Qiong Yang

List of Publications by Year
in descending order

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124 papers	18,553 citations	26630 56 h-index	17105 122 g-index
133 all docs	133 docs citations	133 times ranked	25578 citing authors

#	Article	IF	Citations
1	Accelerometer-Measured, Habitual Physical Activity and Circulating Brain-Derived Neurotrophic Factor: A Cross-Sectional Study. Journal of Alzheimer's Disease, 2022, 85, 805-814.	2.6	2
2	Gene-mapping study of extremes of cerebral small vessel disease reveals TRIM47 as a strong candidate. Brain, 2022, 145, 1992-2007.	7.6	6
3	Genome-wide association study reveals novel genetic loci: a new polygenic risk score for mitral valve prolapse. European Heart Journal, 2022, 43, 1668-1680.	2.2	25
4	Circulating Metabolome and White Matter Hyperintensities in Women and Men. Circulation, 2022, 145, 1040-1052.	1.6	17
5	Elucidating mechanisms of genetic cross-disease associations at the PROCR vascular disease locus. Nature Communications, 2022, 13, 1222.	12.8	5
6	Multiâ€phenotype analyses of hemostatic traits with cardiovascular events reveal novel genetic associations. Journal of Thrombosis and Haemostasis, 2022, 20, 1331-1349.	3.8	12
7	New insights into the genetic etiology of Alzheimerâ€™s disease and related dementias. Nature Genetics, 2022, 54, 412-436.	21.4	700
8	Associations Between Brainstem Volume and Alzheimerâ€™s Disease Pathology in Middle-Aged Individuals of the Framingham Heart Study. Journal of Alzheimer's Disease, 2022, 86, 1603-1609.	2.6	0
9	Blood Phosphorylated Tau 181 as a Biomarker for Amyloid Burden on Brain PET in Cognitively Healthy Adults. Journal of Alzheimer's Disease, 2022, 87, 1517-1526.	2.6	8
10	Genetic loci and prioritization of genes for kidney function decline derived from a meta-analysis of 62 longitudinal genome-wide association studies. Kidney International, 2022, 102, 624-639.	5.2	18
11	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	4.4	17
12	Association of Circulating Metabolites in Plasma or Serum and Risk of Stroke. Neurology, 2021, 96, .	1.1	24
13	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. Kidney International, 2021, 99, 926-939.	5.2	42
14	Proteomic Signatures of Lifestyle Risk Factors for Cardiovascular Disease: A Crossâ€Sectional Analysis of the Plasma Proteome in the Framingham Heart Study. Journal of the American Heart Association, 2021, 10, e018020.	3.7	14
15	An evaluation of approaches for rare variant association analyses of binary traits in related samples. Scientific Reports, 2021, 11, 3145.	3.3	5
16	Proteomic profiling reveals biomarkers and pathways in type 2 diabetes risk. JCI Insight, 2021, 6, .	5.0	26
17	Multiomics integrative analysis identifies APOE allele-specific blood biomarkers associated to Alzheimerâ€™s disease etiopathogenesis. Aging, 2021, 13, 9277-9329.	3.1	15
18	Multiomic Profiling in Black and White Populations Reveals Novel Candidate Pathways in Left Ventricular Hypertrophy and Incident Heart Failure Specific to Black Adults. Circulation Genomic and Precision Medicine, 2021, 14, e003191.	3.6	7

