Jarrett D Morrow

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Blood RNA sequencing shows overlapping gene expression across COPD phenotype domains. Thorax, 2022, 77, 115-122.	2.7	6
2	An interferon-inducible signature of airway disease from blood gene expression profiling. European Respiratory Journal, 2022, 59, 2100569.	3.1	4
3	Protein interaction networks provide insight into fetal origins of chronic obstructive pulmonary disease. Respiratory Research, 2022, 23, 69.	1.4	7
4	Lung tissue shows divergent gene expression between chronic obstructive pulmonary disease and idiopathic pulmonary fibrosis. Respiratory Research, 2022, 23, 97.	1.4	7
5	Sex-specific associations with DNA methylation in lung tissue demonstrate smoking interactions. Epigenetics, 2021, 16, 692-703.	1.3	20
6	DNA methylation perturbations may link altered development and aging in the lung. Aging, 2021, 13, 1742-1764.	1.4	6
7	Peripheral blood microbial signatures in current and former smokers. Scientific Reports, 2021, 11, 19875.	1.6	6
8	Heme metabolism genes Downregulated in COPD Cachexia. Respiratory Research, 2020, 21, 100.	1.4	4
9	Genome-Wide Association Study: Functional Variant rs2076295 Regulates Desmoplakin Expression in Airway Epithelial Cells. American Journal of Respiratory and Critical Care Medicine, 2020, 202, 1225-1236.	2.5	20
10	Integrated transcriptomic correlation network analysis identifies COPD molecular determinants. Scientific Reports, 2020, 10, 3361.	1.6	35
11	DNA Methylation Is Predictive of Mortality in Current and Former Smokers. American Journal of Respiratory and Critical Care Medicine, 2020, 201, 1099-1109.	2.5	15
12	RNA-sequencing across three matched tissues reveals shared and tissue-specific gene expression and pathway signatures of COPD. Respiratory Research, 2019, 20, 65.	1.4	43
13	Genetic landscape of chronic obstructive pulmonary disease identifies heterogeneous cell-type and phenotype associations. Nature Genetics, 2019, 51, 494-505.	9.4	257
14	Do sputum or circulating blood samples reflect the pulmonary transcriptomic differences of COPD patients? A multi-tissue transcriptomic network META-analysis. Respiratory Research, 2019, 20, 5.	1.4	9
15	Human Lung DNA Methylation Quantitative Trait Loci Colocalize with Chronic Obstructive Pulmonary Disease Genome-Wide Association Loci. American Journal of Respiratory and Critical Care Medicine, 2018, 197, 1275-1284.	2.5	56
16	Integrative genomics identifies new genes associated with severe COPD and emphysema. Respiratory Research, 2018, 19, 46.	1.4	20
17	Ensemble genomic analysis in human lung tissue identifies novel genes for chronic obstructive pulmonary disease. Human Genomics, 2018, 12, 1.	1.4	35
18	Functional interactors of three genome-wide association study genes are differentially expressed in severe chronic obstructive pulmonary disease lung tissue. Scientific Reports, 2017, 7, 44232.	1.6	76

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19	Meta-analysis of peripheral blood gene expression modules for COPD phenotypes. PLoS ONE, 2017, 12, e0185682.	1.1	17
20	The Role of Vitamin D in the Transcriptional Program of Human Pregnancy. PLoS ONE, 2016, 11, e0163832.	1.1	34
21	Differential DNA methylation marks and gene comethylation of COPD in African-Americans with COPD exacerbations. Respiratory Research, 2016, 17, 143.	1.4	54
22	DNA methylation profiling in human lung tissue identifies genes associated with COPD. Epigenetics, 2016, 11, 730-739.	1.3	73
23	Exome Array Analysis Identifies a Common Variant in <i>IL27</i> Associated with Chronic Obstructive Pulmonary Disease. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 48-57.	2.5	52
24	Genome-wide site-specific differential methylation in the blood of individuals with Klinefelter syndrome. Molecular Reproduction and Development, 2015, 82, 377-386.	1.0	29
25	The impact of genetic variation and cigarette smoke on DNA methylation in current and former smokers from the COPDGene study. Epigenetics, 2015, 10, 1064-1073.	1.3	31
26	Smoking-Associated Site-Specific Differential Methylation in Buccal Mucosa in the COPDGene Study. American Journal of Respiratory Cell and Molecular Biology, 2015, 53, 246-254.	1.4	49
27	Identifying a gene expression signature of frequent COPD exacerbations in peripheral blood using network methods. BMC Medical Genomics, 2015, 8, 1.	0.7	78
28	A Comparative Study of Tests for Homogeneity of Variances with Application to DNA Methylation Data. PLoS ONE, 2015, 10, e0145295.	1.1	16
29	CallSim: Evaluation of Base Calls Using Sequencing Simulation. , 2012, 2012, 1-10.		0