

# Xingnan Li

## List of Publications by Year in descending order

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Version: 2024-02-01

30  
papers

5,253  
citations

331670

21  
h-index

414414

32  
g-index

32  
all docs

32  
docs citations

32  
times ranked

7794  
citing authors

#	ARTICLE	IF	CITATIONS
1	Lung function, airway and peripheral basophils and eosinophils are associated with molecular pharmacogenomic endotypes of steroid response in severe asthma. <i>Thorax</i> , 2022, 77, 452-460.	5.6	3
2	Genetic Associations and Architecture of Asthma-COPD Overlap. <i>Chest</i> , 2022, 161, 1155-1166.	0.8	15
3	Polygenic transcriptome risk scores for COPD and lung function improve cross-ethnic portability of prediction in the NHLBI TOPMed program. <i>American Journal of Human Genetics</i> , 2022, 109, 857-870.	6.2	7
4	Genetic analyses identify GSDMB associated with asthma severity, exacerbations, and antiviral pathways. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 147, 894-909.	2.9	50
5	Genetic and non-genetic factors affecting the expression of COVID-19-relevant genes in the large airway epithelium. <i>Genome Medicine</i> , 2021, 13, 66.	8.2	21
6	Multiethnic genome-wide and HLA association study of total serum IgE level. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 148, 1589-1595.	2.9	15
7	Genetic variation in genes regulating skeletal muscle regeneration and tissue remodelling associated with weight loss in chronic obstructive pulmonary disease. <i>Journal of Cachexia, Sarcopenia and Muscle</i> , 2021, 12, 1803-1817.	7.3	11
8	Myeloid-associated differentiation marker is a novel SP-A-associated transmembrane protein whose expression on airway epithelial cells correlates with asthma severity. <i>Scientific Reports</i> , 2021, 11, 23392.	3.3	6
9	Investigation of the relationship between IL-6 and type 2 biomarkers in patients with severe asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 145, 430-433.	2.9	38
10	The Effects of Rare <i>SERPINA1</i> Variants on Lung Function and Emphysema in SPIROMICS. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 201, 540-554.	5.6	38
11	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
12	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. <i>Nature Communications</i> , 2020, 11, 6417.	12.8	39
13	Hot Topic: Precision Medicine for Asthma—Has the Time Come?. <i>Current Allergy and Asthma Reports</i> , 2019, 19, 45.	5.3	13
14	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
15	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
16	The effect of <i>BPIFA1/SPLUNC1</i> genetic variation on its expression and function in asthmatic airway epithelium. <i>JCI Insight</i> , 2019, 4, .	5.0	23
17	Genome-wide association study of lung function and clinical implication in heavy smokers. <i>BMC Medical Genetics</i> , 2018, 19, 134.	2.1	28
18	Genome-wide association and HLA fine-mapping studies identify risk loci and genetic pathways underlying allergic rhinitis. <i>Nature Genetics</i> , 2018, 50, 1072-1080.	21.4	106

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19	Association of sputum and blood eosinophil concentrations with clinical measures of COPD severity: an analysis of the SPIROMICS cohort. <i>Lancet Respiratory Medicine</i> , 2017, 5, 956-967.	10.7	211
20	The value of blood cytokines and chemokines in assessing COPD. <i>Respiratory Research</i> , 2017, 18, 180.	3.6	83
21	Expression of asthma susceptibility genes in bronchial epithelial cells and bronchial alveolar lavage in the Severe Asthma Research Program (SARP) cohort. <i>Journal of Asthma</i> , 2016, 53, 775-782.	1.7	23
22	Sputum neutrophil counts are associated with more severe asthma phenotypes using cluster analysis. <i>Journal of Allergy and Clinical Immunology</i> , 2014, 133, 1557-1563.e5.	2.9	488
23	Genome-wide association study identifies TH1 pathway genes associated with lung function in asthmatic patients. <i>Journal of Allergy and Clinical Immunology</i> , 2013, 132, 313-320.e15.	2.9	98
24	Clinical Heterogeneity in the Severe Asthma Research Program. <i>Annals of the American Thoracic Society</i> , 2013, 10, S118-S124.	3.2	74
25	The IL6R variation Asp358Ala is a potential modifier of lung function in subjects with asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2012, 130, 510-515.e1.	2.9	82
26	Genome-wide association studies of asthma indicate opposite immunopathogenesis direction from autoimmune diseases. <i>Journal of Allergy and Clinical Immunology</i> , 2012, 130, 861-868.e7.	2.9	130
27	Importance of hedgehog interacting protein and other lung function genes in asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2011, 127, 1457-1465.	2.9	115
28	Meta-analysis of genome-wide association studies of asthma in ethnically diverse North American populations. <i>Nature Genetics</i> , 2011, 43, 887-892.	21.4	736
29	Genome-wide association study of asthma identifies RAD50-IL13 and HLA-DR/DQ regions. <i>Journal of Allergy and Clinical Immunology</i> , 2010, 125, 328-335.e11.	2.9	295
30	Identification of Asthma Phenotypes Using Cluster Analysis in the Severe Asthma Research Program. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2010, 181, 315-323.	5.6	1,820