Rasika A Mathias

List of Publications by Year
in descending order

118	8,658	71102 41	56724 83
papers	citations	h-index	g-index

128	128	128	16313
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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
2	Whole genome sequence analysis of platelet traits in the NHLBI Trans-Omics for Precision Medicine (TOPMed) initiative. Human Molecular Genetics, 2022, 31, 347-361.	2.9	9
3	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
4	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	6.5	29
5	HLA alleles and sustained peanut consumption promote IgG4 responses in subjects protected from peanut allergy. Journal of Clinical Investigation, 2022, 132, .	8.2	15
6	Rare coding variants in 35 genes associate with circulating lipid levelsâ€"A multi-ancestry analysis of 170,000 exomes. American Journal of Human Genetics, 2022, 109, 81-96.	6.2	24
7	Rare coding variants in RCN3 are associated with blood pressure. BMC Genomics, 2022, 23, 148.	2.8	2
8	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. Nature Genetics, 2022, 54, 263-273.	21.4	156
9	Lipid mediators are detectable in the nasal epithelium and differ by asthma status in female subjects. Journal of Allergy and Clinical Immunology, 2022, , .	2.9	8
10	Secondary analyses for genomeâ€wide association studies using expression quantitative trait loci. Genetic Epidemiology, 2022, , .	1.3	2
11	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	10.3	36
12	The Value of Rare Genetic Variation in the Prediction of Common Obesity in European Ancestry Populations. Frontiers in Endocrinology, 2022, 13, 863893.	3.5	7
13	Telomere shortening and the transition to family caregiving in the Reasons for Geographic and Racial Differences in Stroke (REGARDS) study. PLoS ONE, 2022, 17, e0268689.	2.5	0
14	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. Hypertension, 2022, 79, 1656-1667.	2.7	12
15	Advancing Food Allergy Through Omics Sciences. Journal of Allergy and Clinical Immunology: in Practice, 2021, 9, 119-129.	3.8	13
16	Transcriptional profile of platelets and iPSC-derived megakaryocytes from whole-genome and RNA sequencing. Blood, 2021, 137, 959-968.	1.4	21
17	Whole genome sequence analyses of eGFR in 23,732 people representing multiple ancestries in the NHLBI trans-omics for precision medicine (TOPMed) consortium. EBioMedicine, 2021, 63, 103157.	6.1	14
18	Current insights into the genetics of food allergy. Journal of Allergy and Clinical Immunology, 2021, 147, 15-28.	2.9	40

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19	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
20	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
21	Robust, flexible, and scalable tests for Hardyâ€“Weinberg equilibrium across diverse ancestries. Genetics, 2021, 218, .	2.9	6
22	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
23	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	12.8	17
24	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 874-893.	6.2	28
25	FGL1 as a modulator of plasma Dâ€dimer levels: Exomeâ€wide marker analysis of plasma tPA, PAIâ€1, and Dâ€dimer. Journal of Thrombosis and Haemostasis, 2021, 19, 2019-2028.	3.8	1
26	Gene and protein expression in human megakaryocytes derived from induced pluripotent stem cells. Journal of Thrombosis and Haemostasis, 2021, 19, 1783-1799.	3.8	6
27	Genome sequencing unveils a regulatory landscape of platelet reactivity. Nature Communications, 2021, 12, 3626.	12.8	29
28	Impact of Amerind ancestry and FADS genetic variation on omega-3 deficiency and cardiometabolic traits in Hispanic populations. Communications Biology, 2021, 4, 918.	4.4	11
29	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
30	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
31	Host methylation predicts SARS-CoV-2 infection and clinical outcome. Communications Medicine, 2021, 1, 42.	4.2	35
32	Interpreting Clinical Trials With Omega-3 Supplements in the Context of Ancestry and FADS Genetic Variation. Frontiers in Nutrition, 2021, 8, 808054.	3.7	12
33	FADS genetic and metabolomic analyses identify the âˆ†5 desaturase (FADS1) step as a critical control point in the formation of biologically important lipids. Scientific Reports, 2020, 10, 15873.	3.3	26
34	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
35	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. Nature Genetics, 2020, 52, 969-983.	21.4	146
36	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417.	12.8	39

