

Ma'en Obeidat

List of Publications by Year in descending order

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Version: 2024-02-01

79
papers

5,378
citations

172457

29
h-index

95266

68
g-index

92
all docs

92
docs citations

92
times ranked

9714
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide association study identifies five loci associated with lung function. <i>Nature Genetics</i> , 2010, 42, 36-44.	21.4	518
2	Large-scale association analysis identifies new lung cancer susceptibility loci and heterogeneity in genetic susceptibility across histological subtypes. <i>Nature Genetics</i> , 2017, 49, 1126-1132.	21.4	472
3	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. <i>Nature Genetics</i> , 2011, 43, 1082-1090.	21.4	367
4	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. <i>Nature Genetics</i> , 2019, 51, 481-493.	21.4	350
5	Novel insights into the genetics of smoking behaviour, lung function, and chronic obstructive pulmonary disease (UK BiLEVE): a genetic association study in UK Biobank. <i>Lancet Respiratory Medicine</i> , 2015, 3, 769-781.	10.7	346
6	Genome-wide association analyses for lung function and chronic obstructive pulmonary disease identify new loci and potential druggable targets. <i>Nature Genetics</i> , 2017, 49, 416-425.	21.4	257
7	Genetic landscape of chronic obstructive pulmonary disease identifies heterogeneous cell-type and phenotype associations. <i>Nature Genetics</i> , 2019, 51, 494-505.	21.4	257
8	Genetic variants associated with susceptibility to idiopathic pulmonary fibrosis in people of European ancestry: a genome-wide association study. <i>Lancet Respiratory Medicine</i> , 2017, 5, 869-880.	10.7	233
9	Genome-Wide Association Study of Susceptibility to Idiopathic Pulmonary Fibrosis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 201, 564-574.	5.6	208
10	Identification of <i>TMPRSS2</i> as a Susceptibility Gene for Severe 2009 Pandemic A(H1N1) Influenza and A(H7N9) Influenza. <i>Journal of Infectious Diseases</i> , 2015, 212, 1214-1221.	4.0	170
11	Total Airway Count on Computed Tomography and the Risk of Chronic Obstructive Pulmonary Disease Progression. Findings from a Population-based Study. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018, 197, 56-65.	5.6	147
12	Genome-Wide Joint Meta-Analysis of SNP and SNP-by-Smoking Interaction Identifies Novel Loci for Pulmonary Function. <i>PLoS Genetics</i> , 2012, 8, e1003098.	3.5	130
13	Effect of Five Genetic Variants Associated with Lung Function on the Risk of Chronic Obstructive Lung Disease, and Their Joint Effects on Lung Function. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2011, 184, 786-795.	5.6	128
14	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. <i>Nature Communications</i> , 2015, 6, 8658.	12.8	108
15	Genome-Wide Interaction Analysis of Air Pollution Exposure and Childhood Asthma with Functional Follow-up. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2017, 195, 1373-1383.	5.6	107
16	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. <i>Cancer Research</i> , 2016, 76, 5103-5114.	0.9	100
17	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. <i>Nature Communications</i> , 2018, 9, 2976.	12.8	85
18	BMI is associated with FEV1 decline in chronic obstructive pulmonary disease: a meta-analysis of clinical trials. <i>Respiratory Research</i> , 2019, 20, 236.	3.6	72

