Ming-Huei Chen

List of Publications by Year
in descending order

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81 papers	8,786 citations	57758 44 h-index	54911 84 g-index
84 all docs	84 docs citations	84 times ranked	17359 citing authors

#	Article	IF	Citations
1	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	27.8	1,855
2	Î²-Aminoisobutyric Acid Induces Browning of White Fat and Hepatic Î²-Oxidation and Is Inversely Correlated with Cardiometabolic Risk Factors. Cell Metabolism, 2014, 19, 96-108.	16.2	489
3	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
4	Multiple loci influence erythrocyte phenotypes in the CHARGE Consortium. Nature Genetics, 2009, 41, 1191-1198.	21.4	324
5	Novel Associations of Multiple Genetic Loci With Plasma Levels of Factor VII, Factor VIII, and von Willebrand Factor. Circulation, 2010, 121, 1382-1392.	1.6	311
6	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
7	A Genome-wide Association Study of the Human Metabolome in a Community-Based Cohort. Cell Metabolism, 2013, 18, 130-143.	16.2	274
8	Genome-wide meta-analyses identifies seven loci associated with platelet aggregation in response to agonists. Nature Genetics, 2010, 42, 608-613.	21.4	247
9	GWAF: an R package for genome-wide association analyses with family data. Bioinformatics, 2010, 26, 580-581.	4.1	220
10	Genome-wide association meta-analysis for total serum bilirubin levels. Human Molecular Genetics, 2009, 18, 2700-2710.	2.9	214
11	CUBN Is a Gene Locus for Albuminuria. Journal of the American Society of Nephrology: JASN, 2011, 22, 555-570.	6.1	208
12	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. Human Molecular Genetics, 2011, 20, 2273-2284.	2.9	168
13	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. PLoS Genetics, 2012, 8, e1002584.	3.5	166
14	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. Blood, 2019, 134, 1645-1657.	1.4	162
15	Metabolomic Profiles of Body Mass Index in the Framingham Heart Study Reveal Distinct Cardiometabolic Phenotypes. PLoS ONE, 2016, 11, e0148361.	2.5	155
16	Heritability and a Genome-Wide Linkage Scan for Arterial Stiffness, Wave Reflection, and Mean Arterial Pressure. Circulation, 2005, 112, 194-199.	1.6	139
17	Candidate Gene Association Resource (CARe). Circulation: Cardiovascular Genetics, 2010, 3, 267-275.	5.1	139
18	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. Diabetes, 2016, 65, 803-817.	0.6	131

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19	Multiethnic Meta-Analysis of Genome-Wide Association Studies in >100 000 Subjects Identifies 23 Fibrinogen-Associated Loci but No Strong Evidence of a Causal Association Between Circulating Fibrinogen and Cardiovascular Disease. Circulation, 2013, 128, 1310-1324.	1.6	128
20	Multiple Loci Are Associated with White Blood Cell Phenotypes. PLoS Genetics, 2011, 7, e1002113.	3.5	106
21	Clinical and Genetic Correlates of Growth Differentiation Factor 15 in the Community. Clinical Chemistry, 2012, 58, 1582-1591.	3.2	106
22	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. Journal of Clinical Investigation, 2017, 127, 1798-1812.	8.2	106
23	Genetic association analyses highlight biological pathways underlying mitral valve prolapse. Nature Genetics, 2015, 47, 1206-1211.	21.4	103
24	Genome-Wide Association Transethnic Meta-Analyses Identifies Novel Associations Regulating Coagulation Factor VIII and von Willebrand Factor Plasma Levels. Circulation, 2019, 139, 620-635.	1.6	102
25	Common genetic variation at the IL1RL1 locus regulates IL-33/ST2 signaling. Journal of Clinical Investigation, 2013, 123, 4208-4218.	8.2	101
26	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. Scientific Reports, 2017, 7, 45040.	3.3	98
27	Identification of a specific intronic PEAR1 gene variant associated with greater platelet aggregability and protein expression. Blood, 2011, 118, 3367-3375.	1.4	95
28	Genome-wide association study for circulating levels of PAI-1 provides novel insights into its regulation. Blood, 2012, 120, 4873-4881.	1.4	90
29	Association of Novel Genetic Loci With Circulating Fibrinogen Levels. Circulation: Cardiovascular Genetics, 2009, 2, 125-133.	5.1	86
30	Genomewide metaâ€analysis identifies loci associated with <scp>IGF</scp> â€I and <scp>IGFBP</scp> â€3 levels with impact on ageâ€related traits. Aging Cell, 2016, 15, 811-824.	6.7	83
31	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	6.2	82
32	Circulating Insulin-Like Growth Factor-1 and Its Binding Protein-3. Arteriosclerosis, Thrombosis, and Vascular Biology, 2010, 30, 1479-1484.	2.4	81
33	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. Human Molecular Genetics, 2016, 25, 358-370.	2.9	73
34	A genome-wide association study identifies novel loci associated with circulating IGF-I and IGFBP-3. Human Molecular Genetics, 2011, 20, 1241-1251.	2.9	67
35	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
36	Genetic Predictors of Fibrin D-Dimer Levels in Healthy Adults. Circulation, 2011, 123, 1864-1872.	1.6	60

