Louise V Wain

List of Publications by Year
in descending order

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	Mendelian randomisation of eosinophils and other cell types in relation to lung function and disease. Thorax, 2023, 78, 496-503.	5.6	6
2	Cluster analysis of transcriptomic datasets to identify endotypes of idiopathic pulmonary fibrosis. Thorax, 2023, 78, 551-558.	5.6	8
3	Genome-wide gene-air pollution interaction analysis of lung function in 300,000 individuals. Environment International, 2022, 159, 107041.	10.0	8
4	Genetic Associations and Architecture of Asthma-COPD Overlap. Chest, 2022, 161, 1155-1166.	0.8	15
5	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
6	Genetic overlap between idiopathic pulmonary fibrosis and COVID-19. European Respiratory Journal, 2022, 60, 2103132.	6.7	22
7	Genome-wide association study across five cohorts identifies five novel loci associated with idiopathic pulmonary fibrosis. Thorax, 2022, 77, 829-833.	5.6	47
8	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
9	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
10	Genome-Wide Gene-by-Smoking Interaction Study of Chronic Obstructive Pulmonary Disease. American Journal of Epidemiology, 2021, 190, 875-885.	3.4	21
11	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
12	Shared genetic etiology between idiopathic pulmonary fibrosis and COVID-19 severity. EBioMedicine, 2021, 65, 103277.	6.1	63
13	Pleiotropic associations of heterozygosity for the SERPINA1 Z allele in the UK Biobank. ERJ Open Research, 2021, 7, 00049-2021.	2.6	10
14	Identification of a missense variant in SPDL1 associated with idiopathic pulmonary fibrosis. Communications Biology, 2021, 4, 392.	4.4	28
15	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
16	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
17	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
18	Genetic correlation and causal relationships between cardio-metabolic traits and lung function impairment. Genome Medicine, 2021, 13, 104.	8.2	11

#	Article	IF	Citations
19	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
20	P040â€…Identification and functional characterisation of a rare MTTP variant underlying hereditary non-alcoholic fatty liver disease. , 2021, , .		0
21	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
22	Phenotypic and functional translation of IL33 genetics in asthma. Journal of Allergy and Clinical Immunology, 2021, 147, 144-157.	2.9	29
23	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
24	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
25	Interaction of Cigarette Smoking and Polygenic Risk Score on Reduced Lung Function. JAMA Network Open, 2021, 4, e2139525.	5.9	22
26	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
27	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
28	Defining genetic risk factors for scleroderma-associated interstitial lung disease. Clinical Rheumatology, 2020, 39, 1173-1179.	2.2	12
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	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
31	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
32	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	1.8	3
33	Phenotypic and functional translation of IL1RL1 locus polymorphisms in lung tissue and asthmatic airway epithelium. JCI Insight, 2020, 5, .	5.0	26
34	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	1.8	4
35	Cohort Profile: Extended Cohort for E-health, Environment and DNA (EXCEED). International Journal of Epidemiology, 2019, 48, 678-679j.	1.9	9
36	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

#	Article	IF	Citations
37	Uganda Genome Resource Enables Insights into Population History and Genomic Discovery in Africa. Cell, 2019, 179, 984-1002.e36.	28.9	152
38	Translational genomics and precision medicine: Moving from the lab to the clinic. Science, 2019, 365, 1409-1413.	12.6	133
39	Novel idiopathic pulmonary fibrosis susceptibility variants revealed by deepÂsequencing. ERJ Open Research, 2019, 5, 00071-2019.	2.6	24
40	Adjustment for index event bias in genome-wide association studies of subsequent events. Nature Communications, 2019, 10, 1561.	12.8	87
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	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
45	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. Nature Genetics, 2019, 51, 51-62.	21.4	328
46	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
47	Formalising recall by genotype as an efficient approach to detailed phenotyping and causal inference. Nature Communications, 2018, 9, 711.	12.8	54
48	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
49	ERS International Congress 2018: highlights from best-abstract awardees. Breathe, 2018, 14, e137-e142.	1.3	0
50	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
51	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
52	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
53	The vitamin D binding protein axis modifies disease severity in lymphangioleiomyomatosis. European Respiratory Journal, 2018, 52, 1800951.	6.7	13
54	Identification of susceptibility pathways for the role of chromosome 15q25.1 in modifying lung cancer risk. Nature Communications, 2018, 9, 3221.	12.8	60

