Yongmei Liu

List of Publications by Year
in descending order

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120 papers	18,055 citations	36303 51 h-index	18130 120 g-index
128 all docs	128 docs citations	128 times ranked	27941 citing authors

#	Article	IF	Citations
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
2	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
3	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
4	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
5	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
6	The transcriptional landscape of age in human peripheral blood. Nature Communications, 2015, 6, 8570.	12.8	533
7	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	21.4	426
8	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
9	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	21.4	357
10	Meta-analysis of Correlated Traits via Summary Statistics from GWASs with an Application in Hypertension. American Journal of Human Genetics, 2015, 96, 21-36.	6.2	321
11	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. Nature Communications, 2018, 9, 260.	12.8	295
12	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
13	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
14	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	21.4	284
15	Life-Course Genome-wide Association Study Meta-analysis of Total Body BMD and Assessment of Age-Specific Effects. American Journal of Human Genetics, 2018, 102, 88-102.	6.2	252
16	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	21.4	250
17	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	12.8	245
18	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. Molecular Psychiatry, 2015, 20, 647-656.	7.9	235

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19	Pharmacogenetic meta-analysis of genome-wide association studies of LDL cholesterol response to statins. Nature Communications, 2014, 5, 5068.	12.8	216
20	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
21	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
22	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
23	Age-related variations in the methylome associated with gene expression in human monocytes and T cells. Nature Communications, 2014, 5, 5366.	12.8	168
24	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
25	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. American Journal of Human Genetics, 2017, 101, 888-902.	6.2	154
26	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	12.8	153
27	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	12.8	147
28	Genome-wide association analysis identifies six new loci associated with forced vital capacity. Nature Genetics, 2014, 46, 669-677.	21.4	131
29	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. American Journal of Human Genetics, 2018, 102, 375-400.	6.2	123
30	Genetic architecture of gene expression traits across diverse populations. PLoS Genetics, 2018, 14, e1007586.	3.5	117
31	Multiethnic genome-wide meta-analysis of ectopic fat depots identifies loci associated with adipocyte development and differentiation. Nature Genetics, 2017, 49, 125-130.	21.4	116
32	IL-6 Haplotypes, Inflammation, and Risk for Cardiovascular Disease in a Multiethnic Dialysis Cohort. Journal of the American Society of Nephrology: JASN, 2006, 17, 863-870.	6.1	115
33	Genome-wide association study of kidney function decline in individuals of European descent. Kidney International, 2015, 87, 1017-1029.	5.2	113
34	DNA Methylation of the Aryl Hydrocarbon Receptor Repressor Associations With Cigarette Smoking and Subclinical Atherosclerosis. Circulation: Cardiovascular Genetics, 2015, 8, 707-716.	5.1	107
35	Comparison of Proteomic Assessment Methods in Multiple Cohort Studies. Proteomics, 2020, 20, e1900278.	2.2	103
36	Proteomic Architecture of Human Coronary and Aortic Atherosclerosis. Circulation, 2018, 137, 2741-2756.	1.6	100

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37	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. Scientific Reports, 2017, 7, 45040.	3.3	98
38	Methylomics of gene expression in human monocytes. Human Molecular Genetics, 2013, 22, 5065-5074.	2.9	95
39	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
40	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. Nature Communications, 2018, 9, 2976.	12.8	85
41	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
42	Genomewide metaâ€analysis identifies loci associated with <scp>IGF</scp> â€‐ and <scp>IGFBP</scp> â€‐3 levels with impact on ageâ€related traits. Aging Cell, 2016, 15, 811-824.	6.7	83
43	Alterations of a Cellular Cholesterol Metabolism Network Are a Molecular Feature of Obesity-Related Type 2 Diabetes and Cardiovascular Disease. Diabetes, 2015, 64, 3464-3474.	0.6	82
44	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	6.2	82
45	Association of Lymphopenia With Risk of Mortality Among Adults in the US General Population. JAMA Network Open, 2019, 2, e1916526.	5.9	77
46	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
47	Genome-Wide Association Study for Incident Myocardial Infarction and Coronary Heart Disease in Prospective Cohort Studies: The CHARGE Consortium. PLoS ONE, 2016, 11, e0144997.	2.5	69
48	Comparison of smoking-related DNA methylation between newborns from prenatal exposure and adults from personal smoking. Epigenomics, 2019, 11, 1487-1500.	2.1	64
49	Long-term outdoor air pollution and DNA methylation in circulating monocytes: results from the Multi-Ethnic Study of Atherosclerosis (MESA). Environmental Health, 2016, 15, 119.	4.0	62
50	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. American Journal of Human Genetics, 2016, 99, 8-21.	6.2	60
51	Genetic Determinants of Circulating Estrogen Levels and Evidence of a Causal Effect of Estradiol on Bone Density in Men. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 991-1004.	3.6	60
52	Transcriptomic profiles of aging in purified human immune cells. BMC Genomics, 2015, 16, 333.	2.8	58
53	Trans-ethnic Meta-analysis and Functional Annotation Illuminates theÂGenetic Architecture of Fasting Glucose and Insulin. American Journal of Human Genetics, 2016, 99, 56-75.	6.2	55
54	Meta-analysis of loci associated with age at natural menopause in African-American women. Human Molecular Genetics, 2014, 23, 3327-3342.	2.9	54

