Angel C Y Mak

List of Publications by Year
in descending order

51 papers	**3,171** citations	361045 **20** h-index	233125 **45** g-index
68 all docs	**68** docs citations	**68** times ranked	**8059** citing authors

#	Article	IF	Citations
1	Epigenome-wide association study of lung function in Latino children and youth with asthma. Clinical Epigenetics, 2022, 14, 9.	1.8	12
2	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	3.0	29
3	Nasal airway transcriptome-wide association study of asthma reveals genetically driven mucus pathobiology. Nature Communications, 2022, 13, 1632.	5.8	24
4	Mapping the 17q12â€"21.1 Locus for Variants Associated with Early-Onset Asthma in African Americans. American Journal of Respiratory and Critical Care Medicine, 2021, 203, 424-436.	2.5	16
5	Integrative genomic analysis in African American children with asthma finds three novel loci associated with lung function. Genetic Epidemiology, 2021, 45, 190-208.	0.6	4
6	Genomeâ€wide association study reveals a novel locus for asthma with severe exacerbations in diverse populations. Pediatric Allergy and Immunology, 2021, 32, 106-115.	1.1	17
7	(1) Associations of PAI-1 Promoter Polymorphism and African Ancestry with Asthma in the GALA2 cohort. Journal of Allergy and Clinical Immunology, 2021, 147, AB55.	1.5	0
8	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	13.7	1,069
9	Robust, flexible, and scalable tests for Hardyâ€"Weinberg equilibrium across diverse ancestries. Genetics, 2021, 218, .	1.2	6
10	Native American Ancestry and Air Pollution Interact to Impact Bronchodilator Response in Puerto Rican Children with Asthma. Ethnicity and Disease, 2021, 31, 77-88.	1.0	2
11	Lymph nodeâ€"resident dendritic cells drive T_H2 cell development involving MARCH1. Science Immunology, 2021, 6, eabh0707.	5.6	10
12	Pharmacogenetic studies of long-acting beta agonist and inhaled corticosteroid responsiveness in randomised controlled trials of individuals of African descent with asthma. The Lancet Child and Adolescent Health, 2021, 5, 862-872.	2.7	10
13	Identification of CFTR variants in Latino patients with cystic fibrosis from the Dominican Republic and Puerto Rico. Pediatric Pulmonology, 2020, 55, 533-540.	1.0	5
14	Type 2 and interferon inflammation regulate SARS-CoV-2 entry factor expression in the airway epithelium. Nature Communications, 2020, 11, 5139.	5.8	131
15	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	13.7	376
16	On the cross-population generalizability of gene expression prediction models. PLoS Genetics, 2020, 16, e1008927.	1.5	41
17	Lung Function in African American Children with Asthma Is Associated with Novel Regulatory Variants of the KIT Ligand *KITLG/SCF* and Gene-By-Air-Pollution Interaction. Genetics, 2020, 215, 869-886.	1.2	11
18	Whole-Genome Sequencing Identifies Novel Functional Loci Associated with Lung Function in Puerto Rican Youth. American Journal of Respiratory and Critical Care Medicine, 2020, 202, 962-972.	2.5	11

