Ming-Huei Chen

List of Publications by Year
in descending order

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81	8,786	66250	62345
papers	citations	44 h-index	84 g-index

84	84	84	19127
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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.	1.4	3
2	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.	1.9	1
3	Platelet Reactivity in Individuals Over 65 Years Old Is Not Modulated by Age. Circulation Research, 2020, 127, 394-396.	2.0	3
4	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. Blood, 2019, 134, 1645-1657.	0.6	162
5	A largeâ€scale exome array analysis of venous thromboembolism. Genetic Epidemiology, 2019, 43, 449-457.	0.6	22
6	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
7	A genome-wide association study identifies new loci for factor VII and implicates factor VII in ischemic stroke etiology. Blood, 2019, 133, 967-977.	0.6	34
8	Exome-chip meta-analysis identifies association between variation in ANKRD26 and platelet aggregation. Platelets, 2019, 30, 164-173.	1.1	15
9	Large-scale whole-exome sequencing association studies identify rare functional variants influencing serum urate levels. Nature Communications, 2018, 9, 4228.	5.8	43
10	A Meta-Analysis of Genome-Wide Association Studies of Growth Differentiation Factor-15 Concentration in Blood. Frontiers in Genetics, 2018, 9, 97.	1.1	26
11	Pleiotropic effects of n-6 and n-3 fatty acid-related genetic variants on circulating hemostatic variables. Thrombosis Research, 2018, 168, 53-59.	0.8	1
12	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.	1.1	24
13	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. Scientific Reports, 2017, 7, 45040.	1.6	98
14	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.	1.4	13
15	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.	2.6	45
16	Rare coding variants pinpoint genes that control human hematological traits. PLoS Genetics, 2017, 13, e1006925.	1.5	39
17	Whole exome sequencing in the Framingham Heart Study identifies rare variation in HYAL2 that influences platelet aggregation. Thrombosis and Haemostasis, 2017, 117, 1083-1092.	1.8	11
18	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. Journal of Clinical Investigation, 2017, 127, 1798-1812.	3.9	106

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19	Comparison of HapMap and 1000 Genomes Reference Panels in a Large-Scale Genome-Wide Association Study. PLoS ONE, 2017, 12, e0167742.	1.1	29
20	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.	1.8	5
21	Metabolomic Profiles of Body Mass Index in the Framingham Heart Study Reveal Distinct Cardiometabolic Phenotypes. PLoS ONE, 2016, 11, e0148361.	1.1	155
22	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. American Journal of Human Genetics, 2016, 99, 8-21.	2.6	60
23	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.	3.0	83
24	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.	2.6	45
25	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	2.6	82
26	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.	2.6	50
27	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. Diabetes, 2016, 65, 803-817.	0.3	131
28	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	5.8	412
29	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. Human Molecular Genetics, 2016, 25, 358-370.	1.4	73
30	RVFam: an R package for rare variant association analysis with family data. Bioinformatics, 2016, 32, 624-626.	1.8	10
31	Genome-wide association studies identify genetic loci for low von Willebrand factor levels. European Journal of Human Genetics, 2016, 24, 1035-1040.	1.4	45
32	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. Blood, 2015, 126, e19-e29.	0.6	55
33	Genome-Wide Association Study for Endothelial Growth Factors. Circulation: Cardiovascular Genetics, 2015, 8, 389-397.	5.1	11
34	Left ventricular mechanical function: clinical correlates, heritability, and association with parental heart failure. European Journal of Heart Failure, 2015, 17, 44-50.	2.9	24
35	Genome-Wide Association Analysis of Plasma Bâ€“Type Natriuretic Peptide in Blacks. Circulation: Cardiovascular Genetics, 2015, 8, 122-130.	5.1	32
36	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