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37	Whole genome sequence association analyses of brain volumes in the TOPMed program. Alzheimer's and Dementia, 2020, 16, e040627.	0.8	0
38	Prospective clinical trial examining the impact of genetic variation in FADS1 on the metabolism of linoleic acidâ€“ and É£-linolenic acidâ€“containing botanical oils. American Journal of Clinical Nutrition, 2020, 111, 1068-1078.	4.7	16
39	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
40	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
41	Genomic integrity of human induced pluripotent stem cells across nine studies in the NHLBI NextGen program. Stem Cell Research, 2020, 46, 101803.	0.7	10
42	Genetic loci associated with prevalent and incident myocardial infarction and coronary heart disease in the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium. PLoS ONE, 2020, 15, e0230035.	2.5	5
43	The relationship of family history and risk of type 2 diabetes differs by ancestry. Diabetes and Metabolism, 2019, 45, 261-267.	2.9	1
44	A genome-wide association study identifies genetic loci associated with specific lobar brain volumes. Communications Biology, 2019, 2, 285.	4.4	27
45	The pharmacogenomics of inhaled corticosteroids and lung function decline in COPD. European Respiratory Journal, 2019, 54, 1900521.	6.7	14
46	Replicated methylation changes associated with eczema herpeticum and allergic response. Clinical Epigenetics, 2019, 11, 122.	4.1	22
47	Impact of Rare and Common Genetic Variants on Diabetes Diagnosis by Hemoglobin A1c in Multi-Ancestry Cohorts: The Trans-Omics for Precision Medicine Program. American Journal of Human Genetics, 2019, 105, 706-718.	6.2	44
48	Leveraging linkage evidence to identify low-frequency and rare variants on 16p13 associated with blood pressure using TOPMed whole genome sequencing data. Human Genetics, 2019, 138, 199-210.	3.8	29
49	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. PLoS ONE, 2019, 14, e0216222.	2.5	17
50	The MALT1 locus and peanut avoidance in the risk for peanut allergy. Journal of Allergy and Clinical Immunology, 2019, 143, 2326-2329.	2.9	36
51	Evolution of Hominin Polyunsaturated Fatty Acid Metabolism: From Africa to the New World. Genome Biology and Evolution, 2019, 11, 1417-1430.	2.5	38
52	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
53	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
54	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. American Journal of Human Genetics, 2019, 104, 112-138.	6.2	106

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55	Assembly of a pan-genome from deep sequencing of 910 humans of African descent. Nature Genetics, 2019, 51, 30-35.	21.4	276
56	An admixture mapping meta-analysis implicates genetic variation at 18q21 with asthma susceptibility in Latinos. Journal of Allergy and Clinical Immunology, 2019, 143, 957-969.	2.9	33
57	Efficient Variant Set Mixed Model Association Tests for Continuous and Binary Traits in Large-Scale Whole-Genome Sequencing Studies. American Journal of Human Genetics, 2019, 104, 260-274.	6.2	103
58	Exome-chip meta-analysis identifies association between variation in ANKRD26 and platelet aggregation. Platelets, 2019, 30, 164-173.	2.3	15
59	Targeted deep sequencing of the PEAR1 locus for platelet aggregation in European and African American families. Platelets, 2019, 30, 380-386.	2.3	19
60	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	21.4	426
61	Diabetes and Platelet Response to Low-dose Aspirin. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 4599-4608.	3.6	8
62	Optimized distributed systems achieve significant performance improvement on sorted merging of massive VCF files. GigaScience, 2018, 7, .	6.4	4
63	Exome Chip Analysis Identifies Low-Frequency and Rare Variants in MRPL38 for White Matter Hyperintensities on Brain Magnetic Resonance Imaging. Stroke, 2018, 49, 1812-1819.	2.0	17
64	The genetics of smoking in individuals with chronic obstructive pulmonary disease. Respiratory Research, 2018, 19, 59.	3.6	11
65	Tissue-specific impact of FADS cluster variants on FADS1 and FADS2 gene expression. PLoS ONE, 2018, 13, e0194610.	2.5	29
66	Genome-wide association analyses for lung function and chronic obstructive pulmonary disease identify new loci and potential druggable targets. Nature Genetics, 2017, 49, 416-425.	21.4	257
67	The role of ST2 and ST2 genetic variants in schistosomiasis. Journal of Allergy and Clinical Immunology, 2017, 140, 1416-1422.e6.	2.9	15
68	Identifying tagging SNPs for African specific genetic variation from the African Diaspora Genome. Scientific Reports, 2017, 7, 46398.	3.3	26
69	Effect of polymorphisms on TGFB1 on allergic asthma and helminth infection in an African admixed population. Annals of Allergy, Asthma and Immunology, 2017, 118, 483-488.e1.	1.0	15
70	Surfactant protein D is a causal risk factor for COPD: results of Mendelian randomisation. European Respiratory Journal, 2017, 50, 1700657.	6.7	45
71	Precision Nutrition and Omega-3 Polyunsaturated Fatty Acids: A Case for Personalized Supplementation Approaches for the Prevention and Management of Human Diseases. Nutrients, 2017, 9, 1165.	4.1	88
72	Whole exome sequencing in the Framingham Heart Study identifies rare variation in HYAL2 that influences platelet aggregation. Thrombosis and Haemostasis, 2017, 117, 1083-1092.	3.4	11

