Ian Sayers

List of Publications by Year in descending order

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#	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	Genetics of Asthma: Insights From Genome Wide Association Studies. , 2022, , 308-325.		1
3	Human bronchial epithelial cells from patients with asthma have an altered gene expression profile. ERJ Open Research, 2022, 8, 00625-2021.	1.1	2
4	Genetic Associations and Architecture of Asthma-COPD Overlap. Chest, 2022, 161, 1155-1166.	0.4	15
5	Extended lifespan of bronchial epithelial cells maintains normal cellular phenotype and transcriptome integrity. ERJ Open Research, 2021, 7, 00254-2020.	1.1	Ο
6	Purinergic Receptors in the Airways: Potential Therapeutic Targets for Asthma?. Frontiers in Allergy, 2021, 2, 677677.	1.2	8
7	Functional genomics of GPR126 in airway smooth muscle and bronchial epithelial cells. FASEB Journal, 2021, 35, e21300.	0.2	7
8	Phenotypic and functional translation of IL33 genetics in asthma. Journal of Allergy and Clinical Immunology, 2021, 147, 144-157.	1.5	29
9	Translational Analysis of Moderate to Severe Asthma GWAS Signals Into Candidate Causal Genes and Their Functional, Tissue-Dependent and Disease-Related Associations. Frontiers in Allergy, 2021, 2, 738741.	1.2	3
10	Genome-Wide Association Study of Susceptibility to Idiopathic Pulmonary Fibrosis. American Journal of Respiratory and Critical Care Medicine, 2020, 201, 564-574.	2.5	208
11	Epithelial cell dysfunction, a major driver of asthma development. Allergy: European Journal of Allergy and Clinical Immunology, 2020, 75, 1902-1917.	2.7	151
12	Proinflammatory Effects in <i>Ex Vivo</i> Human Lung Tissue of Respirable Smoke Extracts from Indoor Cooking in Nepal. Annals of the American Thoracic Society, 2020, 17, 688-698.	1.5	8
13	Phenotypic and functional translation of IL1RL1 locus polymorphisms in lung tissue and asthmatic airway epithelium. JCI Insight, 2020, 5, .	2.3	26
14	Defining a role for lung function associated gene GSTCD in cell homeostasis. Respiratory Research, 2019, 20, 172.	1.4	5
15	Exposure to lipopolysaccharide (LPS) reduces contractile response of small airways from GSTCD-/- mice. PLoS ONE, 2019, 14, e0221899.	1.1	1
16	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
17	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
18	Genetic risk factors for the development of pulmonary disease identified by genomeâ€wide association. Respirology, 2019, 24, 204-214.	1.3	44

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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.	9.4	257
20	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
21	Lung function associated gene Integrator Complex subunit 12 regulates protein synthesis pathways. BMC Genomics, 2017, 18, 248.	1.2	15
22	Defining the inflammatory signature of human lung explant tissue in the presence and absence of glucocorticoid. F1000Research, 2017, 6, 460.	0.8	11
23	Targeted Sequencing of Lung Function Loci in Chronic Obstructive Pulmonary Disease Cases and Controls. PLoS ONE, 2017, 12, e0170222.	1.1	9
24	Urokinase plasminogen activator receptor polymorphisms and airway remodelling in asthma. European Respiratory Journal, 2016, 47, 1568-1571.	3.1	7
25	The differential effects of azithromycin on the airway epithelium inÂvitro and inÂvivo. Physiological Reports, 2016, 4, e12960.	0.7	20
26	Traditional and emerging indicators of cardiovascular risk in chronic obstructive pulmonary disease. Chronic Respiratory Disease, 2016, 13, 247-255.	1.0	10
27	Exome-wide analysis of rare coding variation identifies novel associations with COPD and airflow limitation in <i>MOCS3</i> , <i>IFIT3</i> and <i>SERPINA12</i> . Thorax, 2016, 71, 501-509.	2.7	22
28	The Ser82 RAGE Variant Affects Lung Function and Serum RAGE in Smokers and sRAGE Production In Vitro. PLoS ONE, 2016, 11, e0164041.	1.1	34
29	Cigarette Smoke and the Induction of Urokinase Plasminogen Activator ReceptorIn Vivo: Selective Contribution of Isoforms to Bronchial Epithelial Phenotype. American Journal of Respiratory Cell and Molecular Biology, 2015, 53, 174-183.	1.4	6
30	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. Nature Communications, 2015, 6, 8658.	5.8	108
31	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
32	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
33	The impact of azithromycin therapy on the airway microbiota in asthma. Thorax, 2014, 69, 673-674.	2.7	71
34	Genome-wide association analysis identifies six new loci associated with forced vital capacity. Nature Genetics, 2014, 46, 669-677.	9.4	131
35	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.	1.1	11
36	A tailored approach to asthma management: Arg16 holds the key?. Clinical Science, 2013, 124, 517-519.	1.8	6

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37	GSTCD and INTS12 Regulation and Expression in the Human Lung. PLoS ONE, 2013, 8, e74630.	1.1	46
38	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.	2.5	128
39	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. Nature Genetics, 2011, 43, 1082-1090.	9.4	367
40	Genome-wide association study identifies five loci associated with lung function. Nature Genetics, 2010, 42, 36-44.	9.4	518