#	Article	IF	Citations
55	Towards genetic reclassification of idiopathic pulmonary fibrosis. Lancet Respiratory Medicine,the, 2018, 6, 569-570.	10.7	1
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	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. International Journal of Epidemiology, 2017, 46, dyw318.	1.9	36
58	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
59	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
60	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
61	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
62	Age at menarche and lung function: a Mendelian randomization study. European Journal of Epidemiology, 2017, 32, 701-710.	5.7	37
63	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
64	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
65	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744.	12.8	64
66	New Blood Pressureâ€“Associated Loci Identified in Meta-Analyses of 475â€‰000 Individuals. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	48
67	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
68	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. Nature Communications, 2017, 8, 16015.	12.8	149
69	Phenotypic and pharmacogenetic evaluation of patients with thiazide-induced hyponatremia. Journal of Clinical Investigation, 2017, 127, 3367-3374.	8.2	58
70	Targeted Sequencing of Lung Function Loci in Chronic Obstructive Pulmonary Disease Cases and Controls. PLoS ONE, 2017, 12, e0170222.	2.5	9
71	Recurrent mutation at the classical haptoglobin structural polymorphism. Nature Genetics, 2016, 48, 347-348.	21.4	4
72	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

#	Article	IF	Citations
73	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	21.4	261
74	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
75	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
76	Haplotype estimation for biobank-scale data sets. Nature Genetics, 2016, 48, 817-820.	21.4	192
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	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
79	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. Nature Communications, 2015, 6, 8658.	12.8	108
80	Molecular mechanisms underlying variations in lung function: a systems genetics analysis. Lancet Respiratory Medicine,the, 2015, 3, 782-795.	10.7	66
81	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
82	Integrative pathway genomics of lung function and airflow obstruction. Human Molecular Genetics, 2015, 24, 6836-6848.	2.9	28
83	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	27.8	1,014
84	Large-Scale Genome-Wide Association Studies and Meta-Analyses of Longitudinal Change in Adult Lung Function. PLoS ONE, 2014, 9, e100776.	2.5	52
85	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
86	Detection of mutations in KLHL3 and CUL3 in families with FHHt (familial hyperkalaemic) Tj ETQq0 0 0 rgBT /Overlock 10 T	4.3	49
87	Blood Pressure Genetics and Hypertension: Genome-Wide Analysis and Role of Ancestry. Current Genetic Medicine Reports, 2014, 2, 13-22.	1.9	3
88	Rare variants and cardiovascular disease. Briefings in Functional Genomics, 2014, 13, 384-391.	2.7	12
89	Genome-wide association analysis identifies six new loci associated with forced vital capacity. Nature Genetics, 2014, 46, 669-677.	21.4	131
90	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

#	Article	IF	Citations
91	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
92	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
93	GSTCD and INTS12 Regulation and Expression in the Human Lung. PLoS ONE, 2013, 8, e74630.	2.5	46
94	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
95	Genome-wide association studies in lung disease: Figure 1. Thorax, 2012, 67, 271-273.	5.6	16
96	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
97	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
98	Genome-wide association study to identify genetic determinants of severe asthma. Thorax, 2012, 67, 762-768.	5.6	169
99	What can genetics tell us about the cause of fixed airflow obstruction?. Clinical and Experimental Allergy, 2012, 42, 1176-1182.	2.9	7
100	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	27.8	1,855
101	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
102	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
103	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	21.4	403
104	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. Nature Genetics, 2011, 43, 1082-1090.	21.4	367
105	Copy Number Variation. Methods in Molecular Biology, 2011, 713, 167-183.	0.9	3
106	A Comprehensive Evaluation of Potential Lung Function Associated Genes in the SpiroMeta General Population Sample. PLoS ONE, 2011, 6, e19382.	2.5	56
107	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
108	Genome-wide association study identifies five loci associated with lung function. Nature Genetics, 2010, 42, 36-44.	21.4	518

#	Article	IF	Citations
109	A large genome scan for rare CNVs in amyotrophic lateral sclerosis. Human Molecular Genetics, 2010, 19, 4091-4099.	2.9	51
110	Genome-wide association study identifies eight loci associated with blood pressure. Nature Genetics, 2009, 41, 666-676.	21.4	1,104
111	Genomic copy number variation, human health, and disease. Lancet, The, 2009, 374, 340-350.	13.7	172
112	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
113	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
114	Common Variation in the WNK1 Gene and Blood Pressure in Childhood. Hypertension, 2008, 52, 974-979.	2.7	32
115	Adaptation of HIV-1 to Its Human Host. Molecular Biology and Evolution, 2007, 24, 1853-1860.	8.9	100
116	Evolutionary origins of diversity in human viruses. , 2007, , 169-184.		2
117	Chimpanzee Reservoirs of Pandemic and Nonpandemic HIV-1. Science, 2006, 313, 523-526.	12.6	723
118	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	1.8	11
119	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	1.8	1
120	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
121	Genome-wide association study of susceptibility to hospitalised respiratory infections. Wellcome Open Research, 0, 6, 290.	1.8	3
122	Extended Cohort for E-health, Environment and DNA (EXCEED) COVID-19 focus. Wellcome Open Research, 0, 6, 349.	1.8	2