

# Ani W Manichaikul

## List of Publications by Year in descending order

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Version: 2024-02-01

167  
papers

16,556  
citations

28274

55  
h-index

21540

114  
g-index

186  
all docs

186  
docs citations

186  
times ranked

27549  
citing authors

#	ARTICLE	IF	CITATIONS
1	Robust relationship inference in genome-wide association studies. <i>Bioinformatics</i> , 2010, 26, 2867-2873.	4.1	2,328
2	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. <i>Nature Genetics</i> , 2018, 50, 524-537.	21.4	1,124
3	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. <i>Nature</i> , 2021, 590, 290-299.	27.8	1,069
4	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017, 49, 1758-1766.	21.4	470
5	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. <i>Nature Genetics</i> , 2018, 50, 42-53.	21.4	426
6	The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , 2020, 182, 1214-1231.e11.	28.9	388
7	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. <i>JAMA Oncology</i> , 2017, 3, 636.	7.1	376
8	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. <i>Nature Genetics</i> , 2011, 43, 1082-1090.	21.4	367
9	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. <i>Cell</i> , 2020, 182, 1198-1213.e14.	28.9	353
10	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	27.8	353
11	Genetic Loci Associated with Plasma Phospholipid n-3 Fatty Acids: A Meta-Analysis of Genome-Wide Association Studies from the CHARGE Consortium. <i>PLoS Genetics</i> , 2011, 7, e1002193.	3.5	324
12	Genetic loci associated with chronic obstructive pulmonary disease overlap with loci for lung function and pulmonary fibrosis. <i>Nature Genetics</i> , 2017, 49, 426-432.	21.4	306
13	Association of Low-Frequency and Rare Coding-Sequence Variants with Blood Lipids and Coronary Heart Disease in 56,000 Whites and Blacks. <i>American Journal of Human Genetics</i> , 2014, 94, 223-232.	6.2	287
14	Metabolic network reconstruction of <i>Chlamydomonas</i> offers insight into light-driven algal metabolism. <i>Molecular Systems Biology</i> , 2011, 7, 518.	7.2	264
15	Genetic landscape of chronic obstructive pulmonary disease identifies heterogeneous cell-type and phenotype associations. <i>Nature Genetics</i> , 2019, 51, 494-505.	21.4	257
16	Genetic Correlates of Musical Pitch Recognition in Humans. <i>Science</i> , 2001, 291, 1969-1972.	12.6	256
17	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. <i>Molecular Psychiatry</i> , 2015, 20, 647-656.	7.9	235
18	Spectrum of heart disease associated with murine and human GATA4 mutation. <i>Journal of Molecular and Cellular Cardiology</i> , 2007, 43, 677-685.	1.9	218

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19	Loci associated with ischaemic stroke and its subtypes (SiGN): a genome-wide association study. <i>Lancet Neurology</i> , The, 2016, 15, 174-184.	10.2	217
20	Genome-wide meta-analysis of observational studies shows common genetic variants associated with macronutrient intake. <i>American Journal of Clinical Nutrition</i> , 2013, 97, 1395-1402.	4.7	210
21	<i>KLB</i> is associated with alcohol drinking, and its gene product $\beta$ -Klotho is necessary for FGF21 regulation of alcohol preference. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 14372-14377.	7.1	208
22	Genome-Wide Association Study of Susceptibility to Idiopathic Pulmonary Fibrosis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 201, 564-574.	5.6	208
23	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. <i>American Journal of Human Genetics</i> , 2014, 94, 233-245.	6.2	193
24	Allelic Polymorphism within the TAS1R3 Promoter Is Associated with Human Taste Sensitivity to Sucrose. <i>Current Biology</i> , 2009, 19, 1288-1293.	3.9	185
25	Poor Performance of Bootstrap Confidence Intervals for the Location of a Quantitative Trait Locus. <i>Genetics</i> , 2006, 174, 481-489.	2.9	184
26	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , 2017, 8, 14977.	12.8	169
27	Genome-Wide Association Studies Identify <i>CHRNA5/3</i> and <i>HTR4</i> in the Development of Airflow Obstruction. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2012, 186, 622-632.	5.6	164
28	Genome-Wide Association Study of Plasma N6 Polyunsaturated Fatty Acids Within the Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium. <i>Circulation: Cardiovascular Genetics</i> , 2014, 7, 321-331.	5.1	164
29	A Model Selection Approach for the Identification of Quantitative Trait Loci in Experimental Crosses, Allowing Epistasis. <i>Genetics</i> , 2009, 181, 1077-1086.	2.9	149
30	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
31	FTO genetic variants, dietary intake and body mass index: insights from 177 330 individuals. <i>Human Molecular Genetics</i> , 2014, 23, 6961-6972.	2.9	143
32	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. <i>Nature Communications</i> , 2018, 9, 3391.	12.8	140
33	Genome-Wide Analysis of Left Ventricular Image-Derived Phenotypes Identifies Fourteen Loci Associated With Cardiac Morphogenesis and Heart Failure Development. <i>Circulation</i> , 2019, 140, 1318-1330.	1.6	138
34	Genome-wide association analysis identifies six new loci associated with forced vital capacity. <i>Nature Genetics</i> , 2014, 46, 669-677.	21.4	131
35	Genome-Wide Joint Meta-Analysis of SNP and SNP-by-Smoking Interaction Identifies Novel Loci for Pulmonary Function. <i>PLoS Genetics</i> , 2012, 8, e1003098.	3.5	130
36	Identification of additional risk loci for stroke and small vessel disease: a meta-analysis of genome-wide association studies. <i>Lancet Neurology</i> , The, 2016, 15, 695-707.	10.2	130

