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List of Publications by Year
in descending order

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122 papers	16,521 citations	38742 50 h-index	19749 117 g-index
168 all docs	168 docs citations	168 times ranked	24317 citing authors

#	Article	IF	Citations
1	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	27.8	1,855
2	Genome-wide association study identifies eight loci associated with blood pressure. Nature Genetics, 2009, 41, 666-676.	21.4	1,104
3	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	27.8	1,014
4	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
5	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
6	Chimpanzee Reservoirs of Pandemic and Nonpandemic HIV-1. Science, 2006, 313, 523-526.	12.6	723
7	Genome-wide association study identifies five loci associated with lung function. Nature Genetics, 2010, 42, 36-44.	21.4	518
8	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
9	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
10	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	21.4	403
11	Physical, cognitive, and mental health impacts of COVID-19 after hospitalisation (PHOSP-COVID): a UK multicentre, prospective cohort study. Lancet Respiratory Medicine,the, 2021, 9, 1275-1287.	10.7	394
12	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. Nature Genetics, 2011, 43, 1082-1090.	21.4	367
13	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
14	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
15	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
16	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. Nature Genetics, 2019, 51, 51-62.	21.4	328
17	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
18	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	21.4	261

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19	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
20	Genetic landscape of chronic obstructive pulmonary disease identifies heterogeneous cell-type and phenotype associations. Nature Genetics, 2019, 51, 494-505.	21.4	257
21	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
22	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
23	Haplotype estimation for biobank-scale data sets. Nature Genetics, 2016, 48, 817-820.	21.4	192
24	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
25	Genomic copy number variation, human health, and disease. Lancet, The, 2009, 374, 340-350.	13.7	172
26	Genome-wide association study to identify genetic determinants of severe asthma. Thorax, 2012, 67, 762-768.	5.6	169
27	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
28	Uganda Genome Resource Enables Insights into Population History and Genomic Discovery in Africa. Cell, 2019, 179, 984-1002.e36.	28.9	152
29	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. Nature Communications, 2017, 8, 16015.	12.8	149
30	Translational genomics and precision medicine: Moving from the lab to the clinic. Science, 2019, 365, 1409-1413.	12.6	133
31	Genome-wide association analysis identifies six new loci associated with forced vital capacity. Nature Genetics, 2014, 46, 669-677.	21.4	131
32	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
33	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
34	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
35	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. Nature Communications, 2015, 6, 8658.	12.8	108
36	Adaptation of HIV-1 to Its Human Host. Molecular Biology and Evolution, 2007, 24, 1853-1860.	8.9	100

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37	Telomere length and risk of idiopathic pulmonary fibrosis and chronic obstructive pulmonary disease: a mendelian randomisation study. Lancet Respiratory Medicine,the, 2021, 9, 285-294.	10.7	94
38	Common Genetic Variation in the 3â€²- BCL11B Gene Desert Is Associated With Carotid-Femoral Pulse Wave Velocity and Excess Cardiovascular Disease Risk. Circulation: Cardiovascular Genetics, 2012, 5, 81-90.	5.1	90
39	Adjustment for index event bias in genome-wide association studies of subsequent events. Nature Communications, 2019, 10, 1561.	12.8	87
40	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
41	Overlap of Genetic Risk between Interstitial Lung Abnormalities and Idiopathic Pulmonary Fibrosis. American Journal of Respiratory and Critical Care Medicine, 2019, 200, 1402-1413.	5.6	77
42	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
43	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
44	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
45	Molecular mechanisms underlying variations in lung function: a systems genetics analysis. Lancet Respiratory Medicine,the, 2015, 3, 782-795.	10.7	66
46	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
47	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744.	12.8	64
48	Shared genetic etiology between idiopathic pulmonary fibrosis and COVID-19 severity. EBioMedicine, 2021, 65, 103277.	6.1	63
49	Identification of susceptibility pathways for the role of chromosome 15q25.1 in modifying lung cancer risk. Nature Communications, 2018, 9, 3221.	12.8	60
50	Phenotypic and pharmacogenetic evaluation of patients with thiazide-induced hyponatremia. Journal of Clinical Investigation, 2017, 127, 3367-3374.	8.2	58
51	A Comprehensive Evaluation of Potential Lung Function Associated Genes in the SpiroMeta General Population Sample. PLoS ONE, 2011, 6, e19382.	2.5	56
52	Formalising recall by genotype as an efficient approach to detailed phenotyping and causal inference. Nature Communications, 2018, 9, 711.	12.8	54
53	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
54	Large-Scale Genome-Wide Association Studies and Meta-Analyses of Longitudinal Change in Adult Lung Function. PLoS ONE, 2014, 9, e100776.	2.5	52

