

Jarrett D Morrow

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

1,062
citations

516561

16
h-index

501076

28
g-index

33
all docs

33
docs citations

33
times ranked

2463
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic landscape of chronic obstructive pulmonary disease identifies heterogeneous cell-type and phenotype associations. <i>Nature Genetics</i> , 2019, 51, 494-505.	9.4	257
2	Identifying a gene expression signature of frequent COPD exacerbations in peripheral blood using network methods. <i>BMC Medical Genomics</i> , 2015, 8, 1.	0.7	78
3	Functional interactors of three genome-wide association study genes are differentially expressed in severe chronic obstructive pulmonary disease lung tissue. <i>Scientific Reports</i> , 2017, 7, 44232.	1.6	76
4	DNA methylation profiling in human lung tissue identifies genes associated with COPD. <i>Epigenetics</i> , 2016, 11, 730-739.	1.3	73
5	Human Lung DNA Methylation Quantitative Trait Loci Colocalize with Chronic Obstructive Pulmonary Disease Genome-Wide Association Loci. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018, 197, 1275-1284.	2.5	56
6	Differential DNA methylation marks and gene comethylation of COPD in African-Americans with COPD exacerbations. <i>Respiratory Research</i> , 2016, 17, 143.	1.4	54
7	Exome Array Analysis Identifies a Common Variant in <i>IL27</i> Associated with Chronic Obstructive Pulmonary Disease. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016, 194, 48-57.	2.5	52
8	Smoking-Associated Site-Specific Differential Methylation in Buccal Mucosa in the COPD Gene Study. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2015, 53, 246-254.	1.4	49
9	RNA-sequencing across three matched tissues reveals shared and tissue-specific gene expression and pathway signatures of COPD. <i>Respiratory Research</i> , 2019, 20, 65.	1.4	43
10	Ensemble genomic analysis in human lung tissue identifies novel genes for chronic obstructive pulmonary disease. <i>Human Genomics</i> , 2018, 12, 1.	1.4	35
11	Integrated transcriptomic correlation network analysis identifies COPD molecular determinants. <i>Scientific Reports</i> , 2020, 10, 3361.	1.6	35
12	The Role of Vitamin D in the Transcriptional Program of Human Pregnancy. <i>PLoS ONE</i> , 2016, 11, e0163832.	1.1	34
13	The impact of genetic variation and cigarette smoke on DNA methylation in current and former smokers from the COPD Gene study. <i>Epigenetics</i> , 2015, 10, 1064-1073.	1.3	31
14	Genome-wide site-specific differential methylation in the blood of individuals with Klinefelter syndrome. <i>Molecular Reproduction and Development</i> , 2015, 82, 377-386.	1.0	29
15	Integrative genomics identifies new genes associated with severe COPD and emphysema. <i>Respiratory Research</i> , 2018, 19, 46.	1.4	20
16	Genome-Wide Association Study: Functional Variant rs2076295 Regulates Desmoplakin Expression in Airway Epithelial Cells. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 202, 1225-1236.	2.5	20
17	Sex-specific associations with DNA methylation in lung tissue demonstrate smoking interactions. <i>Epigenetics</i> , 2021, 16, 692-703.	1.3	20
18	Meta-analysis of peripheral blood gene expression modules for COPD phenotypes. <i>PLoS ONE</i> , 2017, 12, e0185682.	1.1	17

#	ARTICLE	IF	CITATIONS
19	A Comparative Study of Tests for Homogeneity of Variances with Application to DNA Methylation Data. PLoS ONE, 2015, 10, e0145295.	1.1	16
20	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
21	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
22	Protein interaction networks provide insight into fetal origins of chronic obstructive pulmonary disease. Respiratory Research, 2022, 23, 69.	1.4	7
23	Lung tissue shows divergent gene expression between chronic obstructive pulmonary disease and idiopathic pulmonary fibrosis. Respiratory Research, 2022, 23, 97.	1.4	7
24	DNA methylation perturbations may link altered development and aging in the lung. Aging, 2021, 13, 1742-1764.	1.4	6
25	Blood RNA sequencing shows overlapping gene expression across COPD phenotype domains. Thorax, 2022, 77, 115-122.	2.7	6
26	Peripheral blood microbial signatures in current and former smokers. Scientific Reports, 2021, 11, 19875.	1.6	6
27	Heme metabolism genes Downregulated in COPD Cachexia. Respiratory Research, 2020, 21, 100.	1.4	4
28	An interferon-inducible signature of airway disease from blood gene expression profiling. European Respiratory Journal, 2022, 59, 2100569.	3.1	4
29	CallSim: Evaluation of Base Calls Using Sequencing Simulation. , 2012, 2012, 1-10.		0