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19	Chronic obstructive pulmonary disease and related phenotypes: polygenic risk scores in population-based and case-control cohorts. <i>Lancet Respiratory Medicine</i> , 2020, 8, 696-708.	10.7	69
20	Molecular mechanisms underlying variations in lung function: a systems genetics analysis. <i>Lancet Respiratory Medicine</i> , 2015, 3, 782-795.	10.7	66
21	Identification of susceptibility pathways for the role of chromosome 15q25.1 in modifying lung cancer risk. <i>Nature Communications</i> , 2018, 9, 3221.	12.8	60
22	A Comprehensive Evaluation of Potential Lung Function Associated Genes in the SpiroMeta General Population Sample. <i>PLoS ONE</i> , 2011, 6, e19382.	2.5	56
23	GSTCD and INTS12 Regulation and Expression in the Human Lung. <i>PLoS ONE</i> , 2013, 8, e74630.	2.5	46
24	Surfactant protein D is a causal risk factor for COPD: results of Mendelian randomisation. <i>European Respiratory Journal</i> , 2017, 50, 1700657.	6.7	45
25	Causal and Synthetic Associations of Variants in the SERPINA Gene Cluster with Alpha1-antitrypsin Serum Levels. <i>PLoS Genetics</i> , 2013, 9, e1003585.	3.5	43
26	Functional variants regulating LGALS1 (Galectin 1) expression affect human susceptibility to influenza A(H7N9). <i>Scientific Reports</i> , 2015, 5, 8517.	3.3	43
27	Leveraging lung tissue transcriptome to uncover candidate causal genes in COPD genetic associations. <i>Human Molecular Genetics</i> , 2018, 27, 1819-1829.	2.9	37
28	Introduction to precision medicine in COPD. <i>European Respiratory Journal</i> , 2019, 53, 1802460.	6.7	37
29	Gene expression analysis in asthma using a targeted multiplex array. <i>BMC Pulmonary Medicine</i> , 2017, 17, 189.	2.0	36
30	The Ser82 RAGE Variant Affects Lung Function and Serum RAGE in Smokers and sRAGE Production In Vitro. <i>PLoS ONE</i> , 2016, 11, e0164041.	2.5	34
31	Transcriptome-wide association study reveals candidate causal genes for lung cancer. <i>International Journal of Cancer</i> , 2020, 146, 1862-1878.	5.1	33
32	Network-based analysis reveals novel gene signatures in peripheral blood of patients with chronic obstructive pulmonary disease. <i>Respiratory Research</i> , 2017, 18, 72.	3.6	31
33	Protein-altering germline mutations implicate novel genes related to lung cancer development. <i>Nature Communications</i> , 2020, 11, 2220.	12.8	31
34	Whole Exome Re-Sequencing Implicates CCDC38 and Cilia Structure and Function in Resistance to Smoking Related Airflow Obstruction. <i>PLoS Genetics</i> , 2014, 10, e1004314.	3.5	29
35	Hedgehog signaling in the airway epithelium of patients with chronic obstructive pulmonary disease. <i>Scientific Reports</i> , 2019, 9, 3353.	3.3	29
36	Phenotypic and functional translation of IL33 genetics in asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 147, 144-157.	2.9	29

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37	Integrative pathway genomics of lung function and airflow obstruction. <i>Human Molecular Genetics</i> , 2015, 24, 6836-6848.	2.9	28
38	Airway Epithelial Expression Quantitative Trait Loci Reveal Genes Underlying Asthma and Other Airway Diseases. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2016, 54, 177-187.	2.9	28
39	Integrative Genomics of Emphysema-Associated Genes Reveals Potential Disease Biomarkers. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2017, 57, 411-418.	2.9	28
40	Responsiveness to Ipratropium Bromide in Male and Female Patients with Mild to Moderate Chronic Obstructive Pulmonary Disease. <i>EBioMedicine</i> , 2017, 19, 139-145.	6.1	27
41	Susceptibility to Chronic Mucus Hypersecretion, a Genome Wide Association Study. <i>PLoS ONE</i> , 2014, 9, e91621.	2.5	25
42	COPD GWAS variant at 19q13.2 in relation with DNA methylation and gene expression. <i>Human Molecular Genetics</i> , 2018, 27, 396-405.	2.9	24
43	Macrophages with reduced expressions of classical M1 and M2 surface markers in human bronchoalveolar lavage fluid exhibit pro-inflammatory gene signatures. <i>Scientific Reports</i> , 2021, 11, 8282.	3.3	24
44	Polymorphisms Associated with Expression of BPIFA1/BPIFB1 and Lung Disease Severity in Cystic Fibrosis. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2015, 53, 607-614.	2.9	23
45	Immune-mediated genetic pathways resulting in pulmonary function impairment increase lung cancer susceptibility. <i>Nature Communications</i> , 2020, 11, 27.	12.8	23
46	Understanding the role of the chromosome 15q25.1 in COPD through epigenetics and transcriptomics. <i>European Journal of Human Genetics</i> , 2018, 26, 709-722.	2.8	21
47	Occurrence of Accelerated Epigenetic Aging and Methylation Disruptions in Human Immunodeficiency Virus Infection Before Antiretroviral Therapy. <i>Journal of Infectious Diseases</i> , 2021, 223, 1681-1689.	4.0	19
48	Genome-wide association meta-analysis identifies pleiotropic risk loci for aerodigestive squamous cell cancers. <i>PLoS Genetics</i> , 2021, 17, e1009254.	3.5	19
49	Meta-analysis of exome array data identifies six novel genetic loci for lung function. <i>Wellcome Open Research</i> , 2018, 3, 4.	1.8	19
50	The Effect of Different Case Definitions of Current Smoking on the Discovery of Smoking-Related Blood Gene Expression Signatures in Chronic Obstructive Pulmonary Disease. <i>Nicotine and Tobacco Research</i> , 2016, 18, 1903-1909.	2.6	18
51	The Overlap of Lung Tissue Transcriptome of Smoke Exposed Mice with Human Smoking and COPD. <i>Scientific Reports</i> , 2018, 8, 11881.	3.3	18
52	Genes related to emphysema are enriched for ubiquitination pathways. <i>BMC Pulmonary Medicine</i> , 2014, 14, 187.	2.0	17
53	The Effect of Statins on Blood Gene Expression in COPD. <i>PLoS ONE</i> , 2015, 10, e0140022.	2.5	16
54	Aryl hydrocarbon receptor deficiency causes the development of chronic obstructive pulmonary disease through the integration of multiple pathogenic mechanisms. <i>FASEB Journal</i> , 2021, 35, e21376.	0.5	15

