Genome-wide association study of susceptibility to hospitalised respiratory infections. Wellcome Open Research, 0, 6, 290.	1.8	3
183	Extended Cohort for E-health, Environment and DNA (EXCEED) COVID-19 focus. Wellcome Open Research, 0, 6, 349.	1.8	2