

# 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	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. <i>Nature</i> , 2021, 590, 290-299.	13.7	1,069
2	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. <i>Nature</i> , 2020, 586, 763-768.	13.7	376
3	Assembly of a pan-genome from deep sequencing of 910 humans of African descent. <i>Nature Genetics</i> , 2019, 51, 30-35.	9.4	276
4	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. <i>PLoS Genetics</i> , 2019, 15, e1008500.	1.5	203
5	Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations. <i>Nature Communications</i> , 2019, 10, 880.	5.8	71
6	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
7	clustifyr: an R package for automated single-cell RNA sequencing cluster classification. <i>F1000Research</i> , 2020, 9, 223.	0.8	71
8	Worldwide Frequencies of <i>APOL1</i> Renal Risk Variants. <i>New England Journal of Medicine</i> , 2018, 379, 2571-2572.	13.9	69
9	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. <i>Nature Communications</i> , 2020, 11, 6417.	5.8	39
10	African American ancestry contribution to asthma and atopic dermatitis. <i>Annals of Allergy, Asthma and Immunology</i> , 2019, 122, 456-462.	0.5	33
11	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
12	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
13	clustifyr: an R package for automated single-cell RNA sequencing cluster classification. <i>F1000Research</i> , 2020, 9, 223.	0.8	21
14	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
15	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
16	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
17	The role of ST2 and ST2 genetic variants in schistosomiasis. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 140, 1416-1422.e6.	1.5	15
18	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

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19	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
20	Association of HLA-DRB1*09:01 with tlgE levels among African-ancestry individuals with asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 146, 147-155.	1.5	14
21	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
22	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
23	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
24	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
25	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
26	Whole Genome Sequencing Identifies CRISPLD2 as a Lung Function Gene in Children With Asthma. <i>Chest</i> , 2019, 156, 1068-1079.	0.4	5
27	Identification of novel allergic diathesis genes: Are we closer to novel therapeutic targets?. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, 557-559.	1.5	0
28	Zika Virus Congenital Syndrome and MTOR gene variants: insights from a family of dizygotic twins. <i>Heliyon</i> , 2021, 7, e06878.	1.4	0