Ani W Manichaikul

List of Publications by Year
in descending order

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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	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
2	Whole Genome Sequence Analysis of the Plasma Proteome in Black Adults Provides Novel Insights Into Cardiovascular Disease. Circulation, 2022, 145, 357-370.	1.6	39
3	Polygenic transcriptome risk scores (PTRS) can improve portability of polygenic risk scores across ancestries. Genome Biology, 2022, 23, 23.	8.8	42
4	AtheroSpectrum Reveals Novel Macrophage Foam Cell Gene Signatures Associated With Atherosclerotic Cardiovascular Disease Risk. Circulation, 2022, 145, 206-218.	1.6	29
5	Protein prediction for trait mapping in diverse populations. PLoS ONE, 2022, 17, e0264341.	2.5	13
6	Reticulocalbin 2 as a Potential Biomarker and Therapeutic Target for Atherosclerosis. Cells, 2022, 11, 1107.	4.1	3
7	Polygenic transcriptome risk scores for COPD and lung function improve cross-ethnic portability of prediction in the NHLBI TOPMed program. American Journal of Human Genetics, 2022, 109, 857-870.	6.2	7
8	Genetic Landscape of the ACE2 Coronavirus Receptor. Circulation, 2022, 145, 1398-1411.	1.6	20
9	TOP-LD: A tool to explore linkage disequilibrium with TOPMed whole-genome sequence data. American Journal of Human Genetics, 2022, 109, 1175-1181.	6.2	25
10	Lymphocyte activation gene-3-associated protein networks are associated with HDL-cholesterol and mortality in the Trans-omics for Precision Medicine program. Communications Biology, 2022, 5, 362.	4.4	5
11	Assessing the contribution of rare genetic variants to phenotypes of chronic obstructive pulmonary disease using whole-genome sequence data. Human Molecular Genetics, 2022, 31, 3873-3885.	2.9	2
12	Characterisation of gas exchange in COPD with dissolved-phase hyperpolarised xenon-129 MRI. Thorax, 2021, 76, 178-181.	5.6	16
13	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
14	Robust, flexible, and scalable tests for Hardyâ€“Weinberg equilibrium across diverse ancestries. Genetics, 2021, 218, .	2.9	6
15	Nonclassical Monocytes (CD14dimCD16+) Are Associated With Carotid Intima-Media Thickness Progression for Men but Not Women. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, 1810-1817.	2.4	10
16	Pleiotropy-guided transcriptome imputation from normal and tumor tissues identifies candidate susceptibility genes for breast and ovarian cancer. Human Genetics and Genomics Advances, 2021, 2, 100042.	1.7	6
17	A systematic analysis of protein-altering exonic variants in chronic obstructive pulmonary disease. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2021, 321, L130-L143.	2.9	11
18	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

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19	Population sequencing data reveal a compendium of mutational processes in the human germ line. Science, 2021, 373, 1030-1035.	12.6	43
20	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
21	Rare and low-frequency exonic variants and gene-by-smoking interactions in pulmonary function. Scientific Reports, 2021, 11, 19365.	3.3	2
22	Dynamic changes in immune gene co-expression networks predict development of type 1 diabetes. Scientific Reports, 2021, 11, 22651.	3.3	3
23	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
24	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
25	Genome-Wide Association Study of Susceptibility to Idiopathic Pulmonary Fibrosis. American Journal of Respiratory and Critical Care Medicine, 2020, 201, 564-574.	5.6	208
26	Identification of novel epithelial ovarian cancer loci in women of African ancestry. International Journal of Cancer, 2020, 146, 2987-2998.	5.1	18
27	Genetic linkage of oxidative stress with cardiometabolic traits in an intercross derived from hyperlipidemic mouse strains. Atherosclerosis, 2020, 293, 1-10.	0.8	16
28	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. Nature Communications, 2020, 11, 5182.	12.8	32
29	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	28.9	388
30	Genetic Regulation of Atherosclerosis-Relevant Phenotypes in Human Vascular Smooth Muscle Cells. Circulation Research, 2020, 127, 1552-1565.	4.5	60
31	Data on genetic linkage of oxidative stress with cardiometabolic traits in an intercross derived from hyperlipidemic mouse strains. Data in Brief, 2020, 29, 105165.	1.0	0
32	Chronic obstructive pulmonary disease and related phenotypes: polygenic risk scores in population-based and case-control cohorts. Lancet Respiratory Medicine,the, 2020, 8, 696-708.	10.7	69
33	Multi-omic studies on missense PLG variants in families with otitis media. Scientific Reports, 2020, 10, 15035.	3.3	4
34	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. Cell, 2020, 182, 1198-1213.e14.	28.9	353
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	Association of Dysanapsis With Chronic Obstructive Pulmonary Disease Among Older Adults. JAMA - Journal of the American Medical Association, 2020, 323, 2268.	7.4	104

