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	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
2	Genome partitioning of genetic variation for complex traits using common SNPs. Nature Genetics, 2011, 43, 519-525.	21.4	834
3	Meta-analysis of genome-wide association studies of asthma in ethnically diverse North American populations. Nature Genetics, 2011, 43, 887-892.	21.4	736
4	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	21.4	426
5	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
6	Assembly of a pan-genome from deep sequencing of 910 humans of African descent. Nature Genetics, 2019, 51, 30-35.	21.4	276
7	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
8	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
9	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
10	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173
11	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
12	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. Nature Genetics, 2022, 54, 263-273.	21.4	156
13	Heritability of Platelet Responsiveness to Aspirin in Activation Pathways Directly and Indirectly Related to Cyclooxygenase-1. Circulation, 2007, 115, 2490-2496.	1.6	147
14	Differences in arachidonic acid levels and fatty acid desaturase (<i>FADS</i>) 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
15	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
16	The impact of FADS genetic variants on Ï‰6 polyunsaturated fatty acid metabolism in African Americans. BMC Genetics, 2011, 12, 50.	2.7	116
17	Diet-Gene Interactions and PUFA Metabolism: A Potential Contributor to Health Disparities and Human Diseases. Nutrients, 2014, 6, 1993-2022.	4.1	114
18	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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19	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
20	Identification of a specific intronic PEAR1 gene variant associated with greater platelet aggregability and protein expression. Blood, 2011, 118, 3367-3375.	1.4	95
21	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
22	Adaptive Evolution of the FADS Gene Cluster within Africa. PLoS ONE, 2012, 7, e44926.	2.5	87
23	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	6.2	82
24	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
25	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
26	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
27	Genome-wide interaction studies reveal sex-specific asthma risk alleles. Human Molecular Genetics, 2014, 23, 5251-5259.	2.9	70
28	Challenges and disparities in the application of personalized genomic medicine to populations with African ancestry. Nature Communications, 2016, 7, 12521.	12.8	68
29	Ethnic-specific associations of rare and low-frequency DNA sequence variants with asthma. Nature Communications, 2015, 6, 5965.	12.8	66
30	Resequencing Candidate Genes Implicates Rare Variants in Asthma Susceptibility. American Journal of Human Genetics, 2012, 90, 273-281.	6.2	65
31	Genetic Variants in the FADS Gene: Implications for Dietary Recommendations for Fatty Acid Intake. Current Nutrition Reports, 2014, 3, 139-148.	4.3	61
32	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. American Journal of Human Genetics, 2016, 99, 8-21.	6.2	60
33	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
34	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
35	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
36	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

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37	Large-Scale Genome-Wide Association Studies and Meta-Analyses of Longitudinal Change in Adult Lung Function. PLoS ONE, 2014, 9, e100776.	2.5	52
38	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
39	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
40	Genome-wide association study of platelet aggregation in African Americans. BMC Genetics, 2015, 16, 58.	2.7	50
41	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
42	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
43	Surfactant protein D is a causal risk factor for COPD: results of Mendelian randomisation. European Respiratory Journal, 2017, 50, 1700657.	6.7	45
44	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
45	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
46	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
47	Current insights into the genetics of food allergy. Journal of Allergy and Clinical Immunology, 2021, 147, 15-28.	2.9	40
48	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417.	12.8	39
49	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
50	Evolution of Hominin Polyunsaturated Fatty Acid Metabolism: From Africa to the New World. Genome Biology and Evolution, 2019, 11, 1417-1430.	2.5	38
51	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
52	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	10.3	36
53	Host methylation predicts SARS-CoV-2 infection and clinical outcome. Communications Medicine, 2021, 1, 42.	4.2	35
54	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

