Nick Shrine

List of Publications by Year
in descending order

53 papers	7,014 citations	218381 26 h-index	174990 52 g-index
68 all docs	68 docs citations	68 times ranked	13525 citing authors

#	Article	IF	Citations
1	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	13.7	1,855
2	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	9.4	924
3	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. Nature Genetics, 2017, 49, 403-415.	9.4	492
4	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. Nature Genetics, 2019, 51, 481-493.	9.4	350
5	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.	5.2	346
6	Genetic loci associated with chronic obstructive pulmonary disease overlap with loci for lung function and pulmonary fibrosis. Nature Genetics, 2017, 49, 426-432.	9.4	306
7	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.	9.4	257
8	Genetic landscape of chronic obstructive pulmonary disease identifies heterogeneous cell-type and phenotype associations. Nature Genetics, 2019, 51, 494-505.	9.4	257
9	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.	5.2	233
10	Haplotype estimation for biobank-scale data sets. Nature Genetics, 2016, 48, 817-820.	9.4	192
11	Moderate-to-severe asthma in individuals of European ancestry: a genome-wide association study. Lancet Respiratory Medicine,the, 2019, 7, 20-34.	5.2	183
12	Genome-wide association study to identify genetic determinants of severe asthma. Thorax, 2012, 67, 762-768.	2.7	169
13	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.	2.5	164
14	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. Nature Communications, 2017, 8, 16015.	5.8	149
15	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Hypertension, 2017, 70, .	1.3	123
16	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. Nature Communications, 2015, 6, 8658.	5.8	108
17	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular Psychiatry, 2020, 25, 2392-2409.	4.1	83
18	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.	5.2	69

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19	Genetic and clinical characteristics of treatment-resistant depression using primary care records in two UK cohorts. Molecular Psychiatry, 2021, 26, 3363-3373.	4.1	66
20	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744.	5.8	64
21	Phenotypic and pharmacogenetic evaluation of patients with thiazide-induced hyponatremia. Journal of Clinical Investigation, 2017, 127, 3367-3374.	3.9	58
22	A Comprehensive Evaluation of Potential Lung Function Associated Genes in the SpiroMeta General Population Sample. PLoS ONE, 2011, 6, e19382.	1.1	56
23	Age at menarche and lung function: a Mendelian randomization study. European Journal of Epidemiology, 2017, 32, 701-710.	2.5	37
24	Velocity Scaling of Impact Craters in Water Ice over the Range 1 to 7.3 km sâ^'1. Icarus, 2002, 155, 475-485.	1.1	36
25	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. Nature Communications, 2020, 11, 5182.	5.8	32
26	Whole Exome Re-Sequencing Implicates CCDC38 and Cilia Structure and Function in Resistance to Smoking Related Airflow Obstruction. PLoS Genetics, 2014, 10, e1004314.	1.5	29
27	Phenotypic and functional translation of IL33 genetics in asthma. Journal of Allergy and Clinical Immunology, 2021, 147, 144-157.	1.5	29
28	Phenotypic and functional translation of IL1RL1 locus polymorphisms in lung tissue and asthmatic airway epithelium. JCI Insight, 2020, 5, .	2.3	26
29	Genetic variants affecting cross-sectional lung function in adults show little or no effect on longitudinal lung function decline. Thorax, 2017, 72, 400-408.	2.7	25
30	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.	2.9	25
31	Interaction of Cigarette Smoking and Polygenic Risk Score on Reduced Lung Function. JAMA Network Open, 2021, 4, e2139525.	2.8	22
32	Laboratory investigations of hypervelocity impact cratering in ice. Advances in Space Research, 2001, 28, 1521-1526.	1.2	21
33	Genome-Wide Gene-by-Smoking Interaction Study of Chronic Obstructive Pulmonary Disease. American Journal of Epidemiology, 2021, 190, 875-885.	1.6	21
34	Micro-particle impact flux on the timeband capture cell experiment of the Eureca spacecraft. Advances in Space Research, 1996, 17, 193-199.	1.2	16
35	Laboratory investigations of the survivability of bacteria in hypervelocity impacts. Advances in Space Research, 2001, 28, 707-712.	1.2	15
36	Genetic Associations and Architecture of Asthma-COPD Overlap. Chest, 2022, 161, 1155-1166.	0.4	15

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37	Laboratory investigations of the temperature dependence of hypervelocity impact cratering in ice. Advances in Space Research, 2001, 28, 1527-1532.	1.2	12
38	Microscopic and chemical analyses of major impact sites on timeband capture cell experiment of the eureca spacecraft. Advances in Space Research, 1996, 17, 189-192.	1.2	11
39	Human CCL3L1 copy number variation, gene expression, and the role of the CCL3L1-CCR5 axis in lung function. Wellcome Open Research, 2018, 3, 13.	0.9	10
40	Pleiotropic associations of heterozygosity for the SERPINA1 Z allele in the UK Biobank. ERJ Open Research, 2021, 7, 00049-2021.	1.1	10
41	Cohort Profile: Extended Cohort for E-health, Environment and DNA (EXCEED). International Journal of Epidemiology, 2019, 48, 678-679j.	0.9	9
42	Targeted Sequencing of Lung Function Loci in Chronic Obstructive Pulmonary Disease Cases and Controls. PLoS ONE, 2017, 12, e0170222.	1.1	9
43	Genome-wide gene-air pollution interaction analysis of lung function in 300,000 individuals. Environment International, 2022, 159, 107041.	4.8	8
44	Mendelian randomisation of eosinophils and other cell types in relation to lung function and disease. Thorax, 2023, 78, 496-503.	2.7	6
45	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, .	0.7	6
46	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	0.9	4
47	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	0.9	3
48	Genome-wide association study of susceptibility to hospitalised respiratory infections. Wellcome Open Research, 0, 6, 290.	0.9	3
49	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.	1.4	2
50	Rare and low-frequency exonic variants and gene-by-smoking interactions in pulmonary function. Scientific Reports, 2021, 11, 19365.	1.6	2
51	Human CCL3L1 copy number variation, gene expression, and the role of the CCL3L1-CCR5 axis in lung function. Wellcome Open Research, 0, 3, 13.	0.9	1
52	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
53	P040â€…Identification and functional characterisation of a rare MTTP variant underlying hereditary non-alcoholic fatty liver disease. , 2021, , .		0