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37	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , 2019, 51, 636-648.	21.4	112
38	Association of Dysanapsis With Chronic Obstructive Pulmonary Disease Among Older Adults. <i>JAMA - Journal of the American Medical Association</i> , 2020, 323, 2268.	7.4	104
39	Genome-Wide Association Study Identifies Novel Loci Associated With Concentrations of Four Plasma Phospholipid Fatty Acids in the De Novo Lipogenesis Pathway. <i>Circulation: Cardiovascular Genetics</i> , 2013, 6, 171-183.	5.1	91
40	Genome-Wide Study of Percent Emphysema on Computed Tomography in the General Population. The Multi-Ethnic Study of Atherosclerosis Lung/SNP Health Association Resource Study. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2014, 189, 408-418.	5.6	87
41	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. <i>Nature Communications</i> , 2018, 9, 2976.	12.8	85
42	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , 2019, 188, 1033-1054.	3.4	85
43	Gene-dietary pattern interactions in obesity: analysis of up to 68 317 adults of European ancestry. <i>Human Molecular Genetics</i> , 2015, 24, 4728-4738.	2.9	84
44	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	12.8	84
45	Metabolic network analysis integrated with transcript verification for sequenced genomes. <i>Nature Methods</i> , 2009, 6, 589-592.	19.0	83
46	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. <i>American Journal of Human Genetics</i> , 2016, 99, 40-55.	6.2	82
47	Human airway branch variation and chronic obstructive pulmonary disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E974-E981.	7.1	80
48	Population Structure of Hispanics in the United States: The Multi-Ethnic Study of Atherosclerosis. <i>PLoS Genetics</i> , 2012, 8, e1002640.	3.5	79
49	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. <i>Nature Communications</i> , 2018, 9, 2606.	12.8	79
50	Overlap of Genetic Risk between Interstitial Lung Abnormalities and Idiopathic Pulmonary Fibrosis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2019, 200, 1402-1413.	5.6	77
51	Meta-Analysis Investigating Associations Between Healthy Diet and Fasting Glucose and Insulin Levels and Modification by Loci Associated With Glucose Homeostasis in Data From 15 Cohorts. <i>American Journal of Epidemiology</i> , 2013, 177, 103-115.	3.4	74
52	Consumption of meat is associated with higher fasting glucose and insulin concentrations regardless of glucose and insulin genetic risk scores: a meta-analysis of 50,345 Caucasians. <i>American Journal of Clinical Nutrition</i> , 2015, 102, 1266-1278.	4.7	69
53	Chronic obstructive pulmonary disease and related phenotypes: polygenic risk scores in population-based and case-control cohorts. <i>Lancet Respiratory Medicine</i> , 2020, 8, 696-708.	10.7	69
54	<i>SLC26A4</i> genotype, but not cochlear radiologic structure, is correlated with hearing loss in ears with an enlarged vestibular aqueduct. <i>Laryngoscope</i> , 2010, 120, 384-389.	2.0	68