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73	Integrity of Induced Pluripotent Stem Cell (iPSC) Derived Megakaryocytes as Assessed by Genetic and Transcriptomic Analysis. PLoS ONE, 2017, 12, e0167794.	2.5	9
74	Uncovering the DNA methylation landscape in key regulatory regions within the FADS cluster. PLoS ONE, 2017, 12, e0180903.	2.5	23
75	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. American Journal of Human Genetics, 2016, 99, 8-21.	6.2	60
76	Impact of methods used to express levels of circulating fatty acids on the degree and direction of associations with blood lipids in humans. British Journal of Nutrition, 2016, 115, 251-261.	2.3	42
77	SCARB1 Gene Variants Are Associated With the Phenotype of Combined High High-Density Lipoprotein Cholesterol and High Lipoprotein (a). Circulation: Cardiovascular Genetics, 2016, 9, 408-418.	5.1	29
78	Challenges and disparities in the application of personalized genomic medicine to populations with African ancestry. Nature Communications, 2016, 7, 12521.	12.8	68
79	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	6.2	82
80	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. American Journal of Human Genetics, 2016, 99, 22-39.	6.2	50
81	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. Blood, 2015, 126, e19-e29.	1.4	55
82	Genome-wide association study and admixture mapping reveal new loci associated with total IgE levels in Latinos. Journal of Allergy and Clinical Immunology, 2015, 135, 1502-1510.	2.9	52
83	Targeted deep sequencing identifies rare loss-of-function variants in IFNGR1 for risk of atopic dermatitis complicated by eczema herpeticum. Journal of Allergy and Clinical Immunology, 2015, 136, 1591-1600.	2.9	42
84	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173
85	Genome-Wide Association Study Identification of Novel Loci Associated with Airway Responsiveness in Chronic Obstructive Pulmonary Disease. American Journal of Respiratory Cell and Molecular Biology, 2015, 53, 226-234.	2.9	27
86	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
87	Genome-wide association study of platelet aggregation in African Americans. BMC Genetics, 2015, 16, 58.	2.7	50
88	Greater Collagen-Induced Platelet Aggregation Following Cyclooxygenase 1 Inhibition Predicts Incident Acute Coronary Syndromes. Clinical and Translational Science, 2015, 8, 17-22.	3.1	13
89	Ethnic-specific associations of rare and low-frequency DNA sequence variants with asthma. Nature Communications, 2015, 6, 5965.	12.8	66
90	Exome Sequencing of Phenotypic Extremes Identifies CAV2 and TMC6 as Interacting Modifiers of Chronic Pseudomonas aeruginosa Infection in Cystic Fibrosis. PLoS Genetics, 2015, 11, e1005273.	3.5	39