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19	Plasma amyloid Î² levels are driven by genetic variants near APOE, BACE1, APP, PSEN2: A genomeâ€wide association study in over 12,000 nonâ€demented participants. Alzheimer's and Dementia, 2021, 17, 1663-1674.	0.8	20
20	Allele-specific DNA methylation maps in monozygotic twins discordant for psychiatric disorders reveal that disease-associated switching at the EIPR1 regulatory loci modulates neural function. Molecular Psychiatry, 2021, 26, 6630-6642.	7.9	7
21	Common variants in Alzheimerâ€™s disease and risk stratification by polygenic risk scores. Nature Communications, 2021, 12, 3417.	12.8	140
22	Association of low-frequency and rare coding variants with information processing speed. Translational Psychiatry, 2021, 11, 613.	4.8	2
23	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. Nature Communications, 2020, 11, 4796.	12.8	61
24	Circulating testican-2 is a podocyte-derived marker of kidney health. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 25026-25035.	7.1	19
25	Exome Array Analysis of Early-Onset Ischemic Stroke. Stroke, 2020, 51, 3356-3360.	2.0	5
26	Association of common genetic variants with brain microbleeds. Neurology, 2020, 95, e3331-e3343.	1.1	40
27	The genetics of circulating BDNF: towards understanding the role of BDNF in brain structure and function in middle and old ages. Brain Communications, 2020, 2, fcaa176.	3.3	14
28	Aptamer-Based Proteomic Platform Identifies Novel Protein Predictors of Incident Heart Failure and Echocardiographic Traits. Circulation: Heart Failure, 2020, 13, e006749.	3.9	26
29	Common Genetic Variation Indicates Separate Causes for Periventricular and Deep White Matter Hyperintensities. Stroke, 2020, 51, 2111-2121.	2.0	71
30	The genetic architecture of the human cerebral cortex. Science, 2020, 367, .	12.6	450
31	Genetic Architecture of Circulating Very-Long-Chain (C24:0 and C22:0) Ceramide Concentrations. Journal of Lipid and Atherosclerosis, 2020, 9, 172.	3.5	10
32	A genome-wide association study identifies genetic loci associated with specific lobar brain volumes. Communications Biology, 2019, 2, 285.	4.4	27
33	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	12.8	133
34	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
35	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
36	Proteomics Profiling and Risk of Newâ€Onset Atrial Fibrillation: Framingham Heart Study. Journal of the American Heart Association, 2019, 8, e010976.	3.7	42

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37	Association of variants inHTRA1andNOTCH3with MRI-defined extremes of cerebral small vessel disease in older subjects. Brain, 2019, 142, 1009-1023.	7.6	37
38	Genetic meta-analysis of diagnosed Alzheimerâ€™s disease identifies new risk loci and implicates Aî², tau, immunity and lipid processing. Nature Genetics, 2019, 51, 414-430.	21.4	1,962
39	Profiling of the plasma proteome across different stages of human heart failure. Nature Communications, 2019, 10, 5830.	12.8	53
40	Genetic architecture of subcortical brain structures in 38,851 individuals. Nature Genetics, 2019, 51, 1624-1636.	21.4	192
41	Genetic Architecture of the Cardiovascular Risk Proteome. Circulation, 2018, 137, 1158-1172.	1.6	64
42	Circulating metabolites and general cognitive ability and dementia: Evidence from 11 cohort studies. Alzheimer's and Dementia, 2018, 14, 707-722.	0.8	143
43	Genome-wide association study of 23,500 individuals identifies 7 loci associated with brain ventricular volume. Nature Communications, 2018, 9, 3945.	12.8	31
44	Probing the Virtual Proteome to Identify Novel Disease Biomarkers. Circulation, 2018, 138, 2469-2481.	1.6	42
45	Large-scale whole-exome sequencing association studies identify rare functional variants influencing serum urate levels. Nature Communications, 2018, 9, 4228.	12.8	43
46	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	12.8	484
47	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
48	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
49	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. Nature Genetics, 2017, 49, 946-952.	21.4	279
50	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. Scientific Reports, 2017, 7, 45040.	3.3	98
51	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
52	Heritability of Mitral Regurgitation. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	16
53	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. Nature Genetics, 2017, 49, 1373-1384.	21.4	783
54	Epigenome-wide association studies identify DNA methylation associated with kidney function. Nature Communications, 2017, 8, 1286.	12.8	145