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55	Gain-of-Function Lipoprotein Lipase Variant rs13702 Modulates Lipid Traits through Disruption of a MicroRNA-410 Seed Site. <i>American Journal of Human Genetics</i> , 2013, 92, 5-14.	6.2	67
56	The X Chromosome in Quantitative Trait Locus Mapping. <i>Genetics</i> , 2006, 174, 2151-2158.	2.9	66
57	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019, 10, 376.	12.8	64
58	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. <i>American Journal of Human Genetics</i> , 2016, 99, 8-21.	6.2	60
59	Genetic Regulation of Atherosclerosis-Relevant Phenotypes in Human Vascular Smooth Muscle Cells. <i>Circulation Research</i> , 2020, 127, 1552-1565.	4.5	60
60	A Generalized Family-Based Association Test for Dichotomous Traits. <i>American Journal of Human Genetics</i> , 2009, 85, 364-376.	6.2	59
61	Common genetic variants and subclinical atherosclerosis: The Multi-Ethnic Study of Atherosclerosis (MESA). <i>Atherosclerosis</i> , 2016, 245, 230-236.	0.8	59
62	Oestradiol metabolism and androgen receptor genotypes are associated with right ventricular function. <i>European Respiratory Journal</i> , 2016, 47, 553-563.	6.7	54
63	Bicc1 is a genetic determinant of osteoblastogenesis and bone mineral density. <i>Journal of Clinical Investigation</i> , 2014, 124, 2736-2749.	8.2	51
64	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. <i>American Journal of Human Genetics</i> , 2016, 99, 22-39.	6.2	50
65	Common genes underlying asthma and COPD? Genome-wide analysis on the Dutch hypothesis. <i>European Respiratory Journal</i> , 2014, 44, 860-872.	6.7	49
66	Genetic loci associated with circulating phospholipid trans fatty acids: a meta-analysis of genome-wide association studies from the CHARGE Consortium. <i>American Journal of Clinical Nutrition</i> , 2015, 101, 398-406.	4.7	49
67	Rare and Coding Region Genetic Variants Associated With Risk of Ischemic Stroke. <i>JAMA Neurology</i> , 2015, 72, 781.	9.0	49
68	Higher Magnesium Intake Is Associated with Lower Fasting Glucose and Insulin, with No Evidence of Interaction with Select Genetic Loci, in a Meta-Analysis of 15 CHARGE Consortium Studies. <i>Journal of Nutrition</i> , 2013, 143, 345-353.	2.9	47
69	Genome of the Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. <i>Nature Communications</i> , 2015, 6, 6065.	12.8	45
70	Genome-wide meta-analysis of macronutrient intake of 91,114 European ancestry participants from the cohorts for heart and aging research in genomic epidemiology consortium. <i>Molecular Psychiatry</i> , 2019, 24, 1920-1932.	7.9	44
71	Population sequencing data reveal a compendium of mutational processes in the human germ line. <i>Science</i> , 2021, 373, 1030-1035.	12.6	43
72	Association of <i>SCARB1</i> Variants With Subclinical Atherosclerosis and Incident Cardiovascular Disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2012, 32, 1991-1999.	2.4	42