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19	Expression of SMARCD1 interacts with age in association with asthma control on inhaled corticosteroid therapy. Respiratory Research, 2020, 21, 31.	1.4	6
20	Asthma and its relationship to mitochondrial copy number: Results from the Asthma Translational Genomics Collaborative (ATGC) of the Trans-Omics for Precision Medicine (TOPMed) program. PLoS ONE, 2020, 15, e0242364.	1.1	16
21	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
22	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
23	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
24	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
25	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
26	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
27	Ambient air pollution, asthma drug response, and telomere length in African American youth. Journal of Allergy and Clinical Immunology, 2019, 144, 839-845.e10.	1.5	24
28	Genome of the Komodo dragon reveals adaptations in the cardiovascular and chemosensory systems of monitor lizards. Nature Ecology and Evolution, 2019, 3, 1241-1252.	3.4	67
29	Three patients with homozygous familial hypercholesterolemia: Genomic sequencing and kindred analysis. Molecular Genetics & Genomic Medicine, 2019, 7, e1007.	0.6	5
30	Ancestry-Dependent Enrichment of Deleterious Homozygotes in Runs of Homozygosity. American Journal of Human Genetics, 2019, 105, 747-762.	2.6	36
31	Whole Genome Sequencing Identifies CRISPLD2 as a Lung Function Gene in Children With Asthma. Chest, 2019, 156, 1068-1079.	0.4	5
32	A genome-wide association and admixture mapping study of bronchodilator drug response in African Americans with asthma. Pharmacogenomics Journal, 2019, 19, 249-259.	0.9	54
33	Dysregulated invertebrate tropomyosinâ€"dectin-1 interaction confers susceptibility to allergic diseases. Science Immunology, 2018, 3, .	5.6	51
34	Whole-Genome Sequencing of Pharmacogenetic Drug Response in Racially Diverse Children with Asthma. American Journal of Respiratory and Critical Care Medicine, 2018, 197, 1552-1564.	2.5	102
35	A comprehensive evaluation of the genetic architecture of sudden cardiac arrest. European Heart Journal, 2018, 39, 3961-3969.	1.0	59
36	Genetic Determinants of Telomere Length in African American Youth. Scientific Reports, 2018, 8, 13265.	1.6	20

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37	Secondhand smoke exposure and asthma outcomes among African-American and Latino children with asthma. Thorax, 2018, 73, 1041-1048.	2.7	30
38	High-throughput single-molecule mapping links subtelomeric variants and long-range haplotypes with specific telomeres. Nucleic Acids Research, 2017, 45, e73-e73.	6.5	22
39	Identification of a novel locus associated with skin colour in African-admixed populations. Scientific Reports, 2017, 7, 44548.	1.6	31
40	The Effects of Migration and Assortative Mating on Admixture Linkage Disequilibrium. Genetics, 2017, 205, 375-383.	1.2	31
41	OMSV enables accurate and comprehensive identification of large structural variations from nanochannel-based single-molecule optical maps. Genome Biology, 2017, 18, 230.	3.8	28
42	In the Wrong Place with the Wrong SNP. Epidemiology, 2016, 27, 656-662.	1.2	5
43	Towards a More Accurate Error Model for BioNano Optical Maps. Lecture Notes in Computer Science, 2016, , 67-79.	1.0	8
44	Brief Report: Whole‐Exome Sequencing for Identification of Potential Causal Variants for Diffuse Cutaneous Systemic Sclerosis. Arthritis and Rheumatology, 2016, 68, 2257-2262.	2.9	35
45	Genome-Wide Structural Variation Detection by Genome Mapping on Nanochannel Arrays. Genetics, 2016, 202, 351-362.	1.2	126
46	Air Pollution and Lung Function in Minority Youth with Asthma in the GALA II (Genes–Environments) Tj ETQq0 0 0 rgBT /Overlock 10 T	2.5	54
47	Effects of the Absence of Apolipoprotein E on Lipoproteins, Neurocognitive Function, and Retinal Function. JAMA Neurology, 2014, 71, 1228.	4.5	79
48	Finished sequence and assembly of the DUF1220-rich 1q21 region using a haploid human genome. BMC Genomics, 2014, 15, 387.	1.2	47
49	Common variation in fatty acid metabolic genes and risk of incident sudden cardiac arrest. Heart Rhythm, 2014, 11, 471-477.	0.3	16
50	SOX9 Governs Differentiation Stage-Specific Gene Expression in Growth Plate Chondrocytes via Direct Concomitant Transactivation and Repression. PLoS Genetics, 2011, 7, e1002356.	1.5	174
51	Differential and overlapping expression pattern of SOX2 and SOX9 in inner ear development. Gene Expression Patterns, 2009, 9, 444-453.	0.3	73