

# Jiang Li

## List of Publications by Year in descending order

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Version: 2024-02-01

20  
papers

422  
citations

1040056

9  
h-index

839539

18  
g-index

23  
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23  
docs citations

23  
times ranked

1171  
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	Blood miRNAs Are Linked to Frequent Asthma Exacerbations in Childhood Asthma and Adult COPD. <i>Non-coding RNA</i> , 2022, 8, 27.	2.6	3
3	Enhancing the prediction of childhood asthma remission: Integrating clinical factors with microRNAs. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 147, 1093-1095.e1.	2.9	6
4	Circulating MicroRNA: Incident Asthma Prediction and Vitamin D Effect Modification. <i>Journal of Personalized Medicine</i> , 2021, 11, 307.	2.5	7
5	COPD-associated miR-145-5p is downregulated in early-decline FEV1 trajectories in childhood asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 147, 2181-2190.	2.9	26
6	Commercially Available Blocking Oligonucleotides Effectively Suppress Unwanted Hemolysis-Related miRNAs in a Large Whole-Blood RNA Cohort. <i>Journal of Molecular Diagnostics</i> , 2021, 23, 671-682.	2.8	8
7	Identification of ROBO2 as a Potential Locus Associated with Inhaled Corticosteroid Response in Childhood Asthma. <i>Journal of Personalized Medicine</i> , 2021, 11, 733.	2.5	6
8	Seasonal Variation in miR-328-3p and let-7d-3p Are Associated With Seasonal Allergies and Asthma Symptoms in Children. <i>Allergy, Asthma and Immunology Research</i> , 2021, 13, 576.	2.9	7
9	Genome-wide association study of asthma exacerbations despite inhaled corticosteroid use. <i>European Respiratory Journal</i> , 2021, 57, 2003388.	6.7	17
10	COMPSRA: a COMprehensive Platform for Small RNA-Seq data Analysis. <i>Scientific Reports</i> , 2020, 10, 4552.	3.3	18
11	Circulating MicroRNAs and Treatment Response in Childhood Asthma. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 202, 65-72.	5.6	42
12	A nuclease-polymerase chain reaction enables amplification of probes used for capture-based DNA target enrichment. <i>Nucleic Acids Research</i> , 2019, 47, e147-e147.	14.5	6
13	Violent Crime and Park Use in Low-Income Urban Neighborhoods. <i>American Journal of Preventive Medicine</i> , 2018, 54, 352-358.	3.0	63
14	A rare variant in MLKL confers susceptibility to ApoE $\epsilon$ 4-negative Alzheimer's disease in Hong Kong Chinese population. <i>Neurobiology of Aging</i> , 2018, 68, 160.e1-160.e7.	3.1	23
15	Robust and rapid algorithms facilitate large-scale whole genome sequencing downstream analysis in an integrative framework. <i>Nucleic Acids Research</i> , 2017, 45, gkx019.	14.5	36
16	Genome-wide protein-protein interactions and protein function exploration in cyanobacteria. <i>Scientific Reports</i> , 2015, 5, 15519.	3.3	21
17	SPS: A Simulation Tool for Calculating Power of Set-Based Genetic Association Tests. <i>Genetic Epidemiology</i> , 2015, 39, 395-397.	1.3	3
18	MGAS: a powerful tool for multivariate gene-based genome-wide association analysis. <i>Bioinformatics</i> , 2015, 31, 1007-1015.	4.1	39

#	ARTICLE	IF	CITATIONS
19	Exploring virus relationships based on virus-host protein-protein interaction network. BMC Systems Biology, 2011, 5, S11.	3.0	7
20	Nucleosome structure incorporated histone acetylation site prediction in arabidopsis thaliana. BMC Genomics, 2010, 11, S7.	2.8	2