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37	Trans-ethnic meta-analysis of white blood cell phenotypes. Human Molecular Genetics, 2014, 23, 6944-6960.	2.9	60
38	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. American Journal of Human Genetics, 2016, 99, 8-21.	6.2	60
39	The Relation of Genetic and Environmental Factors to Systemic Inflammatory Biomarker Concentrations. Circulation: Cardiovascular Genetics, 2009, 2, 229-237.	5.1	58
40	Cardiometabolic Correlates and Heritability of Fetuin-A, Retinol-Binding Protein 4, and Fatty-Acid Binding Protein 4 in the Framingham Heart Study. Journal of Clinical Endocrinology and Metabolism, 2012, 97, E1943-E1947.	3.6	56
41	Genetic variation associated with circulating monocyte count in the eMERGE Network. Human Molecular Genetics, 2013, 22, 2119-2127.	2.9	56
42	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
43	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. Blood, 2015, 126, e19-e29.	1.4	55
44	Genome-Wide Association Study of <scp>l</scp> -Arginine and Dimethylarginines Reveals Novel Metabolic Pathway for Symmetric Dimethylarginine. Circulation: Cardiovascular Genetics, 2014, 7, 864-872.	5.1	53
45	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
46	Whole-Exome Sequencing Identifies Loci Associated with Blood Cell Traits and Reveals a Role for Alternative GFI1B Splice Variants in Human Hematopoiesis. American Journal of Human Genetics, 2016, 99, 481-488.	6.2	45
47	Genome-wide association studies identify genetic loci for low von Willebrand factor levels. European Journal of Human Genetics, 2016, 24, 1035-1040.	2.8	45
48	Genome-wide Trans-ethnic Meta-analysis Identifies Seven Genetic Loci Influencing Erythrocyte Traits and a Role for RBPMS in Erythropoiesis. American Journal of Human Genetics, 2017, 100, 51-63.	6.2	45
49	Genome-Wide Association Study for Circulating Tissue Plasminogen Activator Levels and Functional Follow-Up Implicates Endothelial STXBP5 and STX2. Arteriosclerosis, Thrombosis, and Vascular Biology, 2014, 34, 1093-1101.	2.4	43
50	Large-scale whole-exome sequencing association studies identify rare functional variants influencing serum urate levels. Nature Communications, 2018, 9, 4228.	12.8	43
51	Rare coding variants pinpoint genes that control human hematological traits. PLoS Genetics, 2017, 13, e1006925.	3.5	39
52	Validated SNPs for eGFR and their associations with albuminuria. Human Molecular Genetics, 2012, 21, 3293-3298.	2.9	37
53	A genome-wide association study identifies new loci for factor VII and implicates factor VII in ischemic stroke etiology. Blood, 2019, 133, 967-977.	1.4	34
54	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