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55	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
56	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
57	Tissue-specific impact of FADS cluster variants on FADS1 and FADS2 gene expression. PLoS ONE, 2018, 13, e0194610.	2.5	29
58	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
59	Genome sequencing unveils a regulatory landscape of platelet reactivity. Nature Communications, 2021, 12, 3626.	12.8	29
60	An IL-13 Promoter Polymorphism Associated with Liver Fibrosis in Patients with Schistosoma japonicum. PLoS ONE, 2015, 10, e0135360.	2.5	29
61	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	6.5	29
62	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
63	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
64	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
65	A genome-wide association study identifies genetic loci associated with specific lobar brain volumes. Communications Biology, 2019, 2, 285.	4.4	27
66	Identifying tagging SNPs for African specific genetic variation from the African Diaspora Genome. Scientific Reports, 2017, 7, 46398.	3.3	26
67	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
68	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
69	Uncovering the DNA methylation landscape in key regulatory regions within the FADS cluster. PLoS ONE, 2017, 12, e0180903.	2.5	23
70	Replicated methylation changes associated with eczema herpeticum and allergic response. Clinical Epigenetics, 2019, 11, 122.	4.1	22
71	Transcriptional profile of platelets and iPSC-derived megakaryocytes from whole-genome and RNA sequencing. Blood, 2021, 137, 959-968.	1.4	21
72	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

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73	Targeted deep sequencing of the PEAR1 locus for platelet aggregation in European and African American families. Platelets, 2019, 30, 380-386.	2.3	19
74	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
75	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
76	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. PLoS ONE, 2019, 14, e0216222.	2.5	17
77	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	12.8	17
78	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
79	The role of ST2 and ST2 genetic variants in schistosomiasis. Journal of Allergy and Clinical Immunology, 2017, 140, 1416-1422.e6.	2.9	15
80	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
81	Exome-chip meta-analysis identifies association between variation in ANKRD26 and platelet aggregation. Platelets, 2019, 30, 164-173.	2.3	15
82	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
83	HLA alleles and sustained peanut consumption promote IgG4 responses in subjects protected from peanut allergy. Journal of Clinical Investigation, 2022, 132, .	8.2	15
84	The pharmacogenomics of inhaled corticosteroids and lung function decline in COPD. European Respiratory Journal, 2019, 54, 1900521.	6.7	14
85	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
86	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
87	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
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	Advancing Food Allergy Through Omics Sciences. Journal of Allergy and Clinical Immunology: in Practice, 2021, 9, 119-129.	3.8	13
90	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

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91	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
92	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
93	The genetics of smoking in individuals with chronic obstructive pulmonary disease. Respiratory Research, 2018, 19, 59.	3.6	11
94	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
95	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
96	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
97	Environmental covariates: Effects on the power of sibâ€pair linkage methods. Genetic Epidemiology, 1999, 17, S643-8.	1.3	9
98	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
99	Integrity of Induced Pluripotent Stem Cell (iPSC) Derived Megakaryocytes as Assessed by Genetic and Transcriptomic Analysis. PLoS ONE, 2017, 12, e0167794.	2.5	9
100	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
101	Diabetes and Platelet Response to Low-dose Aspirin. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 4599-4608.	3.6	8
102	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
103	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
104	The Robustness of Generalized Estimating Equations for Association Tests in Extended Family Data. Human Heredity, 2012, 74, 17-26.	0.8	7
105	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
106	Robust, flexible, and scalable tests for Hardyâ€“Weinberg equilibrium across diverse ancestries. Genetics, 2021, 218, .	2.9	6
107	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
108	Possible linkage of alcoholism, monoamine oxidase activity and P300 amplitude to markers on chromosome 12q24. Genetic Epidemiology, 1999, 17, S193-8.	1.3	5

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109	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
110	Optimized distributed systems achieve significant performance improvement on sorted merging of massive VCF files. GigaScience, 2018, 7, .	6.4	4
111	Rare coding variants in RCN3 are associated with blood pressure. BMC Genomics, 2022, 23, 148.	2.8	2
112	Secondary analyses for genomeâ€wide association studies using expression quantitative trait loci. Genetic Epidemiology, 2022, , .	1.3	2
113	The relationship of family history and risk of type 2 diabetes differs by ancestry. Diabetes and Metabolism, 2019, 45, 261-267.	2.9	1
114	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
115	Whole genome sequence association analyses of brain volumes in the TOPMed program. Alzheimer's and Dementia, 2020, 16, e040627.	0.8	0
116	Genome-Wide Association Study of Platelet Function in African Americans. Blood, 2012, 120, 1068-1068.	1.4	0
117	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
118	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