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55	Genetic risk score and risk of stage 3 chronic kidney disease. BMC Nephrology, 2017, 18, 32.	1.8	30
56	Whole exome sequence-based association analyses of plasma amyloid-Î² in African and European Americans; the Atherosclerosis Risk in Communities-Neurocognitive Study. PLoS ONE, 2017, 12, e0180046.	2.5	18
57	Dimethylguanidino valeric acid is a marker of liver fat and predicts diabetes. Journal of Clinical Investigation, 2017, 127, 4394-4402.	8.2	115
58	An exome array study of the plasma metabolome. Nature Communications, 2016, 7, 12360.	12.8	69
59	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. Diabetes, 2016, 65, 803-817.	0.6	131
60	Causal Assessment of Serum Urate Levels inÂCardiometabolic Diseases Through a Mendelian Randomization Study. Journal of the American College of Cardiology, 2016, 67, 407-416.	2.8	138
61	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
62	RVFam: an R package for rare variant association analysis with family data. Bioinformatics, 2016, 32, 624-626.	4.1	10
63	Lipid and lipoprotein measurements and the risk of ischemic vascular events. Neurology, 2015, 84, 472-479.	1.1	62
64	Association of Alzheimer's disease GWAS loci with MRI markers of brain aging. Neurobiology of Aging, 2015, 36, 1765.e7-1765.e16.	3.1	82
65	Multiethnic Genome-Wide Association Study of Cerebral White Matter Hyperintensities on MRI. Circulation: Cardiovascular Genetics, 2015, 8, 398-409.	5.1	162
66	Geneâ€¢centric approach identifies new and known loci for <scp>F</scp>VIII activity and <scp>VWF</scp> antigen levels in <scp>E</scp>uropean <scp>A</scp>mericans and <scp>A</scp>frican <scp>A</scp>mericans. American Journal of Hematology, 2015, 90, 534-540.	4.1	20
67	Genome-Wide Meta-Analysis of Homocysteine and Methionine Metabolism Identifies Five One Carbon Metabolism Loci and a Novel Association of ALDH1L1 with Ischemic Stroke. PLoS Genetics, 2014, 10, e1004214.	3.5	69
68	A genetic association study of D-dimer levels with 50K SNPs from a candidate gene chip in four ethnic groups. Thrombosis Research, 2014, 134, 462-467.	1.7	8
69	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	21.4	675
70	Common Variants in Mendelian Kidney Disease Genes and Their Association with Renal Function. Journal of the American Society of Nephrology: JASN, 2013, 24, 2105-2117.	6.1	33
71	A Combined Epidemiologic and Metabolomic Approach Improves CKD Prediction. Journal of the American Society of Nephrology: JASN, 2013, 24, 1330-1338.	6.1	233
72	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. PLoS Genetics, 2012, 8, e1002584.	3.5	166