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73	Genome-wide meta-analyses identify novel loci associated with n-3 and n-6 polyunsaturated fatty acid levels in Chinese and European-ancestry populations. <i>Human Molecular Genetics</i> , 2016, 25, 1215-1224.	2.9	42
74	Polygenic transcriptome risk scores (PTRS) can improve portability of polygenic risk scores across ancestries. <i>Genome Biology</i> , 2022, 23, 23.	8.8	42
75	A Genome-Wide Association Study of Chronic Obstructive Pulmonary Disease in Hispanics. <i>Annals of the American Thoracic Society</i> , 2015, 12, 340-348.	3.2	41
76	Meta-analysis of rare and common exome chip variants identifies S1PR4 and other loci influencing blood cell traits. <i>Nature Genetics</i> , 2016, 48, 867-876.	21.4	41
77	D-Dimer in African Americans. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2017, 37, 2220-2227.	2.4	40
78	A Genetic Risk Score Associated with Chronic Obstructive Pulmonary Disease Susceptibility and Lung Structure on Computed Tomography. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2019, 200, 721-731.	5.6	40
79	Whole Genome Sequence Analysis of the Plasma Proteome in Black Adults Provides Novel Insights Into Cardiovascular Disease. <i>Circulation</i> , 2022, 145, 357-370.	1.6	39
80	Genetic loci associated with circulating levels of very long-chain saturated fatty acids. <i>Journal of Lipid Research</i> , 2015, 56, 176-184.	4.2	38
81	APOM and high-density lipoprotein cholesterol are associated with lung function and per cent emphysema. <i>European Respiratory Journal</i> , 2014, 43, 1003-1017.	6.7	37
82	A Genome-Wide Association Study in Hispanics/Latinos Identifies Novel Signals for Lung Function. The Hispanic Community Health Study/Study of Latinos. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018, 198, 208-219.	5.6	37
83	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. <i>International Journal of Epidemiology</i> , 2017, 46, dyw318.	1.9	36
84	Meta-analysis of 49â€¦549 individuals imputed with the 1000 Genomes Project reveals an exonic damaging variant in <i>ANGPTL4</i> determining fasting TG levels. <i>Journal of Medical Genetics</i> , 2016, 53, 441-449.	3.2	34
85	Racial/ethnic differences in the epidemiology of ovarian cancer: a pooled analysis of 12 case-control studies. <i>International Journal of Epidemiology</i> , 2018, 47, 460-472.	1.9	33
86	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. <i>Nature Communications</i> , 2020, 11, 5182.	12.8	32
87	Lymphocyte activation gene 3 and coronary artery disease. <i>JCI Insight</i> , 2016, 1, e88628.	5.0	32
88	Genome-wide association study of subclinical interstitial lung disease in MESA. <i>Respiratory Research</i> , 2017, 18, 97.	3.6	31
89	Genetic variants associated with VLDL, LDL and HDL particle size differ with race/ethnicity. <i>Human Genetics</i> , 2013, 132, 405-413.	3.8	30
90	Genetic ancestry and the relationship of cigarette smoking to lung function and per cent emphysema in four race/ethnic groups: a cross-sectional study. <i>Thorax</i> , 2013, 68, 634-642.	5.6	30

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91	Fine-mapping of lipid regions in global populations discovers ethnic-specific signals and refines previously identified lipid loci. <i>Human Molecular Genetics</i> , 2016, 25, 5500-5512.	2.9	29
92	AtheroSpectrum Reveals Novel Macrophage Foam Cell Gene Signatures Associated With Atherosclerotic Cardiovascular Disease Risk. <i>Circulation</i> , 2022, 145, 206-218.	1.6	29
93	Integrative pathway genomics of lung function and airflow obstruction. <i>Human Molecular Genetics</i> , 2015, 24, 6836-6848.	2.9	28
94	Plasma Soluble Receptor for Advanced Glycation End Products in Idiopathic Pulmonary Fibrosis. <i>Annals of the American Thoracic Society</i> , 2017, 14, 628-635.	3.2	28
95	Evaluation of the Thyroid in Patients With Hearing Loss and Enlarged Vestibular Aqueducts. <i>JAMA Otolaryngology</i> , 2009, 135, 670.	1.2	27
96	<i>KCNK3</i> Variants Are Associated With Hyperaldosteronism and Hypertension. <i>Hypertension</i> , 2016, 68, 356-364.	2.7	27
97	Association of the Lipoprotein Receptor SCARB1 Common Missense Variant rs4238001 with Incident Coronary Heart Disease. <i>PLoS ONE</i> , 2015, 10, e0125497.	2.5	26
98	Significance Thresholds for Quantitative Trait Locus Mapping Under Selective Genotyping. <i>Genetics</i> , 2007, 177, 1963-1966.	2.9	25
99	Characterization of <i>Ath29</i> , a major mouse atherosclerosis susceptibility locus, and identification of <i>Rcn2</i> as a novel regulator of cytokine expression. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2011, 301, H1056-H1061.	3.2	25
100	TOP-LD: A tool to explore linkage disequilibrium with TOPMed whole-genome sequence data. <i>American Journal of Human Genetics</i> , 2022, 109, 1175-1181.	6.2	25
101	Variant Discovery and Fine Mapping of Genetic Loci Associated with Blood Pressure Traits in Hispanics and African Americans. <i>PLoS ONE</i> , 2016, 11, e0164132.	2.5	24
102	Interaction of methylation-related genetic variants with circulating fatty acids on plasma lipids: a meta-analysis of 7 studies and methylation analysis of 3 studies in the Cohorts for Heart and Aging Research in Genomic Epidemiology consortium. <i>American Journal of Clinical Nutrition</i> , 2016, 103, 567-578.	4.7	24
103	Genetic association of long-chain acyl-CoA synthetase 1 variants with fasting glucose, diabetes, and subclinical atherosclerosis. <i>Journal of Lipid Research</i> , 2016, 57, 433-442.	4.2	24
104	Prognostic Significance of Large Airway Dimensions on Computed Tomography in the General Population. The Multi-Ethnic Study of Atherosclerosis (MESA) Lung Study. <i>Annals of the American Thoracic Society</i> , 2018, 15, 718-727.	3.2	24
105	APOE genotype modifies the association between plasma omega-3 fatty acids and plasma lipids in the Multi-Ethnic Study of Atherosclerosis (MESA). <i>Atherosclerosis</i> , 2013, 228, 181-187.	0.8	22
106	Whole-Genome Sequencing in Severe Chronic Obstructive Pulmonary Disease. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2018, 59, 614-622.	2.9	22
107	Modifiers of von Willebrand factor identified by natural variation in inbred strains of mice. <i>Blood</i> , 2009, 114, 5368-5374.	1.4	20
108	Integrative genomics identifies new genes associated with severe COPD and emphysema. <i>Respiratory Research</i> , 2018, 19, 46.	3.6	20

