

Nick Shrine

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8924334/publications.pdf>

Version: 2024-02-01

53
papers

7,014
citations

218592

26
h-index

175177

52
g-index

68
all docs

68
docs citations

68
times ranked

13525
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.	2.7	6
2	Genome-wide gene-air pollution interaction analysis of lung function in 300,000 individuals. Environment International, 2022, 159, 107041.	4.8	8
3	Genetic Associations and Architecture of Asthma-COPD Overlap. Chest, 2022, 161, 1155-1166.	0.4	15
4	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
5	Genome-Wide Gene-by-Smoking Interaction Study of Chronic Obstructive Pulmonary Disease. American Journal of Epidemiology, 2021, 190, 875-885.	1.6	21
6	Pleiotropic associations of heterozygosity for the <i>SERPINA1</i> Z allele in the UK Biobank. ERJ Open Research, 2021, 7, 00049-2021.	1.1	10
7	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
8	Familial hypereosinophilia associated with eosinophilic gastrointestinal symptoms in individuals with a missense mutation in <i>CKLF↞like MARVEL transmembrane domain containing 3</i>. Clinical and Experimental Allergy, 2021, 51, 1501-1504.	1.4	2
9	P040–Identification and functional characterisation of a rare MTTP variant underlying hereditary non-alcoholic fatty liver disease. , 2021, , .		0
10	Rare and low-frequency exonic variants and gene-by-smoking interactions in pulmonary function. Scientific Reports, 2021, 11, 19365.	1.6	2
11	Phenotypic and functional translation of IL33 genetics in asthma. Journal of Allergy and Clinical Immunology, 2021, 147, 144-157.	1.5	29
12	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
13	Interaction of Cigarette Smoking and Polygenic Risk Score on Reduced Lung Function. JAMA Network Open, 2021, 4, e2139525.	2.8	22
14	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
15	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. Nature Communications, 2020, 11, 5182.	5.8	32
16	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
17	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	0.9	3
18	Phenotypic and functional translation of IL1RL1 locus polymorphisms in lung tissue and asthmatic airway epithelium. JCI Insight, 2020, 5, .	2.3	26

#	ARTICLE	IF	CITATIONS
19	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	0.9	4
20	Cohort Profile: Extended Cohort for E-health, Environment and DNA (EXCEED). International Journal of Epidemiology, 2019, 48, 678-679j.	0.9	9
21	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
22	Genetic landscape of chronic obstructive pulmonary disease identifies heterogeneous cell-type and phenotypic associations. Nature Genetics, 2019, 51, 494-505.	9.4	257
23	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
24	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
25	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
26	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
27	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
28	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
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	Age at menarche and lung function: a Mendelian randomization study. European Journal of Epidemiology, 2017, 32, 701-710.	2.5	37
31	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
32	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744.	5.8	64
33	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
34	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. Nature Communications, 2017, 8, 16015.	5.8	149
35	Phenotypic and pharmacogenetic evaluation of patients with thiazide-induced hyponatremia. Journal of Clinical Investigation, 2017, 127, 3367-3374.	3.9	58
36	Targeted Sequencing of Lung Function Loci in Chronic Obstructive Pulmonary Disease Cases and Controls. PLoS ONE, 2017, 12, e0170222.	1.1	9

#	ARTICLE	IF	CITATIONS
37	Genome-wide association study of copy number variation with lung function identifies a novel signal of association near BNP for forced vital capacity. BMC Genetics, 2016, 17, 116.	2.7	0
38	Haplotype estimation for biobank-scale data sets. Nature Genetics, 2016, 48, 817-820.	9.4	192
39	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. Nature Communications, 2015, 6, 8658.	5.8	108
40	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, 2015, 3, 769-781.	5.2	346
41	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
42	Genome-Wide Association Studies Identify <i>CHRNA5/3</i> and <i>HTR4</i> in the Development of Airflow Obstruction. American Journal of Respiratory and Critical Care Medicine, 2012, 186, 622-632.	2.5	164
43	Genome-wide association study to identify genetic determinants of severe asthma. Thorax, 2012, 67, 762-768.	2.7	169
44	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	13.7	1,855
45	A Comprehensive Evaluation of Potential Lung Function Associated Genes in the SpiroMeta General Population Sample. PLoS ONE, 2011, 6, e19382.	1.1	56
46	Velocity Scaling of Impact Craters in Water Ice over the Range 1 to 7.3 km s ⁻¹ . Icarus, 2002, 155, 475-485.	1.1	36
47	Laboratory investigations of the survivability of bacteria in hypervelocity impacts. Advances in Space Research, 2001, 28, 707-712.	1.2	15
48	Laboratory investigations of hypervelocity impact cratering in ice. Advances in Space Research, 2001, 28, 1521-1526.	1.2	21
49	Laboratory investigations of the temperature dependence of hypervelocity impact cratering in ice. Advances in Space Research, 2001, 28, 1527-1532.	1.2	12
50	Microscopic and chemical analyses of major impact sites on timeband capture cell experiment of the eureka spacecraft. Advances in Space Research, 1996, 17, 189-192.	1.2	11
51	Micro-particle impact flux on the timeband capture cell experiment of the Eureka spacecraft. Advances in Space Research, 1996, 17, 193-199.	1.2	16
52	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
53	Genome-wide association study of susceptibility to hospitalised respiratory infections. Wellcome Open Research, 0, 6, 290.	0.9	3