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55	The pharmacogenomics of inhaled corticosteroids and lung function decline in COPD. <i>European Respiratory Journal</i> , 2019, 54, 1900521.	6.7	14
56	Latrophilin receptors: novel bronchodilator targets in asthma. <i>Thorax</i> , 2017, 72, 74-82.	5.6	12
57	Widespread Sexual Dimorphism in the Transcriptome of Human Airway Epithelium in Response to Smoking. <i>Scientific Reports</i> , 2019, 9, 17600.	3.3	12
58	Informed Genome-Wide Association Analysis With Family History As a Secondary Phenotype Identifies Novel Loci of Lung Cancer. <i>Genetic Epidemiology</i> , 2015, 39, 197-206.	1.3	11
59	The Well-Known Gene <i>HHIP</i> and Novel Gene <i>MECR</i> Are Implicated in Small Airway Obstruction. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016, 194, 1299-1302.	5.6	11
60	Identification of Drug Candidates to Suppress Cigarette Smoke-induced Inflammation via Connectivity Map Analyses. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2018, 58, 727-735.	2.9	11
61	The genetics of smoking in individuals with chronic obstructive pulmonary disease. <i>Respiratory Research</i> , 2018, 19, 59.	3.6	11
62	Meta-analysis of exome array data identifies six novel genetic loci for lung function. <i>Wellcome Open Research</i> , 0, 3, 4.	1.8	11
63	Genetics of complex respiratory diseases: implications for pathophysiology and pharmacology studies. <i>British Journal of Pharmacology</i> , 2011, 163, 96-105.	5.4	10
64	Total particulate matter concentration skews cigarette smoke's gene expression profile. <i>ERJ Open Research</i> , 2016, 2, 00029-2016.	2.6	10
65	Lung cancer susceptibility genetic variants modulate <i>HOXB2</i> expression in the lung. <i>International Journal of Developmental Biology</i> , 2018, 62, 857-864.	0.6	8
66	Differential lung tissue gene expression in males and females: implications for the susceptibility to develop COPD. <i>European Respiratory Journal</i> , 2019, 54, 1702567.	6.7	8
67	Genetic regulation of gene expression of MIF family members in lung tissue. <i>Scientific Reports</i> , 2020, 10, 16980.	3.3	8
68	Precision health: treating the individual patient with chronic obstructive pulmonary disease. <i>Medical Journal of Australia</i> , 2019, 210, 424-428.	1.7	6
69	Impact of Statins on Gene Expression in Human Lung Tissues. <i>PLoS ONE</i> , 2015, 10, e0142037.	2.5	4
70	Variants associated with <i>HHIP</i> expression have sex-differential effects on lung function. <i>Wellcome Open Research</i> , 2020, 5, 111.	1.8	4
71	Variants associated with <i>HHIP</i> expression have sex-differential effects on lung function. <i>Wellcome Open Research</i> , 2020, 5, 111.	1.8	3
72	MA03.09 Transcriptome-Wide Association Study Reveals Candidate Causal Genes for Lung Cancer. <i>Journal of Thoracic Oncology</i> , 2018, 13, S365.	1.1	1

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73	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	1.8	1
74	GDF11: a fountain of youth for the ageing COPD lung?. Thorax, 2017, 72, 874-875.	5.6	0
75	The Causal Effect of Body Mass Index on Mortality in COPD: Investigating the "Obesity Paradox" Using Non-Linear Mendelian Randomization. , 2020, , .		0
76	Integrative -Omics Identify Potential Biomarkers and Therapeutic Targets for Idiopathic Pulmonary Fibrosis. , 2020, , .		0
77	A Polygenic Score for Asthma Is Associated with Airway Hyperresponsiveness in People with Chronic Obstructive Pulmonary Disease. , 2020, , .		0
78	Gene Expression Signature of Human Alveolar Macrophages Recovered from Human Broncho-Alveolar Lavage. , 2020, , .		0
79	Meta-analysis of idiopathic pulmonary fibrosis genome-wide analyses identifies three novel genetic signals associated with disease susceptibility. , 2019, , .		0