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91	An IL-13 Promoter Polymorphism Associated with Liver Fibrosis in Patients with Schistosoma japonicum. PLoS ONE, 2015, 10, e0135360.	2.5	29
92	DNA Methylation in an Enhancer Region of the FADS Cluster Is Associated with FADS Activity in Human Liver. PLoS ONE, 2014, 9, e97510.	2.5	56
93	Large-Scale Genome-Wide Association Studies and Meta-Analyses of Longitudinal Change in Adult Lung Function. PLoS ONE, 2014, 9, e100776.	2.5	52
94	Diet-Gene Interactions and PUFA Metabolism: A Potential Contributor to Health Disparities and Human Diseases. Nutrients, 2014, 6, 1993-2022.	4.1	114
95	Meta-Analysis of Genome-Wide Association Studies in African Americans Provides Insights into the Genetic Architecture of Type 2 Diabetes. PLoS Genetics, 2014, 10, e1004517.	3.5	191
96	Relationship between a Common Variant in the Fatty Acid Desaturase (FADS) Cluster and Eicosanoid Generation in Humans. Journal of Biological Chemistry, 2014, 289, 22482-22489.	3.4	59
97	Genome-wide interaction studies reveal sex-specific asthma risk alleles. Human Molecular Genetics, 2014, 23, 5251-5259.	2.9	70
98	Genome-wide association study of lung function phenotypes in a founder population. Journal of Allergy and Clinical Immunology, 2014, 133, 248-255.e10.	2.9	50
99	Genetic Variants in the FADS Gene: Implications for Dietary Recommendations for Fatty Acid Intake. Current Nutrition Reports, 2014, 3, 139-148.	4.3	61
100	A Simple Scalable Association Hypothesis Test Combining Gene-wide Evidence from Multiple Polymorphisms. British Journal of Medicine and Medical Research, 2014, 4, 1413-1422.	0.2	0
101	A meta-analysis of genome-wide association studies for serum total IgE in diverse study populations. Journal of Allergy and Clinical Immunology, 2013, 131, 1176-1184.	2.9	58
102	African Ancestry is a Risk Factor for Asthma and High Total IgE Levels in African Admixed Populations. Genetic Epidemiology, 2013, 37, 393-401.	1.3	46
103	Targeted Deep Resequencing Identifies Coding Variants in the PEAR1 Gene That Play a Role in Platelet Aggregation. PLoS ONE, 2013, 8, e64179.	2.5	28
104	Differences in arachidonic acid levels and fatty acid desaturase (FADS) gene variants in African Americans and European Americans with diabetes or the metabolic syndrome. British Journal of Nutrition, 2012, 107, 547-555.	2.3	147
105	The Robustness of Generalized Estimating Equations for Association Tests in Extended Family Data. Human Heredity, 2012, 74, 17-26.	0.8	7
106	Adaptive Evolution of the FADS Gene Cluster within Africa. PLoS ONE, 2012, 7, e44926.	2.5	87
107	Resequencing Candidate Genes Implicates Rare Variants in Asthma Susceptibility. American Journal of Human Genetics, 2012, 90, 273-281.	6.2	65
108	Genome-Wide Association Study of Platelet Function in African Americans. Blood, 2012, 120, 1068-1068.	1.4	0

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109	The impact of FADS genetic variants on ï‰6 polyunsaturated fatty acid metabolism in African Americans. BMC Genetics, 2011, 12, 50.	2.7	116
110	Meta-analysis of genome-wide association studies of asthma in ethnically diverse North American populations. Nature Genetics, 2011, 43, 887-892.	21.4	736
111	Identification of a specific intronic PEAR1 gene variant associated with greater platelet aggregability and protein expression. Blood, 2011, 118, 3367-3375.	1.4	95
112	Genome partitioning of genetic variation for complex traits using common SNPs. Nature Genetics, 2011, 43, 519-525.	21.4	834
113	A combined genome-wide linkage and association approach to find susceptibility loci for platelet function phenotypes in European American and African American families with coronary artery disease. BMC Medical Genomics, 2010, 3, 22.	1.5	31
114	FADS genetic variants and Ï‰-6 polyunsaturated fatty acid metabolism in a homogeneous island population. Journal of Lipid Research, 2010, 51, 2766-2774.	4.2	74
115	Heritability of Platelet Responsiveness to Aspirin in Activation Pathways Directly and Indirectly Related to Cyclooxygenase-1. Circulation, 2007, 115, 2490-2496.	1.6	147
116	Inheritance of Total Serum IgE in the Isolated Tangier Island Population from Virginia: Complexities Associated with Genealogical Depth of Pedigrees in Segregation Analyses. Human Heredity, 2005, 59, 228-238.	0.8	8
117	Possible linkage of alcoholism, monoamine oxidase activity and P300 amplitude to markers on chromosome 12q24. Genetic Epidemiology, 1999, 17, S193-8.	1.3	5
118	Environmental covariates: Effects on the power of sibâ€pair linkage methods. Genetic Epidemiology, 1999, 17, S643-8.	1.3	9