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55	Large-Scale Genome-Wide Association Studies and Meta-Analyses of Longitudinal Change in Adult Lung Function. PLoS ONE, 2014, 9, e100776.	2.5	52
56	<scp>GWAS</scp> analysis of handgrip and lower body strength in older adults in the <scp>CHARGE</scp> consortium. Aging Cell, 2016, 15, 792-800.	6.7	51
57	Blood monocyte transcriptome and epigenome analyses reveal loci associated with human atherosclerosis. Nature Communications, 2017, 8, 393.	12.8	51
58	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
59	The FoxO3 gene and causeâ€specific mortality. Aging Cell, 2016, 15, 617-624.	6.7	48
60	T-786C Polymorphism of the Endothelial Nitric Oxide Synthase Gene Is Associated with Albuminuria in the Diabetes Heart Study. Journal of the American Society of Nephrology: JASN, 2005, 16, 1085-1090.	6.1	45
61	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
62	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
63	A Peripheral Blood DNA Methylation Signature of Hepatic Fat Reveals a Potential Causal Pathway for Nonalcoholic Fatty Liver Disease. Diabetes, 2019, 68, 1073-1083.	0.6	41
64	SOS2 and ACP1 Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. Journal of the American Society of Nephrology: JASN, 2017, 28, 981-994.	6.1	39
65	Bayesian shrinkage estimation of high dimensional causal mediation effects in omics studies. Biometrics, 2020, 76, 700-710.	1.4	39
66	Disentangling the genetics of lean mass. American Journal of Clinical Nutrition, 2019, 109, 276-287.	4.7	38
67	Genetic Investigation Into the Differential Risk of Atrial Fibrillation Among Black and White Individuals. JAMA Cardiology, 2016, 1, 442.	6.1	35
68	Declines in inflammation predict greater white matter microstructure in older adults. Neurobiology of Aging, 2015, 36, 948-954.	3.1	33
69	Transethnic Evaluation Identifies Low-Frequency Loci Associated With 25-Hydroxyvitamin D Concentrations. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 1380-1392.	3.6	33
70	Penalized Multimarkervs.Single-Marker Regression Methods for Genome-Wide Association Studies of Quantitative Traits. Genetics, 2015, 199, 205-222.	2.9	32
71	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. Human Molecular Genetics, 2021, 30, 393-409.	2.9	32
72	Inflammation as a Mediator of the Association Between Race and AtrialÂFibrillation. JACC: Clinical Electrophysiology, 2015, 1, 248-255.	3.2	31