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37	Genetic association analyses highlight biological pathways underlying mitral valve prolapse. Nature Genetics, 2015, 47, 1206-1211.	9.4	103
38	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.	1.1	8
39	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.	1.1	43
40	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.	7.2	489
41	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
42	Trans-ethnic meta-analysis of white blood cell phenotypes. Human Molecular Genetics, 2014, 23, 6944-6960.	1.4	60
43	Overlap Between Common Genetic Polymorphisms Underpinning Kidney Traits and Cardiovascular Disease Phenotypes: The CKDGen Consortium. American Journal of Kidney Diseases, 2013, 61, 889-898.	2.1	31
44	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.	3.0	33
45	A Genome-wide Association Study of the Human Metabolome in a Community-Based Cohort. Cell Metabolism, 2013, 18, 130-143.	7.2	274
46	SORCS1 contributes to the development of renal disease in rats and humans. Physiological Genomics, 2013, 45, 720-728.	1.0	17
47	Genetic variation associated with circulating monocyte count in the eMERGE Network. Human Molecular Genetics, 2013, 22, 2119-2127.	1.4	56
48	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
49	Common genetic variation at the IL1RL1 locus regulates IL-33/ST2 signaling. Journal of Clinical Investigation, 2013, 123, 4208-4218.	3.9	101
50	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. PLoS Genetics, 2012, 8, e1002584.	1.5	166
51	Validated SNPs for eGFR and their associations with albuminuria. Human Molecular Genetics, 2012, 21, 3293-3298.	1.4	37
52	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. Human Molecular Genetics, 2012, 21, 5329-5343.	1.4	64
53	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.	1.8	56
54	Genome-wide association study for circulating levels of PAI-1 provides novel insights into its regulation. Blood, 2012, 120, 4873-4881.	0.6	90

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55	Clinical and Genetic Correlates of Growth Differentiation Factor 15 in the Community. Clinical Chemistry, 2012, 58, 1582-1591.	1.5	106
56	Using Family-Based Imputation in Genome-Wide Association Studies with Large Complex Pedigrees: The Framingham Heart Study. PLoS ONE, 2012, 7, e51589.	1.1	17
57	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	13.7	1,855
58	Identification of a specific intronic PEAR1 gene variant associated with greater platelet aggregability and protein expression. Blood, 2011, 118, 3367-3375.	0.6	95
59	A comparison of strategies for analyzing dichotomous outcomes in genome-wide association studies with general pedigrees. Genetic Epidemiology, 2011, 35, 650-657.	0.6	15
60	CUBN Is a Gene Locus for Albuminuria. Journal of the American Society of Nephrology: JASN, 2011, 22, 555-570.	3.0	208
61	A genome-wide association study identifies novel loci associated with circulating IGF-I and IGFBP-3. Human Molecular Genetics, 2011, 20, 1241-1251.	1.4	67
62	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.	1.4	168
63	Genetic Predictors of Fibrin D-Dimer Levels in Healthy Adults. Circulation, 2011, 123, 1864-1872.	1.6	60
64	Multiple Loci Are Associated with White Blood Cell Phenotypes. PLoS Genetics, 2011, 7, e1002113.	1.5	106
65	A three-stage approach for genome-wide association studies with family data for quantitative traits. BMC Genetics, 2010, 11, 40.	2.7	8
66	Genome-wide meta-analyses identifies seven loci associated with platelet aggregation in response to agonists. Nature Genetics, 2010, 42, 608-613.	9.4	247
67	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
68	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
69	GWAF: an R package for genome-wide association analyses with family data. Bioinformatics, 2010, 26, 580-581.	1.8	220
70	Circulating Insulin-Like Growth Factor-1 and Its Binding Protein-3. Arteriosclerosis, Thrombosis, and Vascular Biology, 2010, 30, 1479-1484.	1.1	81
71	Candidate Gene Association Resource (CARe). Circulation: Cardiovascular Genetics, 2010, 3, 267-275.	5.1	139
72	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

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73	Evaluation of Approaches to Identify Associated SNPs That Explain the Linkage Evidence in Nuclear Families with Affected Siblings. Human Heredity, 2010, 69, 104-119.	0.4	4
74	The Relation of Genetic and Environmental Factors to Systemic Inflammatory Biomarker Concentrations. Circulation: Cardiovascular Genetics, 2009, 2, 229-237.	5.1	58
75	Association of Novel Genetic Loci With Circulating Fibrinogen Levels. Circulation: Cardiovascular Genetics, 2009, 2, 125-133.	5.1	86
76	Genome-wide association meta-analysis for total serum bilirubin levels. Human Molecular Genetics, 2009, 18, 2700-2710.	1.4	214
77	Multiple loci influence erythrocyte phenotypes in the CHARGE Consortium. Nature Genetics, 2009, 41, 1191-1198.	9.4	324
78	Joint modeling of linkage and association using affected sib-pair data. BMC Proceedings, 2007, 1, S38.	1.8	3
79	Using linkage and association to identify and model genetic effects: summary of GAW15 Group 4. Genetic Epidemiology, 2007, 31, S34-S42.	0.6	3
80	Identification of polymorphisms explaining a linkage signal: application to the GAW14 simulated data. BMC Genetics, 2005, 6, S88.	2.7	7
81	Heritability and a Genome-Wide Linkage Scan for Arterial Stiffness, Wave Reflection, and Mean Arterial Pressure. Circulation, 2005, 112, 194-199.	1.6	139