Michael A Portelli

List of Publications by Year
in descending order

28 papers	792 citations	1039880 9 h-index	1199470 12 g-index
32 all docs	32 docs citations	32 times ranked	2276 citing authors

#	Article	IF	Citations
1	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
2	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
3	Genetic risk factors for the development of allergic disease identified by genomeâ€wide association. Clinical and Experimental Allergy, 2015, 45, 21-31.	1.4	158
4	Genetic basis for personalized medicine in asthma. Expert Review of Respiratory Medicine, 2012, 6, 223-236.	1.0	39
5	Genomeâ€wide protein QTL mapping identifies human plasma kallikrein as a postâ€translational regulator of serum uPAR levels. FASEB Journal, 2014, 28, 923-934.	0.2	29
6	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
7	Phenotypic and functional translation of IL33 genetics in asthma. Journal of Allergy and Clinical Immunology, 2021, 147, 144-157.	1.5	29
8	Phenotypic and functional translation of IL1RL1 locus polymorphisms in lung tissue and asthmatic airway epithelium. JCI Insight, 2020, 5, .	2.3	26
9	Airway and peripheral urokinase plasminogen activator receptor is elevated in asthma, and identifies a severe, nonatopic subset of patients. Allergy: European Journal of Allergy and Clinical Immunology, 2017, 72, 473-482.	2.7	18
10	Urokinase plasminogen activator receptor polymorphisms and airway remodelling in asthma. European Respiratory Journal, 2016, 47, 1568-1571.	3.1	7
11	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
12	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
13	Human bronchial epithelial cells from patients with asthma have an altered gene expression profile. ERJ Open Research, 2022, 8, 00625-2021.	1.1	2
14	Genetics of Asthma: Insights From Genome Wide Association Studies. , 2022, , 308-325.		1
15	IL33 receptor activation is IL33 isoform and receptor genotype specific. , 2019, , .		1
16	Investigating Soluble Cleaved Upar As A Biomarker For COPD. , 2011, , .		0
17	GWAS Identifies That A Human Plasma Kallikrein Single Nucleotide Polymorphism Regulates Serum PLAUR Levels In Asthma And COPD. , 2012, , .		0
18	Cigarette Smoke Modulates PLAUR Expression In Bronchial Epithelial Cells Via A 3`UTR Mechanism. , 2012, , .		0

#	Article	IF	Citations
19	Letters to the Editor. FASEB Journal, 2015, 29, 4758-4759.	0.2	0
20	Functional Translation of IL33 Locus Polymorphisms Into Altered Epithelial Cell Function Underlying Asthma. , 2019, , .		0
21	Extended lifespan of bronchial epithelial cells maintains normal cellular phenotype and transcriptome integrity. ERJ Open Research, 2021, 7, 00254-2020.	1.1	0
22	Urokinase plasminogen activator receptor variants drive distinct phenotypes in the bronchial epithelium. , 2015, , .		0
23	Differential expression of uPAR in cultured bronchial epithelial cells from asthma patients. , 2015, , .		0
24	A Genome Wide Association Study of Moderate-Severe Asthma in subjects from the United Kingdom. , 2017, , .		0
25	Using transcriptomics to understand the potential functions of lung function associated gene, GPR126 in human airway smooth muscle cells. , 2019, , .		0
26	Type 2 cytokines and biomarkers in asthma patient sera show coordinated expression and identify patient subsets. , 2019, , .		0
27	Investigating the effects of interleukin-33 on rhinovirus A induced changes in asthmatic bronchial epithelial cells. , 2020, , .		0
28	Rhinovirus & IL33 driven HBEC gene signatures are disease & IL1RL1 polymorphism dependent. , 2020, , .		0