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55	A large genome scan for rare CNVs in amyotrophic lateral sclerosis. Human Molecular Genetics, 2010, 19, 4091-4099.	2.9	51
56	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
57	Detection of mutations in KLHL3 and CUL3 in families with FHHt (familial hyperkalaemic) Tj ETQq1 1 0.784314 rgBT /Over	4.3	49
58	New Blood Pressureâ€“Associated Loci Identified in Meta-Analyses of 475â€‰000 Individuals. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	48
59	Genome-wide association study across five cohorts identifies five novel loci associated with idiopathic pulmonary fibrosis. Thorax, 2022, 77, 829-833.	5.6	47
60	GSTCD and INTS12 Regulation and Expression in the Human Lung. PLoS ONE, 2013, 8, e74630.	2.5	46
61	Bi-allelic Loss-of-Function CACNA1B Mutations in Progressive Epilepsy-Dyskinesia. American Journal of Human Genetics, 2019, 104, 948-956.	6.2	45
62	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
63	Age at menarche and lung function: a Mendelian randomization study. European Journal of Epidemiology, 2017, 32, 701-710.	5.7	37
64	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
65	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. International Journal of Epidemiology, 2017, 46, dyw318.	1.9	36
66	Common Variation in the WNK1 Gene and Blood Pressure in Childhood. Hypertension, 2008, 52, 974-979.	2.7	32
67	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. Nature Communications, 2020, 11, 5182.	12.8	32
68	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
69	Phenotypic and functional translation of IL33 genetics in asthma. Journal of Allergy and Clinical Immunology, 2021, 147, 144-157.	2.9	29
70	Integrative pathway genomics of lung function and airflow obstruction. Human Molecular Genetics, 2015, 24, 6836-6848.	2.9	28
71	Identification of a missense variant in SPDL1 associated with idiopathic pulmonary fibrosis. Communications Biology, 2021, 4, 392.	4.4	28
72	Understanding the burden of interstitial lung disease post-COVID-19: the UK Interstitial Lung Disease-Long COVID Study (UKILD-Long COVID). BMJ Open Respiratory Research, 2021, 8, e001049.	3.0	28

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73	Phenotypic and functional translation of IL1RL1 locus polymorphisms in lung tissue and asthmatic airway epithelium. JCI Insight, 2020, 5, .	5.0	26
74	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
75	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
76	Novel idiopathic pulmonary fibrosis susceptibility variants revealed by deepÂsequencing. ERJ Open Research, 2019, 5, 00071-2019.	2.6	24
77	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
78	Interaction of Cigarette Smoking and Polygenic Risk Score on Reduced Lung Function. JAMA Network Open, 2021, 4, e2139525.	5.9	22
79	Genetic overlap between idiopathic pulmonary fibrosis and COVID-19. European Respiratory Journal, 2022, 60, 2103132.	6.7	22
80	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
81	Genome-Wide Gene-by-Smoking Interaction Study of Chronic Obstructive Pulmonary Disease. American Journal of Epidemiology, 2021, 190, 875-885.	3.4	21
82	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 2018, 3, 4.	1.8	19
83	Reversal of Agingâ€Induced Increases in Aortic Stiffness by Targeting Cytoskeletal Proteinâ€Protein Interfaces. Journal of the American Heart Association, 2018, 7, .	3.7	17
84	Proportion of Idiopathic Pulmonary Fibrosis Risk Explained by Known Common Genetic Loci in European Populations. American Journal of Respiratory and Critical Care Medicine, 2021, 203, 775-778.	5.6	17
85	Genome-wide association studies in lung disease: Figure 1. Thorax, 2012, 67, 271-273.	5.6	16
86	Genetic Associations and Architecture of Asthma-COPD Overlap. Chest, 2022, 161, 1155-1166.	0.8	15
87	The vitamin D binding protein axis modifies disease severity in lymphangioleiomyomatosis. European Respiratory Journal, 2018, 52, 1800951.	6.7	13
88	Rare variants and cardiovascular disease. Briefings in Functional Genomics, 2014, 13, 384-391.	2.7	12
89	Defining genetic risk factors for scleroderma-associated interstitial lung disease. Clinical Rheumatology, 2020, 39, 1173-1179.	2.2	12
90	Genetic correlation and causal relationships between cardio-metabolic traits and lung function impairment. Genome Medicine, 2021, 13, 104.	8.2	11