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37	Fatty Acid Desaturase Geneâ€Induced Omegaâ€3 Deficiency in Amerindianâ€Ancestry Hispanic Populations. FASEB Journal, 2020, 34, 1-1.	0.5	2
38	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. Molecular Psychiatry, 2019, 24, 1920-1932.	7.9	44
39	Overlap of Genetic Risk between Interstitial Lung Abnormalities and Idiopathic Pulmonary Fibrosis. American Journal of Respiratory and Critical Care Medicine, 2019, 200, 1402-1413.	5.6	77
40	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
41	Sequencing Analysis at 8p23 Identifies Multiple Rare Variants in DLC1 Associated with Sleep-Related Oxyhemoglobin Saturation Level. American Journal of Human Genetics, 2019, 105, 1057-1068.	6.2	10
42	Genome-Wide Analysis of Left Ventricular Image-Derived Phenotypes Identifies Fourteen Loci Associated With Cardiac Morphogenesis and Heart Failure Development. Circulation, 2019, 140, 1318-1330.	1.6	138
43	Whole Genome Sequencing Identifies CRISPLD2 as a Lung Function Gene in Children With Asthma. Chest, 2019, 156, 1068-1079.	0.8	5
44	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
45	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
46	Positive Associations of Dietary Marine Omega-3 Polyunsaturated Fatty Acids with Lung Function: A Meta-analysis (P18-087-19). Current Developments in Nutrition, 2019, 3, nzz039.P18-087-19.	0.3	1
47	Evaluation of vitamin D biosynthesis and pathway target genes reveals UGT2A1/2 and EGFR polymorphisms associated with epithelial ovarian cancer in African American Women. Cancer Medicine, 2019, 8, 2503-2513.	2.8	6
48	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
49	A Genetic Risk Score Associated with Chronic Obstructive Pulmonary Disease Susceptibility and Lung Structure on Computed Tomography. American Journal of Respiratory and Critical Care Medicine, 2019, 200, 721-731.	5.6	40
50	Genetic landscape of chronic obstructive pulmonary disease identifies heterogeneous cell-type and phenotype associations. Nature Genetics, 2019, 51, 494-505.	21.4	257
51	Omega-3 Fatty Acids and Genome-Wide Interaction Analyses Reveal DPP10â€“Pulmonary Function Association. American Journal of Respiratory and Critical Care Medicine, 2019, 199, 631-642.	5.6	14
52	A Genome-Wide Association Study in Hispanics/Latinos Identifies Novel Signals for Lung Function. The Hispanic Community Health Study/Study of Latinos. American Journal of Respiratory and Critical Care Medicine, 2018, 198, 208-219.	5.6	37
53	Human airway branch variation and chronic obstructive pulmonary disease. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E974-E981.	7.1	80
54	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	21.4	426