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73	Meta-analyses identify DNA methylation associated with kidney function and damage. Nature Communications, 2021, 12, 7174.	12.8	30
74	Secondhand Tobacco Smoke Exposure Associations with DNA Methylation of the Aryl Hydrocarbon Receptor Repressor. Nicotine and Tobacco Research, 2017, 19, ntw219.	2.6	29
75	Tobacco exposure-related alterations in DNA methylation and gene expression in human monocytes: the Multi-Ethnic Study of Atherosclerosis (MESA). Epigenetics, 2017, 12, 1092-1100.	2.7	29
76	Meta-analysis of genome-wide association studies of HDL cholesterol response to statins. Journal of Medical Genetics, 2016, 53, 835-845.	3.2	28
77	Association of a Cystatin C Gene Variant With Cystatin C Levels, CKD, and Risk of Incident Cardiovascular Disease and Mortality. American Journal of Kidney Diseases, 2014, 63, 16-22.	1.9	27
78	Epigenome-wide association analysis of daytime sleepiness in the Multi-Ethnic Study of Atherosclerosis reveals African-American-specific associations. Sleep, 2019, 42, .	1.1	27
79	Prospective Associations of Coronary Heart Disease Loci in African Americans Using the MetaboChip: The PAGE Study. PLoS ONE, 2014, 9, e113203.	2.5	27
80	Identification of Smoking-Associated Differentially Methylated Regions Using Reduced Representation Bisulfite Sequencing and Cell typeâ€“Specific Enhancer Activation and Gene Expression. Environmental Health Perspectives, 2018, 126, 047015.	6.0	26
81	Genome-Wide Association Study Meta-Analysis of Stroke in 22 000 Individuals of African Descent Identifies Novel Associations With Stroke. Stroke, 2020, 51, 2454-2463.	2.0	26
82	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
83	Elevations in neutrophils with obstructive sleep apnea: The Multi-Ethnic Study of Atherosclerosis (MESA). International Journal of Cardiology, 2018, 257, 318-323.	1.7	24
84	Neurotransmitter Pathway Genes in Cognitive Decline During Aging: Evidence forGNG4andKCNQ2Genes. American Journal of Alzheimer's Disease and Other Dementias, 2018, 33, 153-165.	1.9	24
85	Genetic and Environmental Factors Are Associated with Serum 25-Hydroxyvitamin D Concentrations in Older African Americans. Journal of Nutrition, 2015, 145, 799-805.	2.9	23
86	Longevity-AssociatedFOXO3Genotype and its Impact on Coronary Artery Disease Mortality in Japanese, Whites, and Blacks: A Prospective Study of Three American Populations. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2017, 72, glw196.	3.6	23
87	Variants in angiopoietin-2 (ANGPT2) contribute to variation in nocturnal oxyhaemoglobin saturation level. Human Molecular Genetics, 2016, 25, ddw324.	2.9	21
88	Contrasting effects of Western vs Mediterranean diets on monocyte inflammatory gene expression and social behavior in a primate model. ELife, 2021, 10, .	6.0	19
89	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 2018, 3, 4.	1.8	19
90	Association of Arachidonate 12-Lipoxygenase Genotype Variation and Glycemic Control With Albuminuria in Type 2 Diabetes. American Journal of Kidney Diseases, 2008, 52, 242-250.	1.9	18

