Michelle Daya

List of Publications by Year
in descending order

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	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
2	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
3	Assembly of a pan-genome from deep sequencing of 910 humans of African descent. Nature Genetics, 2019, 51, 30-35.	21.4	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. PLoS Genetics, 2019, 15, e1008500.	3.5	203
5	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
6	De novo mutations across 1,465 diverse genomes reveal mutational insights and reductions in the Amish founder population. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 2560-2569.	7.1	71
7	clustifyr: an R package for automated single-cell RNA sequencing cluster classification. F1000Research, 2020, 9, 223.	1.6	71
8	Worldwide Frequencies of APOL1 Renal Risk Variants. New England Journal of Medicine, 2018, 379, 2571-2572.	27.0	69
9	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417.	12.8	39
10	African American ancestry contribution to asthma and atopic dermatitis. Annals of Allergy, Asthma and Immunology, 2019, 122, 456-462.	1.0	33
11	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. Nature Communications, 2020, 11, 5182.	12.8	32
12	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	6.5	29
13	clustifyr: an R package for automated single-cell RNA sequencing cluster classification. F1000Research, 2020, 9, 223.	1.6	21
14	Whole genome sequencing identifies novel genetic mutations in patients with eczema herpeticum. Allergy: European Journal of Allergy and Clinical Immunology, 2021, 76, 2510-2523.	5.7	20
15	Genome-wide association study of asthma, total IgE, and lung function in a cohort of Peruvian children. Journal of Allergy and Clinical Immunology, 2021, 148, 1493-1504.	2.9	19
16	Easy-HLA: a validated web application suite to reveal the full details of HLA typing. Bioinformatics, 2020, 36, 2157-2164.	4.1	17
17	The role of ST2 and ST2 genetic variants in schistosomiasis. Journal of Allergy and Clinical Immunology, 2017, 140, 1416-1422.e6.	2.9	15
18	Multiethnic genome-wide and HLA association study of total serum IgE level. Journal of Allergy and Clinical Immunology, 2021, 148, 1589-1595.	2.9	15

#	Article	IF	Citations
19	Hunter-gatherer genomes reveal diverse demographic trajectories during the rise of farming in Eastern Africa. Current Biology, 2022, 32, 1852-1860.e5.	3.9	15
20	Association of HLA-DRB1âˆ—09:01 with tIgE levels among African-ancestry individuals with asthma. Journal of Allergy and Clinical Immunology, 2020, 146, 147-155.	2.9	14
21	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 1836-1851.	6.2	14
22	Polygenic prediction of atopic dermatitis improves with atopic training and filaggrin factors. Journal of Allergy and Clinical Immunology, 2022, 149, 145-155.	2.9	11
23	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.	5.6	10
24	Discovering metabolite quantitative trait loci in asthma using an isolated population. Journal of Allergy and Clinical Immunology, 2022, 149, 1807-1811.e16.	2.9	8
25	A regulatory variant in the C1Q gene cluster is associated with tuberculosis susceptibility and C1qA plasma levels in a South African population. Immunogenetics, 2020, 72, 305-314.	2.4	7
26	Whole Genome Sequencing Identifies CRISPLD2 as a Lung Function Gene in Children With Asthma. Chest, 2019, 156, 1068-1079.	0.8	5
27	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
28	Zika Virus Congenital Syndrome and MTOR gene variants: insights from a family of dizygotic twins. Heliyon, 2021, 7, e06878.	3.2	0