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55	Genome-Wide Association Analysis of Plasma Bâ€“Type Natriuretic Peptide in Blacks. Circulation: Cardiovascular Genetics, 2015, 8, 122-130.	5.1	32
56	Overlap Between Common Genetic Polymorphisms Underpinning Kidney Traits and Cardiovascular Disease Phenotypes: The CKDGen Consortium. American Journal of Kidney Diseases, 2013, 61, 889-898.	1.9	31
57	Comparison of HapMap and 1000 Genomes Reference Panels in a Large-Scale Genome-Wide Association Study. PLoS ONE, 2017, 12, e0167742.	2.5	29
58	A Meta-Analysis of Genome-Wide Association Studies of Growth Differentiation Factor-15 Concentration in Blood. Frontiers in Genetics, 2018, 9, 97.	2.3	26
59	Left ventricular mechanical function: clinical correlates, heritability, and association with parental heart failure. European Journal of Heart Failure, 2015, 17, 44-50.	7.1	24
60	Genome-Wide Meta-Analyses of Plasma Renin Activity and Concentration Reveal Association With the Kininogen 1 and Prekallikrein Genes. Circulation: Cardiovascular Genetics, 2015, 8, 131-140.	5.1	24
61	Novel Thrombotic Function of a Human SNP in STXBP5 Revealed by CRISPR/Cas9 Gene Editing in Mice. Arteriosclerosis, Thrombosis, and Vascular Biology, 2017, 37, 264-270.	2.4	24
62	A largeâ€scale exome array analysis of venous thromboembolism. Genetic Epidemiology, 2019, 43, 449-457.	1.3	22
63	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
64	SORCS1 contributes to the development of renal disease in rats and humans. Physiological Genomics, 2013, 45, 720-728.	2.3	17
65	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
66	Exome-chip meta-analysis identifies association between variation in ANKRD26 and platelet aggregation. Platelets, 2019, 30, 164-173.	2.3	15
67	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
68	Genome-Wide Association Study for Endothelial Growth Factors. Circulation: Cardiovascular Genetics, 2015, 8, 389-397.	5.1	11
69	Whole exome sequencing in the Framingham Heart Study identifies rare variation in HYAL2 that influences platelet aggregation. Thrombosis and Haemostasis, 2017, 117, 1083-1092.	3.4	11
70	RVFam: an R package for rare variant association analysis with family data. Bioinformatics, 2016, 32, 624-626.	4.1	10
71	A three-stage approach for genome-wide association studies with family data for quantitative traits. BMC Genetics, 2010, 11, 40.	2.7	8
72	No Evidence for Genome-Wide Interactions on Plasma Fibrinogen by Smoking, Alcohol Consumption and Body Mass Index: Results from Meta-Analyses of 80,607 Subjects. PLoS ONE, 2014, 9, e111156.	2.5	8

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73	Identification of polymorphisms explaining a linkage signal: application to the GAW14 simulated data. BMC Genetics, 2005, 6, S88.	2.7	7
74	Genome-wide association reveals that common genetic variation in the kallikrein-kinin system is associated with serum L-arginine levels. Thrombosis and Haemostasis, 2016, 116, 1041-1049.	3.4	5
75	Evaluation of Approaches to Identify Associated SNPs That Explain the Linkage Evidence in Nuclear Families with Affected Siblings. Human Heredity, 2010, 69, 104-119.	0.8	4
76	Joint modeling of linkage and association using affected sib-pair data. BMC Proceedings, 2007, 1, S38.	1.6	3
77	Using linkage and association to identify and model genetic effects: summary of GAW15 Group 4. Genetic Epidemiology, 2007, 31, S34-S42.	1.3	3
78	Platelet Reactivity in Individuals Over 65 Years Old Is Not Modulated by Age. Circulation Research, 2020, 127, 394-396.	4.5	3
79	Whole-exome sequencing of 14â€‰389 individuals from the ESP and CHARGE consortia identifies novel rare variation associated with hemostatic factors. Human Molecular Genetics, 2022, 31, 3120-3132.	2.9	3
80	Pleiotropic effects of n-6 and n-3 fatty acid-related genetic variants on circulating hemostatic variables. Thrombosis Research, 2018, 168, 53-59.	1.7	1
81	FGL1 as a modulator of plasma Dâ€dimer levels: Exomeâ€wide marker analysis of plasma tPA, PAIâ€1, and Dâ€dimer. Journal of Thrombosis and Haemostasis, 2021, 19, 2019-2028.	3.8	1