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73	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. Human Molecular Genetics, 2012, 21, 5329-5343.	2.9	64
74	Methods for Analyzing Multivariate Phenotypes in Genetic Association Studies. Journal of Probability and Statistics, 2012, 2012, 1-13.	0.7	90
75	Genome-wide association study for circulating levels of PAI-1 provides novel insights into its regulation. Blood, 2012, 120, 4873-4881.	1.4	90
76	Association of Genetic Variation in the Mitochondrial Genome With Blood Pressure and Metabolic Traits. Hypertension, 2012, 60, 949-956.	2.7	38
77	Using Family-Based Imputation in Genome-Wide Association Studies with Large Complex Pedigrees: The Framingham Heart Study. PLoS ONE, 2012, 7, e51589.	2.5	17
78	Flexible Semiparametric Analysis of Longitudinal Genetic Studies by Reduced Rank Smoothing. Journal of the Royal Statistical Society Series C: Applied Statistics, 2012, 61, 1-24.	1.0	16
79	Association of Estimated Glomerular Filtration Rate and Urinary Uromodulin Concentrations with Rare Variants Identified by UMOD Gene Region Sequencing. PLoS ONE, 2012, 7, e38311.	2.5	24
80	Association of genomic loci from a cardiovascular gene SNP array with fibrinogen levels in European Americans and African-Americans from six cohort studies: the Candidate Gene Association Resource (CARe). Blood, 2011, 117, 268-275.	1.4	36
81	A comparison of strategies for analyzing dichotomous outcomes in genome-wide association studies with general pedigrees. Genetic Epidemiology, 2011, 35, 650-657.	1.3	15
82	CUBN Is a Gene Locus for Albuminuria. Journal of the American Society of Nephrology: JASN, 2011, 22, 555-570.	6.1	208
83	Genome-wide association study for serum urate concentrations and gout among African Americans identifies genomic risk loci and a novel URAT1 loss-of-function allele. Human Molecular Genetics, 2011, 20, 4056-4068.	2.9	101
84	Identification of cis - and trans -Acting Genetic Variants Explaining Up to Half the Variation in Circulating Vascular Endothelial Growth Factor Levels. Circulation Research, 2011, 109, 554-563.	4.5	72
85	Genetic Predictors of Fibrin D-Dimer Levels in Healthy Adults. Circulation, 2011, 123, 1864-1872.	1.6	60
86	Association of eGFR-Related Loci Identified by GWAS with Incident CKD and ESRD. PLoS Genetics, 2011, 7, e1002292.	3.5	172
87	Assessment of Genetic Determinants of the Association of Î³â€² Fibrinogen in Relation to Cardiovascular Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2011, 31, 2345-2352.	2.4	44
88	Analyze multivariate phenotypes in genetic association studies by combining univariate association tests. Genetic Epidemiology, 2010, 34, 444-454.	1.3	137
89	A three-stage approach for genome-wide association studies with family data for quantitative traits. BMC Genetics, 2010, 11, 40.	2.7	8
90	New loci associated with kidney function and chronic kidney disease. Nature Genetics, 2010, 42, 376-384.	21.4	710

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91	Genome-wide meta-analyses identifies seven loci associated with platelet aggregation in response to agonists. Nature Genetics, 2010, 42, 608-613.	21.4	247
92	Clinical and Genetic Correlates of Circulating Angiopoietin-2 and Soluble Tie-2 in the Community. Circulation: Cardiovascular Genetics, 2010, 3, 300-306.	5.1	55
93	Association of Single Nucleotide Polymorphisms on Chromosome 9p21.3 With Platelet Reactivity. Circulation: Cardiovascular Genetics, 2010, 3, 445-453.	5.1	61
94	GWAF: an R package for genome-wide association analyses with family data. Bioinformatics, 2010, 26, 580-581.	4.1	220
95	Candidate Gene Association Resource (CARe). Circulation: Cardiovascular Genetics, 2010, 3, 267-275.	5.1	139
96	Genome-Wide Association Studies of Serum Magnesium, Potassium, and Sodium Concentrations Identify Six Loci Influencing Serum Magnesium Levels. PLoS Genetics, 2010, 6, e1001045.	3.5	185
97	Multiple Genetic Loci Influence Serum Urate Levels and Their Relationship With Gout and Cardiovascular Disease Risk Factors. Circulation: Cardiovascular Genetics, 2010, 3, 523-530.	5.1	285
98	Association of Novel Genetic Loci With Circulating Fibrinogen Levels. Circulation: Cardiovascular Genetics, 2009, 2, 125-133.	5.1	86
99	Common variants at 30 loci contribute to polygenic dyslipidemia. Nature Genetics, 2009, 41, 56-65.	21.4	1,234
100	Multiple loci associated with indices of renal function and chronic kidney disease. Nature Genetics, 2009, 41, 712-717.	21.4	553
101	Multiple loci influence erythrocyte phenotypes in the CHARGE Consortium. Nature Genetics, 2009, 41, 1191-1198.	21.4	324
102	CDKN1C/p57kip2is a candidate tumor suppressor gene in human breast cancer. BMC Cancer, 2008, 8, 68.	2.6	50
103	Association of three genetic loci with uric acid concentration and risk of gout: a genome-wide association study. Lancet, The, 2008, 372, 1953-1961.	13.7	610
104	The Third Generation Cohort of the National Heart, Lung, and Blood Institute's Framingham Heart Study: Design, Recruitment, and Initial Examination. American Journal of Epidemiology, 2007, 165, 1328-1335.	3.4	752
105	Joint modeling of linkage and association using affected sib-pair data. BMC Proceedings, 2007, 1, S38.	1.6	3
106	Maternal influence on blood pressure suggests involvement of mitochondrial DNA in the pathogenesis of hypertension: the Framingham Heart Study. Journal of Hypertension, 2007, 25, 2067-2073.	0.5	47
107	Handling linkage disequilibrium in linkage analysis using dense single-nucleotide polymorphisms. BMC Proceedings, 2007, 1, S161.	1.6	7
108	Evidence for linkage of red blood cell size and count: Genome-wide scans in the Framingham Heart Study. American Journal of Hematology, 2007, 82, 605-610.	4.1	37