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55	Racial/ethnic differences in the epidemiology of ovarian cancer: a pooled analysis of 12 case-control studies. International Journal of Epidemiology, 2018, 47, 460-472.	1.9	33
56	Prognostic Significance of Large Airway Dimensions on Computed Tomography in the General Population. The Multi-Ethnic Study of Atherosclerosis (MESA) Lung Study. Annals of the American Thoracic Society, 2018, 15, 718-727.	3.2	24
57	Associations between emphysema-like lung on CT and incident airflow limitation: a general population-based cohort study. Thorax, 2018, 73, 486-488.	5.6	19
58	Lp-PLA2, scavenger receptor class B type I gene (SCARB1) rs10846744 variant, and cardiovascular disease. PLoS ONE, 2018, 13, e0204352.	2.5	2
59	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. British Journal of Nutrition, 2018, 120, 1159-1170.	2.3	9
60	Genome-wide association meta-analysis of circulating odd-numbered chain saturated fatty acids: Results from the CHARGE Consortium. PLoS ONE, 2018, 13, e0196951.	2.5	14
61	Whole-Genome Sequencing in Severe Chronic Obstructive Pulmonary Disease. American Journal of Respiratory Cell and Molecular Biology, 2018, 59, 614-622.	2.9	22
62	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. Nature Communications, 2018, 9, 2606.	12.8	79
63	Integrative genomics identifies new genes associated with severe COPD and emphysema. Respiratory Research, 2018, 19, 46.	3.6	20
64	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. Nature Communications, 2018, 9, 3391.	12.8	140
65	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. Nature Communications, 2018, 9, 2976.	12.8	85
66	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. Nature Genetics, 2018, 50, 524-537.	21.4	1,124
67	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 2018, 3, 4.	1.8	19
68	Meta-analysis of genome-wide association studies identifies three novel loci for saturated fatty acids in East Asians. European Journal of Nutrition, 2017, 56, 1477-1484.	3.9	10
69	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. International Journal of Epidemiology, 2017, 46, dyw318.	1.9	36
70	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. JAMA Oncology, 2017, 3, 636.	7.1	376
71	Genetic loci associated with chronic obstructive pulmonary disease overlap with loci for lung function and pulmonary fibrosis. Nature Genetics, 2017, 49, 426-432.	21.4	306
72	Plasma Soluble Receptor for Advanced Glycation End Products in Idiopathic Pulmonary Fibrosis. Annals of the American Thoracic Society, 2017, 14, 628-635.	3.2	28

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73	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	12.8	169
74	Discovery and fine-mapping of loci associated with MUFAs through trans-ethnic meta-analysis in Chinese and European populations. Journal of Lipid Research, 2017, 58, 974-981.	4.2	18
75	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470
76	D-Dimer in African Americans. Arteriosclerosis, Thrombosis, and Vascular Biology, 2017, 37, 2220-2227.	2.4	40
77	Genetic studies as a tool for identifying novel potential targets for treatment ofÂCOPD. European Respiratory Journal, 2017, 50, 1702042.	6.7	1
78	Genome-wide association study of subclinical interstitial lung disease in MESA. Respiratory Research, 2017, 18, 97.	3.6	31
79	Distribution of the FMR1 gene in females by race/ethnicity: women with diminished ovarian reserve versus women with normal fertility (SWAN study). Fertility and Sterility, 2017, 107, 205-211.e1.	1.0	18
80	Genome-wide association meta-analysis of fish and EPA+DHA consumption in 17 US and European cohorts. PLoS ONE, 2017, 12, e0186456.	2.5	18
81	Acculturation and Plasma Fatty Acid Concentrations in Hispanic and Chinese-American Adults: The Multi-Ethnic Study of Atherosclerosis. PLoS ONE, 2016, 11, e0149267.	2.5	7
82	Variant Discovery and Fine Mapping of Genetic Loci Associated with Blood Pressure Traits in Hispanics and African Americans. PLoS ONE, 2016, 11, e0164132.	2.5	24
83	Meta-analysis of rare and common exome chip variants identifies S1PR4 and other loci influencing blood cell traits. Nature Genetics, 2016, 48, 867-876.	21.4	41
84	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. American Journal of Human Genetics, 2016, 99, 8-21.	6.2	60
85	Meta-analysis of 49â€…549 individuals imputed with the 1000 Genomes Project reveals an exonic damaging variant inANGPTL4determining fasting TG levels. Journal of Medical Genetics, 2016, 53, 441-449.	3.2	34
86	Data on genetic analysis of atherosclerosis identifies a major susceptibility locus in the major histocompatibility complex of mice. Data in Brief, 2016, 9, 1067-1069.	1.0	0
87	Identification of additional risk loci for stroke and small vessel disease: a meta-analysis of genome-wide association studies. Lancet Neurology, The, 2016, 15, 695-707.	10.2	130
88	Detailed analysis of association between common single nucleotide polymorphisms and subclinical atherosclerosis: The Multi-ethnic Study of Atherosclerosis. Data in Brief, 2016, 7, 229-242.	1.0	12
89	Genetic analysis of atherosclerosis identifies a major susceptibility locus in the major histocompatibility complex of mice. Atherosclerosis, 2016, 254, 124-132.	0.8	12
90	KLB is associated with alcohol drinking, and its gene product Î²-Klotho is necessary for FGF21 regulation of alcohol preference. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14372-14377.	7.1	208