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109	Genetic Landscape of the ACE2 Coronavirus Receptor. <i>Circulation</i> , 2022, 145, 1398-1411.	1.6	20
110	Dissecting the genetics of chronic mucus hypersecretion in smokers with and without COPD. <i>European Respiratory Journal</i> , 2015, 45, 60-75.	6.7	19
111	Associations between emphysema-like lung on CT and incident airflow limitation: a general population-based cohort study. <i>Thorax</i> , 2018, 73, 486-488.	5.6	19
112	Meta-analysis of exome array data identifies six novel genetic loci for lung function. <i>Wellcome Open Research</i> , 2018, 3, 4.	1.8	19
113	A Functionally Significant Polymorphism in ID3 Is Associated with Human Coronary Pathology. <i>PLoS ONE</i> , 2014, 9, e90222.	2.5	18
114	Discovery and fine-mapping of loci associated with MUFAs through trans-ethnic meta-analysis in Chinese and European populations. <i>Journal of Lipid Research</i> , 2017, 58, 974-981.	4.2	18
115	Distribution of the FMR1 gene in females by race/ethnicity: women with diminished ovarian reserve versus women with normal fertility (SWAN study). <i>Fertility and Sterility</i> , 2017, 107, 205-211.e1.	1.0	18
116	Genome-wide association meta-analysis of fish and EPA+DHA consumption in 17 US and European cohorts. <i>PLoS ONE</i> , 2017, 12, e0186456.	2.5	18
117	Identification of novel epithelial ovarian cancer loci in women of African ancestry. <i>International Journal of Cancer</i> , 2020, 146, 2987-2998.	5.1	18
118	Atherosclerosis Susceptibility Loci Identified in an Extremely Atherosclerosis-Resistant Mouse Strain. <i>Journal of the American Heart Association</i> , 2013, 2, e000260.	3.7	17
119	Genetic linkage of oxidative stress with cardiometabolic traits in an intercross derived from hyperlipidemic mouse strains. <i>Atherosclerosis</i> , 2020, 293, 1-10.	0.8	16
120	Characterisation of gas exchange in COPD with dissolved-phase hyperpolarised xenon-129 MRI. <i>Thorax</i> , 2021, 76, 178-181.	5.6	16
121	Analysis of family- and population-based samples in cohort genome-wide association studies. <i>Human Genetics</i> , 2012, 131, 275-287.	3.8	15
122	Genome-wide association meta-analysis of circulating odd-numbered chain saturated fatty acids: Results from the CHARGE Consortium. <i>PLoS ONE</i> , 2018, 13, e0196951.	2.5	14
123	Omega-3 Fatty Acids and Genome-Wide Interaction Analyses Reveal <i>DPP10</i> Pulmonary Function Association. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2019, 199, 631-642.	5.6	14
124	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
125	Protein prediction for trait mapping in diverse populations. <i>PLoS ONE</i> , 2022, 17, e0264341.	2.5	13
126	Genetic Contributors to Otitis Media: Agnostic Discovery Approaches. <i>Current Allergy and Asthma Reports</i> , 2014, 14, 411.	5.3	12



