

# Michelle Daya

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6729802/publications.pdf>

Version: 2024-02-01

28  
papers

2,543  
citations

623188

14  
h-index

476904

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.   | 1.5  | 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.   | 1.5  | 8         |
| 3  | Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. <i>Cell Genomics</i> , 2022, 2, 100084.   | 3.0  | 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.   | 1.8  | 15        |
| 5  | Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. <i>Nature</i> , 2021, 590, 290-299.  | 13.7 | 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.  | 1.5  | 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.  | 2.7  | 20        |
| 8  | Zika Virus Congenital Syndrome and MTOR gene variants: insights from a family of dizygotic twins. <i>Heliyon</i> , 2021, 7, e06878.  | 1.4  | 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.  | 1.5  | 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.   | 2.6  | 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. | 2.7  | 10        |
| 12 | Easy-HLA: a validated web application suite to reveal the full details of HLA typing. <i>Bioinformatics</i> , 2020, 36, 2157-2164.   | 1.8  | 17        |
| 13 | Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. <i>Nature Communications</i> , 2020, 11, 5182.  | 5.8  | 32        |
| 14 | Inherited causes of clonal haematopoiesis in 97,691 whole genomes. <i>Nature</i> , 2020, 586, 763-768.   | 13.7 | 376       |
| 15 | Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. <i>Nature Communications</i> , 2020, 11, 6417.   | 5.8  | 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.   | 1.2  | 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.       | 3.3  | 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.   | 1.5  | 14        |

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 19 | clustifyr: an R package for automated single-cell RNA sequencing cluster classification. F1000Research, 2020, 9, 223.   | 0.8  | 71        |
| 20 | clustifyr: an R package for automated single-cell RNA sequencing cluster classification. F1000Research, 2020, 9, 223.   | 0.8  | 21        |
| 21 | Whole Genome Sequencing Identifies CRISPLD2 as a Lung Function Gene in Children With Asthma. Chest, 2019, 156, 1068-1079.   | 0.4  | 5         |
| 22 | Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations. Nature Communications, 2019, 10, 880.   | 5.8  | 71        |
| 23 | African American ancestry contribution to asthma and atopic dermatitis. Annals of Allergy, Asthma and Immunology, 2019, 122, 456-462.   | 0.5  | 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. | 1.5  | 203       |
| 25 | Assembly of a pan-genome from deep sequencing of 910 humans of African descent. Nature Genetics, 2019, 51, 30-35.   | 9.4  | 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.  | 1.5  | 0         |
| 27 | Worldwide Frequencies of <i>APOL1</i> Renal Risk Variants. New England Journal of Medicine, 2018, 379, 2571-2572.   | 13.9 | 69        |
| 28 | The role of ST2 and ST2 genetic variants in schistosomiasis. Journal of Allergy and Clinical Immunology, 2017, 140, 1416-1422.e6.   | 1.5  | 15        |