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91	Fine-mapping of lipid regions in global populations discovers ethnic-specific signals and refines previously identified lipid loci. Human Molecular Genetics, 2016, 25, 5500-5512.	2.9	29
92	KCNK3 Variants Are Associated With Hyperaldosteronism and Hypertension. Hypertension, 2016, 68, 356-364.	2.7	27
93	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	6.2	82
94	FMRI CGG Repeats:Reference Levels and Race-Ethnic Variation in Women With Normal Fertility (Study) Tj ETQq0 0 0 rgBT /Overlock 10 T	2.5	12
95	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
96	Genome-wide meta-analyses identify novel loci associated with n-3 and n-6 polyunsaturated fatty acid levels in Chinese and European-ancestry populations. Human Molecular Genetics, 2016, 25, 1215-1224.	2.9	42
97	Common genetic variants and subclinical atherosclerosis: The Multi-Ethnic Study of Atherosclerosis (MESA). Atherosclerosis, 2016, 245, 230-236.	0.8	59
98	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. American Journal of Clinical Nutrition, 2016, 103, 567-578.	4.7	24
99	Loci associated with ischaemic stroke and its subtypes (SiGN): a genome-wide association study. Lancet Neurology, The, 2016, 15, 174-184.	10.2	217
100	Oestradiol metabolism and androgen receptor genotypes are associated with right ventricular function. European Respiratory Journal, 2016, 47, 553-563.	6.7	54
101	Genetic association of long-chain acyl-CoA synthetase 1 variants with fasting glucose, diabetes, and subclinical atherosclerosis. Journal of Lipid Research, 2016, 57, 433-442.	4.2	24
102	Lymphocyte activation gene 3 and coronary artery disease. JCI Insight, 2016, 1, e88628.	5.0	32
103	Fine mapping the CETP region reveals a common intronic insertion associated to HDL-C. Npj Aging and Mechanisms of Disease, 2015, 1, 15011.	4.5	8
104	Genetic linkage of hyperglycemia and dyslipidemia in an intercross between BALB/cJ and SM/J Apoe-deficient mouse strains. BMC Genetics, 2015, 16, 133.	2.7	12
105	Association of the Lipoprotein Receptor SCARB1 Common Missense Variant rs4238001 with Incident Coronary Heart Disease. PLoS ONE, 2015, 10, e0125497.	2.5	26
106	Gene Ã— dietary pattern interactions in obesity: analysis of up to 68 317 adults of European ancestry. Human Molecular Genetics, 2015, 24, 4728-4738.	2.9	84
107	Genetic loci associated with circulating phospholipid trans fatty acids: a meta-analysis of genome-wide association studies from the CHARGE Consortium. American Journal of Clinical Nutrition, 2015, 101, 398-406.	4.7	49
108	Genetic loci associated with circulating levels of very long-chain saturated fatty acids. Journal of Lipid Research, 2015, 56, 176-184.	4.2	38