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91	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
92	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	1.8	11
93	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
94	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
95	Pleiotropic associations of heterozygosity for the SERPINA1 Z allele in the UK Biobank. ERJ Open Research, 2021, 7, 00049-2021.	2.6	10
96	Cohort Profile: Extended Cohort for E-health, Environment and DNA (EXCEED). International Journal of Epidemiology, 2019, 48, 678-679j.	1.9	9
97	Krebs von den Lungenâ€6 (KLâ€6) is a pathophysiological biomarker of earlyâ€stage acute hypersensitivity pneumonitis among pigeon fanciers. Clinical and Experimental Allergy, 2020, 50, 1391-1399.	2.9	9
98	Genetically increased circulating FUT3 level leads to reduced risk of Idiopathic Pulmonary Fibrosis: a Mendelian Randomisation Study. European Respiratory Journal, 2021, , 2003979.	6.7	9
99	Targeted Sequencing of Lung Function Loci in Chronic Obstructive Pulmonary Disease Cases and Controls. PLoS ONE, 2017, 12, e0170222.	2.5	9
100	Genome-wide gene-air pollution interaction analysis of lung function in 300,000 individuals. Environment International, 2022, 159, 107041.	10.0	8
101	Cluster analysis of transcriptomic datasets to identify endotypes of idiopathic pulmonary fibrosis. Thorax, 2023, 78, 551-558.	5.6	8
102	What can genetics tell us about the cause of fixed airflow obstruction?. Clinical and Experimental Allergy, 2012, 42, 1176-1182.	2.9	7
103	Mendelian randomisation of eosinophils and other cell types in relation to lung function and disease. Thorax, 2023, 78, 496-503.	5.6	6
104	Exome-wide analysis of copy number variation shows association of the human leukocyte antigen region with asthma in UK Biobank. BMC Medical Genomics, 2022, 15, .	1.5	6
105	Recurrent mutation at the classical haptoglobin structural polymorphism. Nature Genetics, 2016, 48, 347-348.	21.4	4
106	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	1.8	4
107	Blood Pressure Genetics and Hypertension: Genome-Wide Analysis and Role of Ancestry. Current Genetic Medicine Reports, 2014, 2, 13-22.	1.9	3
108	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	1.8	3

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109	Copy Number Variation. Methods in Molecular Biology, 2011, 713, 167-183.	0.9	3
110	Genome-wide association study of susceptibility to hospitalised respiratory infections. Wellcome Open Research, 0, 6, 290.	1.8	3
111	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
112	Evolutionary origins of diversity in human viruses. , 2007, , 169-184.		2
113	Extended Cohort for E-health, Environment and DNA (EXCEED) COVID-19 focus. Wellcome Open Research, 0, 6, 349.	1.8	2
114	Joint Effect of Single-Nucleotide Polymorphisms and Smoking Exposure in Chronic Obstructive Pulmonary Disease Risk. American Journal of Respiratory and Critical Care Medicine, 2012, 185, 683-684.	5.6	1
115	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
116	Towards genetic reclassification of idiopathic pulmonary fibrosis. Lancet Respiratory Medicine,the, 2018, 6, 569-570.	10.7	1
117	Call for Papers: â€œMorphology is the link between genetics and functionâ€¦ a tribute to Ewald R. Weibel. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2021, 320, L254-L256.	2.9	1
118	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	1.8	1
119	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
120	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
121	ERS International Congress 2018: highlights from best-abstract awardees. Breathe, 2018, 14, e137-e142.	1.3	0
122	P040â€…Identification and functional characterisation of a rare MTTP variant underlying hereditary non-alcoholic fatty liver disease. , 2021, , .		0