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91	An Empirical Comparison of Joint and Stratified Frameworks for Studying G Ã— E Interactions: Systolic Blood Pressure and Smoking in the CHARGE Geneâ€Lifestyle Interactions Working Group. Genetic Epidemiology, 2016, 40, 404-415.	1.3	18
92	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
93	Genome-Wide Association Analysis of the Sense of Smell in U.S. Older Adults: Identification of Novel Risk Loci in African-Americans and European-Americans. Molecular Neurobiology, 2017, 54, 8021-8032.	4.0	17
94	Genetics of progressive renal failure in diabetic kidney disease. Kidney International, 2005, 68, S94-S97.	5.2	16
95	Transcriptomic profiles of aging in naÃ¯ve and memory CD4+ cells from mice. Immunity and Ageing, 2017, 14, 15.	4.2	16
96	Gene-gene Interaction Analyses for Atrial Fibrillation. Scientific Reports, 2016, 6, 35371.	3.3	15
97	Pulmonary Function and Blood DNA Methylation: A Multiancestry Epigenome-Wide Association Meta-analysis. American Journal of Respiratory and Critical Care Medicine, 2022, 206, 321-336.	5.6	15
98	Functional Variants in the Lymphotoxin-Î± Gene Predict Cardiovascular Disease in Dialysis Patients. Journal of the American Society of Nephrology: JASN, 2006, 17, 3158-3166.	6.1	14
99	Transcriptome prediction performance across machine learning models and diverse ancestries. Human Genetics and Genomics Advances, 2021, 2, 100019.	1.7	14
100	Detection of genetic loci associated with plasma fetuin-A: a meta-analysis of genome-wide association studies from the CHARGE Consortium. Human Molecular Genetics, 2017, 26, 2156-2163.	2.9	13
101	Protein prediction for trait mapping in diverse populations. PLoS ONE, 2022, 17, e0264341.	2.5	13
102	Genetic diversity is a predictor of mortality in humans. BMC Genetics, 2014, 15, 159.	2.7	12
103	Association between sleep disordered breathing and epigenetic age acceleration: Evidence from the Multi-Ethnic Study of Atherosclerosis. EBioMedicine, 2019, 50, 387-394.	6.1	12
104	Epigenome-wide analysis of long-term air pollution exposure and DNA methylation in monocytes: results from the Multi-Ethnic Study of Atherosclerosis. Epigenetics, 2022, 17, 1-17.	2.7	11
105	P-selectin gene haplotype associations with albuminuria in the Diabetes Heart Study. Kidney International, 2005, 68, 741-746.	5.2	9
106	Genomeâ€Wide Interactions with Dairy Intake for Body Mass Index in Adults of European Descent. Molecular Nutrition and Food Research, 2018, 62, 1700347.	3.3	9
107	Bayesian hierarchical models for highâ€dimensional mediation analysis with coordinated selection of correlated mediators. Statistics in Medicine, 2021, 40, 6038-6056.	1.6	8
108	Î²-Fibrinogen Haplotypes and the Risk for Cardiovascular Disease in a Dialysis Cohort. American Journal of Kidney Diseases, 2005, 46, 78-85.	1.9	7

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109	Mitochondrial DNA Sequence Variation Associated With Peripheral Nerve Function in the Elderly. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2015, 70, 1400-1408.	3.6	7
110	Low oxygen saturation during sleep reduces CD1D and RAB20 expressions that are reversed by CPAP therapy. EBioMedicine, 2020, 56, 102803.	6.1	7
111	Monocyte miRNAs Are Associated With Type 2 Diabetes. Diabetes, 2022, 71, 853-861.	0.6	7
112	A functional polymorphism in the lymphotoxin-Î± gene is associated with carotid artery wall thickness: The Diabetes Heart Study. European Journal of Cardiovascular Prevention and Rehabilitation, 2006, 13, 655-657.	2.8	6
113	Targeted Genome Sequencing Identifies Multiple Rare Variants in Caveolin-1 Associated with Obstructive Sleep Apnea. American Journal of Respiratory and Critical Care Medicine, 0, , .	5.6	5
114	Rare and low-frequency exonic variants and gene-by-smoking interactions in pulmonary function. Scientific Reports, 2021, 11, 19365.	3.3	2
115	[P4â€“079]: AGINGâ€RELATED MITOCHONDRIAL DYSFUNCTION AND COGNITIVE FUNCTION: A TRANSCRIPTOMIC ANALYSIS OF MONOCYTES IN A COMMUNITYâ€BASED POPULATION. Alzheimer's and Dementia, 2017, 13, P1288.	0.8	1
116	P3-190: DECLINES IN INFLAMMATION PREDICT GREATER WHITE MATTER INTEGRITY IN OLDER ADULTS. , 2014, 10, P699-P699.		0
117	Differentially conserved transcriptomic response to adversity related to self-rated health in the multi-ethnic study of atherosclerosis. Experimental Biology and Medicine, 2017, 242, 1812-1819.	2.4	0
118	P3â€115: THE ASSOCIATIONS OF AGEâ€RELATED TRANSCRIPTIONAL NETWORKS WITH VASCULAR AND COGNITIVE FUNCTION: THE MULTIâ€ETHNIC STUDY OF ATHEROSCLEROSIS. Alzheimer's and Dementia, 2018, 14, P1111.	0.8	0
119	0291 Sleep Disordered Breathing Associated with Epigenetic Age Acceleration: Evidence from the Multi-Ethnic Study of Atherosclerosis. Sleep, 2019, 42, A118-A119.	1.1	0
120	0021 Lower Oxygen Saturation During Sleep Is Associated With Reduced Expressions Of Cd1d And Rab20 That Is Potentially Reversed By CPAP Therapy. Sleep, 2019, 42, A8-A9.	1.1	0