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109	A Genome-Wide Association Study of Chronic Obstructive Pulmonary Disease in Hispanics. Annals of the American Thoracic Society, 2015, 12, 340-348.	3.2	41
110	Rare and Coding Region Genetic Variants Associated With Risk of Ischemic Stroke. JAMA Neurology, 2015, 72, 781.	9.0	49
111	Integrative pathway genomics of lung function and airflow obstruction. Human Molecular Genetics, 2015, 24, 6836-6848.	2.9	28
112	Genome of the Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. Nature Communications, 2015, 6, 6065.	12.8	45
113	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. American Journal of Clinical Nutrition, 2015, 102, 1266-1278.	4.7	69
114	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. Molecular Psychiatry, 2015, 20, 647-656.	7.9	235
115	Dissecting the genetics of chronic mucus hypersecretion in smokers with and without COPD. European Respiratory Journal, 2015, 45, 60-75.	6.7	19
116	A Functionally Significant Polymorphism in ID3 Is Associated with Human Coronary Pathology. PLoS ONE, 2014, 9, e90222.	2.5	18
117	Evaluation of Replication of Variants Associated with Genetic Risk of Otitis Media. PLoS ONE, 2014, 9, e104212.	2.5	8
118	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. American Journal of Respiratory and Critical Care Medicine, 2014, 189, 408-418.	5.6	87
119	Genome-Wide Association Study of Plasma N6 Polyunsaturated Fatty Acids Within the Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium. Circulation: Cardiovascular Genetics, 2014, 7, 321-331.	5.1	164
120	APOM and high-density lipoprotein cholesterol are associated with lung function and per cent emphysema. European Respiratory Journal, 2014, 43, 1003-1017.	6.7	37
121	FTO genetic variants, dietary intake and body mass index: insights from 177 330 individuals. Human Molecular Genetics, 2014, 23, 6961-6972.	2.9	143
122	Genetic Contributors to Otitis Media: Agnostic Discovery Approaches. Current Allergy and Asthma Reports, 2014, 14, 411.	5.3	12
123	Association of Low-Frequency and Rare Coding-Sequence Variants with Blood Lipids and Coronary Heart Disease in 56,000 Whites and Blacks. American Journal of Human Genetics, 2014, 94, 223-232.	6.2	287
124	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	6.2	193
125	Genome-wide association analysis identifies six new loci associated with forced vital capacity. Nature Genetics, 2014, 46, 669-677.	21.4	131
126	Resistance to Noise-Induced Hearing Loss in 129S6 and MOLF Mice: Identification of Independent, Overlapping, and Interacting Chromosomal Regions. JARO - Journal of the Association for Research in Otolaryngology, 2014, 15, 721-738.	1.8	11

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127	Common genes underlying asthma and COPD? Genome-wide analysis on the Dutch hypothesis. European Respiratory Journal, 2014, 44, 860-872.	6.7	49
128	Bicc1 is a genetic determinant of osteoblastogenesis and bone mineral density. Journal of Clinical Investigation, 2014, 124, 2736-2749.	8.2	51
129	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. American Journal of Epidemiology, 2013, 177, 103-115.	3.4	74
130	Gain-of-Function Lipoprotein Lipase Variant rs13702 Modulates Lipid Traits through Disruption of a MicroRNA-410 Seed Site. American Journal of Human Genetics, 2013, 92, 5-14.	6.2	67
131	APOE genotype modifies the association between plasma omega-3 fatty acids and plasma lipids in the Multi-Ethnic Study of Atherosclerosis (MESA). Atherosclerosis, 2013, 228, 181-187.	0.8	22
132	Genetic variants associated with VLDL, LDL and HDL particle size differ with race/ethnicity. Human Genetics, 2013, 132, 405-413.	3.8	30
133	Atherosclerosis Susceptibility Loci Identified in an Extremely AtherosclerosisâEResistant Mouse Strain. Journal of the American Heart Association, 2013, 2, e000260.	3.7	17
134	Genome-wide meta-analysis of observational studies shows common genetic variants associated with macronutrient intake. American Journal of Clinical Nutrition, 2013, 97, 1395-1402.	4.7	210
135	Genetic ancestry and the relationship of cigarette smoking to lung function and per cent emphysema in four race/ethnic groups: a cross-sectional study. Thorax, 2013, 68, 634-642.	5.6	30
136	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. Journal of Nutrition, 2013, 143, 345-353.	2.9	47
137	Genome-Wide Association Study Identifies Novel Loci Associated With Concentrations of Four Plasma Phospholipid Fatty Acids in the De Novo Lipogenesis Pathway. Circulation: Cardiovascular Genetics, 2013, 6, 171-183.	5.1	91
138	Population Structure of Hispanics in the United States: The Multi-Ethnic Study of Atherosclerosis. PLoS Genetics, 2012, 8, e1002640.	3.5	79
139	Genome-Wide Joint Meta-Analysis of SNP and SNP-by-Smoking Interaction Identifies Novel Loci for Pulmonary Function. PLoS Genetics, 2012, 8, e1003098.	3.5	130
140	Genome-Wide Association Studies Identify CHRNA5/3 and HTR4 in the Development of Airflow Obstruction. American Journal of Respiratory and Critical Care Medicine, 2012, 186, 622-632.	5.6	164
141	Association of SCARB1 Variants With Subclinical Atherosclerosis and Incident Cardiovascular Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2012, 32, 1991-1999.	2.4	42
142	Single Nucleotide Polymorphisms In The Apolipoprotein M Gene Are Associated With Percent Emphysema, HDL And HDL Subfractions Among European- And African-Americans: The MESA Lung And SNP Health Association Resource (SHARe) Studies. , 2012, , .		0
143	Analysis of family- and population-based samples in cohort genome-wide association studies. Human Genetics, 2012, 131, 275-287.	3.8	15
144	Metabolic network reconstruction of Chlamydomonas offers insight into lightâEdriven algal metabolism. Molecular Systems Biology, 2011, 7, 518.	7.2	264