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109	Using linkage and association to identify and model genetic effects: summary of GAW15 Group 4. Genetic Epidemiology, 2007, 31, S34-S42.	1.3	3
110	Effect of linkage disequilibrium between markers in linkage and association analyses. Genetic Epidemiology, 2007, 31, S139-S148.	1.3	1
111	The Framingham Heart Study 100K SNP genome-wide association study resource: overview of 17 phenotype working group reports. BMC Medical Genetics, 2007, 8, S1.	2.1	169
112	A genome-wide association for kidney function and endocrine-related traits in the NHLBI's Framingham Heart Study. BMC Medical Genetics, 2007, 8, S10.	2.1	80
113	Genome-wide association and linkage analyses of hemostatic factors and hematological phenotypes in the Framingham Heart Study. BMC Medical Genetics, 2007, 8, S12.	2.1	66
114	Common Genetic Variation in Five Thrombosis Genes and Relations to Plasma Hemostatic Protein Level and Cardiovascular Disease Risk. Arteriosclerosis, Thrombosis, and Vascular Biology, 2006, 26, 1405-1412.	2.4	59
115	Genome-wide linkage analysis to urinary microalbuminuria in a community-based sample: The Framingham Heart Study. Kidney International, 2005, 67, 70-74.	5.2	44
116	Genome-wide linkage analyses and candidate gene fine mapping for HDL3 cholesterol: the Framingham Study. Journal of Lipid Research, 2005, 46, 1416-1425.	4.2	23
117	Comprehensive Survey of Common Genetic Variation at the Plasminogen Activator Inhibitor-1 Locus and Relations to Circulating Plasminogen Activator Inhibitor-1 Levels. Circulation, 2005, 112, 1728-1735.	1.6	70
118	Genome-wide search for genes affecting serum uric acid levels: the Framingham Heart Study. Metabolism: Clinical and Experimental, 2005, 54, 1435-1441.	3.4	101
119	Genomewide Linkage Analysis to Serum Creatinine, GFR, and Creatinine Clearance in a Community-Based Population. Journal of the American Society of Nephrology: JASN, 2004, 15, 2457-2461.	6.1	161
120	Quantitative DNA Fingerprinting May Distinguish New Primary Breast Cancer From Disease Recurrence. Journal of Clinical Oncology, 2004, 22, 1830-1838.	1.6	45
121	Description of the Framingham Heart Study data for Genetic Analysis Workshop 13. BMC Genetics, 2003, 4, S2.	2.7	22
122	Genetic analyses of longitudinal phenotype data: a comparison of univariate methods and a multivariate approach. BMC Genetics, 2003, 4, S29.	2.7	9
123	A genome-wide search for genes affecting circulating fibrinogen levels in the Framingham Heart Study. Thrombosis Research, 2003, 110, 57-64.	1.7	29
124	Rare and Common Variants in COL4A1 in Chinese Patients With Intracerebral Hemorrhage. Frontiers in Neurology, 0, 13, .	2.4	0