

# Michelle Daya

## List of Publications by Year in descending order

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Version: 2024-02-01

28  
papers

2,543  
citations

623734

14  
h-index

477307

29  
g-index

31  
all docs

31  
docs citations

31  
times ranked

5808  
citing authors

#	ARTICLE	IF	CITATIONS
1	Polygenic prediction of atopic dermatitis improves with atopic training and filaggrin factors. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 149, 145-155.	2.9	11
2	Discovering metabolite quantitative trait loci in asthma using an isolated population. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 149, 1807-1811.e16.	2.9	8
3	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. <i>Cell Genomics</i> , 2022, 2, 100084.	6.5	29
4	Hunter-gatherer genomes reveal diverse demographic trajectories during the rise of farming in Eastern Africa. <i>Current Biology</i> , 2022, 32, 1852-1860.e5.	3.9	15
5	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. <i>Nature</i> , 2021, 590, 290-299.	27.8	1,069
6	Genome-wide association study of asthma, total IgE, and lung function in a cohort of Peruvian children. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 148, 1493-1504.	2.9	19
7	Whole genome sequencing identifies novel genetic mutations in patients with eczema herpeticum. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2021, 76, 2510-2523.	5.7	20
8	Zika Virus Congenital Syndrome and MTOR gene variants: insights from a family of dizygotic twins. <i>Heliyon</i> , 2021, 7, e06878.	3.2	0
9	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
10	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. <i>American Journal of Human Genetics</i> , 2021, 108, 1836-1851.	6.2	14
11	Pharmacogenetic studies of long-acting beta agonist and inhaled corticosteroid responsiveness in randomised controlled trials of individuals of African descent with asthma. <i>The Lancet Child and Adolescent Health</i> , 2021, 5, 862-872.	5.6	10
12	Easy-HLA: a validated web application suite to reveal the full details of HLA typing. <i>Bioinformatics</i> , 2020, 36, 2157-2164.	4.1	17
13	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. <i>Nature Communications</i> , 2020, 11, 5182.	12.8	32
14	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. <i>Nature</i> , 2020, 586, 763-768.	27.8	376
15	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. <i>Nature Communications</i> , 2020, 11, 6417.	12.8	39
16	A regulatory variant in the C1Q gene cluster is associated with tuberculosis susceptibility and C1qA plasma levels in a South African population. <i>Immunogenetics</i> , 2020, 72, 305-314.	2.4	7
17	De novo mutations across 1,465 diverse genomes reveal mutational insights and reductions in the Amish founder population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 2560-2569.	7.1	71
18	Association of HLA-DRB1*09:01 with tIgE levels among African-ancestry individuals with asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 146, 147-155.	2.9	14

#	ARTICLE	IF	CITATIONS
19	clustifyr: an R package for automated single-cell RNA sequencing cluster classification. F1000Research, 2020, 9, 223.	1.6	71
20	clustifyr: an R package for automated single-cell RNA sequencing cluster classification. F1000Research, 2020, 9, 223.	1.6	21
21	Whole Genome Sequencing Identifies CRISPLD2 as a Lung Function Gene in Children With Asthma. Chest, 2019, 156, 1068-1079.	0.8	5
22	Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations. Nature Communications, 2019, 10, 880.	12.8	71
23	African American ancestry contribution to asthma and atopic dermatitis. Annals of Allergy, Asthma and Immunology, 2019, 122, 456-462.	1.0	33
24	Use of >100,000 NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium whole genome sequences improves imputation quality and detection of rare variant associations in admixed African and Hispanic/Latino populations. PLoS Genetics, 2019, 15, e1008500.	3.5	203
25	Assembly of a pan-genome from deep sequencing of 910 humans of African descent. Nature Genetics, 2019, 51, 30-35.	21.4	276
26	Identification of novel allergic diathesis genes: Are we closer to novel therapeutic targets?. Journal of Allergy and Clinical Immunology, 2019, 143, 557-559.	2.9	0
27	Worldwide Frequencies of <i>APOL1</i> Renal Risk Variants. New England Journal of Medicine, 2018, 379, 2571-2572.	27.0	69
28	The role of ST2 and ST2 genetic variants in schistosomiasis. Journal of Allergy and Clinical Immunology, 2017, 140, 1416-1422.e6.	2.9	15