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127	Genetic linkage of hyperglycemia and dyslipidemia in an intercross between BALB/cj and SM/J Apoe-deficient mouse strains. <i>BMC Genetics</i> , 2015, 16, 133.	2.7	12
128	Detailed analysis of association between common single nucleotide polymorphisms and subclinical atherosclerosis: The Multi-ethnic Study of Atherosclerosis. <i>Data in Brief</i> , 2016, 7, 229-242.	1.0	12
129	Genetic analysis of atherosclerosis identifies a major susceptibility locus in the major histocompatibility complex of mice. <i>Atherosclerosis</i> , 2016, 254, 124-132.	0.8	12
130	FMRI CGG Repeats:Reference Levels and Race-Ethnic Variation in Women With Normal Fertility (Study) <i>Tj ETQq0 0 0 rgBT /Overlock 10 T</i>	2.5	12
131	Interpreting Clinical Trials With Omega-3 Supplements in the Context of Ancestry and FADS Genetic Variation. <i>Frontiers in Nutrition</i> , 2021, 8, 808054.	3.7	12
132	Resistance to Noise-Induced Hearing Loss in 129S6 and MOLF Mice: Identification of Independent, Overlapping, and Interacting Chromosomal Regions. <i>JARO - Journal of the Association for Research in Otolaryngology</i> , 2014, 15, 721-738.	1.8	11
133	A systematic analysis of protein-altering exonic variants in chronic obstructive pulmonary disease. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2021, 321, L130-L143.	2.9	11
134	Impact of Amerind ancestry and FADS genetic variation on omega-3 deficiency and cardiometabolic traits in Hispanic populations. <i>Communications Biology</i> , 2021, 4, 918.	4.4	11
135	Meta-analysis of exome array data identifies six novel genetic loci for lung function. <i>Wellcome Open Research</i> , 0, 3, 4.	1.8	11
136	Meta-analysis of genome-wide association studies identifies three novel loci for saturated fatty acids in East Asians. <i>European Journal of Nutrition</i> , 2017, 56, 1477-1484.	3.9	10
137	Sequencing Analysis at 8p23 Identifies Multiple Rare Variants in DLC1 Associated with Sleep-Related Oxyhemoglobin Saturation Level. <i>American Journal of Human Genetics</i> , 2019, 105, 1057-1068.	6.2	10
138	Nonclassical Monocytes (CD14dimCD16+) Are Associated With Carotid Intima-Media Thickness Progression for Men but Not Women. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2021, 41, 1810-1817.	2.4	10
139	Meta-analysis across Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium provides evidence for an association of serum vitamin D with pulmonary function. <i>British Journal of Nutrition</i> , 2018, 120, 1159-1170.	2.3	9
140	Whole genome sequence analysis of platelet traits in the NHLBI Trans-Omics for Precision Medicine (TOPMed) initiative. <i>Human Molecular Genetics</i> , 2022, 31, 347-361.	2.9	9
141	Evaluation of Replication of Variants Associated with Genetic Risk of Otitis Media. <i>PLoS ONE</i> , 2014, 9, e104212.	2.5	8
142	Fine mapping the CETP region reveals a common intronic insertion associated to HDL-C. <i>Npj Aging and Mechanisms of Disease</i> , 2015, 1, 15011.	4.5	8
143	Acculturation and Plasma Fatty Acid Concentrations in Hispanic and Chinese-American Adults: The Multi-Ethnic Study of Atherosclerosis. <i>PLoS ONE</i> , 2016, 11, e0149267.	2.5	7
144	Polygenic transcriptome risk scores for COPD and lung function improve cross-ethnic portability of prediction in the NHLBI TOPMed program. <i>American Journal of Human Genetics</i> , 2022, 109, 857-870.	6.2	7

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145	Binary Trait Mapping in Experimental Crosses With Selective Genotyping. <i>Genetics</i> , 2009, 182, 863-874.	2.9	6
146	Evaluation of vitamin D biosynthesis and pathway target genes reveals UGT2A1/2 and EGFR polymorphisms associated with epithelial ovarian cancer in African American Women. <i>Cancer Medicine</i> , 2019, 8, 2503-2513.	2.8	6
147	Robust, flexible, and scalable tests for Hardy-Weinberg equilibrium across diverse ancestries. <i>Genetics</i> , 2021, 218, .	2.9	6
148	Pleiotropy-guided transcriptome imputation from normal and tumor tissues identifies candidate susceptibility genes for breast and ovarian cancer. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100042.	1.7	6
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