

Sameer Chavan

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

1,993
citations

623734

14
h-index

580821

25
g-index

32
all docs

32
docs citations

32
times ranked

4570
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	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. <i>Science Advances</i> , 2022, 8, eabl6579.	10.3	36
3	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
4	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
5	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. <i>Nature Communications</i> , 2021, 12, 2182.	12.8	17
6	Genome sequencing unveils a regulatory landscape of platelet reactivity. <i>Nature Communications</i> , 2021, 12, 3626.	12.8	29
7	Variant-specific inflation factors for assessing population stratification at the phenotypic variance level. <i>Nature Communications</i> , 2021, 12, 3506.	12.8	1
8	Mapping the human genetic architecture of COVID-19. <i>Nature</i> , 2021, 600, 472-477.	27.8	640
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	A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. <i>Nature Genetics</i> , 2021, 53, 1504-1516.	21.4	69
12	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. <i>Nature</i> , 2020, 586, 763-768.	27.8	376
13	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. <i>Nature Genetics</i> , 2020, 52, 969-983.	21.4	146
14	Genetic Determinants of Peanut-Specific IgG4 in The Learning Early About Peanut Allergy (LEAP) Study. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 145, AB50.	2.9	0
15	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
16	Replicated methylation changes associated with eczema herpeticum and allergic response. <i>Clinical Epigenetics</i> , 2019, 11, 122.	4.1	22
17	Whole Genome Sequencing Identifies CRISPLD2 as a Lung Function Gene in Children With Asthma. <i>Chest</i> , 2019, 156, 1068-1079.	0.8	5
18	The MALT1 locus and peanut avoidance in the risk for peanut allergy. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, 2326-2329.	2.9	36

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19	Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations. <i>Nature Communications</i> , 2019, 10, 880.	12.8	71
20	Assembly of a pan-genome from deep sequencing of 910 humans of African descent. <i>Nature Genetics</i> , 2019, 51, 30-35.	21.4	276
21	Whole Genome Sequencing Identifies Four Novel Variants in the Epidermal Differentiation Complex That Increase Risk and Severity for Atopic Dermatitis. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, AB85.	2.9	0
22	Synthesizer: Expediting synthesis studies from context-free data with information retrieval techniques. <i>PLoS ONE</i> , 2017, 12, e0175860.	2.5	0
23	Filaggrin Associated Risk for Atopic Dermatitis Is Offset By Protective Missense Variants in Rptn and LCE1B Genes in the Epidermal Differentiation Complex. <i>Journal of Allergy and Clinical Immunology</i> , 2016, 137, AB182.	2.9	0
24	Imputation from 328 African Ancestry Genomes Reveals New Associations with Asthma in DPP10. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 135, AB162.	2.9	0
25	Identifying Genetic Determinants of Atopic Dermatitis and Bacterial Colonization Using Whole Genome Sequencing. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 135, AB391.	2.9	2
26	Preserving biological heterogeneity with a permuted surrogate variable analysis for genomics batch correction. <i>Bioinformatics</i> , 2014, 30, 2757-2763.	4.1	102
27	Molecular basis of antigenic drift in Influenza A/H3N2 strains (1968-2007) in the light of antigen-antibody interactions. <i>Bioinformatics</i> , 2011, 6, 266-270.	0.5	16
28	Antigenic variability in Neuraminidase protein of Influenza A/H3N2 vaccine strains (1968-2009). <i>Bioinformatics</i> , 2011, 7, 76-81.	0.5	9