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145	A Genome-Wide Association Study To Assess Loci Associated With Lung Function Among Hispanic-Americans And Asian-Americans: The Mesa Lung Share Study. , 2011, , .		0
146	Genome-Wide Association Study (GWAS) Of Lung Function Among African-Americans In 5 National Heart, Lung, And Blood Institute (NHLBI) Cohorts. The Candidate-Gene Association Resource (CARE). , 2011, , .		0
147	Identifying variants that contribute to linkage for dichotomous and quantitative traits in extended pedigrees. BMC Proceedings, 2011, 5, S68.	1.6	1
148	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. Nature Genetics, 2011, 43, 1082-1090.	21.4	367
149	Characterization of Ath29, a major mouse atherosclerosis susceptibility locus, and identification of Rcn2 as a novel regulator of cytokine expression. American Journal of Physiology - Heart and Circulatory Physiology, 2011, 301, H1056-H1061.	3.2	25
150	Genetic Loci Associated with Plasma Phospholipid n-3 Fatty Acids: A Meta-Analysis of Genome-Wide Association Studies from the CHARGE Consortium. PLoS Genetics, 2011, 7, e1002193.	3.5	324
151	SLC26A4 genotype, but not cochlear radiologic structure, is correlated with hearing loss in ears with an enlarged vestibular aqueduct. Laryngoscope, 2010, 120, 384-389.	2.0	68
152	Robust relationship inference in genome-wide association studies. Bioinformatics, 2010, 26, 2867-2873.	4.1	2,328
153	Binary Trait Mapping in Experimental Crosses With Selective Genotyping. Genetics, 2009, 182, 863-874.	2.9	6
154	A Model Selection Approach for the Identification of Quantitative Trait Loci in Experimental Crosses, Allowing Epistasis. Genetics, 2009, 181, 1077-1086.	2.9	149
155	Allelic Polymorphism within the TAS1R3 Promoter Is Associated with Human Taste Sensitivity to Sucrose. Current Biology, 2009, 19, 1288-1293.	3.9	185
156	NK gene complex and chromosome 19 loci enhance MHC resistance to murine cytomegalovirus infection. Immunogenetics, 2009, 61, 755-764.	2.4	5
157	Metabolic network analysis integrated with transcript verification for sequenced genomes. Nature Methods, 2009, 6, 589-592.	19.0	83
158	A Generalized Family-Based Association Test for Dichotomous Traits. American Journal of Human Genetics, 2009, 85, 364-376.	6.2	59
159	Evaluation of the Thyroid in Patients With Hearing Loss and Enlarged Vestibular Aqueducts. JAMA Otolaryngology, 2009, 135, 670.	1.2	27
160	Modifiers of von Willebrand factor identified by natural variation in inbred strains of mice. Blood, 2009, 114, 5368-5374.	1.4	20
161	Significance Thresholds for Quantitative Trait Locus Mapping Under Selective Genotyping. Genetics, 2007, 177, 1963-1966.	2.9	25
162	Spectrum of heart disease associated with murine and human GATA4 mutation. Journal of Molecular and Cellular Cardiology, 2007, 43, 677-685.	1.9	218

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163	Poor Performance of Bootstrap Confidence Intervals for the Location of a Quantitative Trait Locus. Genetics, 2006, 174, 481-489.	2.9	184
164	The X Chromosome in Quantitative Trait Locus Mapping. Genetics, 2006, 174, 2151-2158.	2.9	66
165	Genetic Correlates of Musical Pitch Recognition in Humans. Science, 2001, 291, 1969-1972.	12.6	256
166	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	1.8	11
167	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	1.8	1