Han-Yang Chen

List of Publications by Year
in descending order

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73 papers	9,155 citations	201385 27 h-index	88477 70 g-index

96 all docs	96 docs citations	96 times ranked	15761 citing authors

#	Article	IF	Citations
1	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. Nature Genetics, 2012, 44, 981-990.	9.4	1,748
2	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	9.4	959
3	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
4	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. Nature Genetics, 2012, 44, 659-669.	9.4	762
5	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	9.4	746
6	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.3	615
7	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	9.4	365
8	Control for Population Structure and Relatedness for Binary Traits in Genetic Association Studies via Logistic Mixed Models. American Journal of Human Genetics, 2016, 98, 653-666.	2.6	347
9	Genome-Wide Association Identifies Nine Common Variants Associated With Fasting Proinsulin Levels and Provides New Insights Into the Pathophysiology of Type 2 Diabetes. Diabetes, 2011, 60, 2624-2634.	0.3	335
10	Genetic association testing using the GENESIS R/Bioconductor package. Bioinformatics, 2019, 35, 5346-5348.	1.8	260
11	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. Nature Genetics, 2016, 48, 1162-1170.	9.4	223
12	Sequence Kernel Association Test for Quantitative Traits in Family Samples. Genetic Epidemiology, 2013, 37, 196-204.	0.6	193
13	A Method of Moments Estimator for Random Effect Multivariate Metaâ€Analysis. Biometrics, 2012, 68, 1278-1284.	0.8	159
14	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.	9.4	146
15	Genetic Associations with Obstructive Sleep Apnea Traits in Hispanic/Latino Americans. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 886-897.	2.5	107
16	Efficient Variant Set Mixed Model Association Tests for Continuous and Binary Traits in Large-Scale Whole-Genome Sequencing Studies. American Journal of Human Genetics, 2019, 104, 260-274.	2.6	103
17	Test for Rare Variants by Environment Interactions in Sequencing Association Studies. Biometrics, 2016, 72, 156-164.	0.8	68
18	Genome-Wide Association Study of the Modified Stumvoll Insulin Sensitivity Index Identifies BCL2 and FAM19A2 as Novel Insulin Sensitivity Loci. Diabetes, 2016, 65, 3200-3211.	0.3	67

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19	Multiethnic Meta-Analysis Identifies RAI1 as a Possible Obstructive Sleep Apneaâ€“related Quantitative Trait Locus in Men. American Journal of Respiratory Cell and Molecular Biology, 2018, 58, 391-401.	1.4	65
20	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. Nature Communications, 2019, 10, 5121.	5.8	62
21	Sequence Kernel Association Test for Survival Traits. Genetic Epidemiology, 2014, 38, 191-197.	0.6	58
22	African Ancestryâ€“Specific Alleles and Kidney Disease Risk in Hispanics/Latinos. Journal of the American Society of Nephrology: JASN, 2017, 28, 915-922.	3.0	57
23	Exome Array Analysis Identifies a Common Variant in IL27 Associated with Chronic Obstructive Pulmonary Disease. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 48-57.	2.5	52
24	A Genome-wide Association Study Discovers 46 Loci of the Human Metabolome in the Hispanic Community Health Study/Study of Latinos. American Journal of Human Genetics, 2020, 107, 849-863.	2.6	48
25	Dynamic Scan Procedure for Detecting Rare-Variant Association Regions in Whole-Genome Sequencing Studies. American Journal of Human Genetics, 2019, 104, 802-814.	2.6	43
26	Admixture mapping identifies novel loci for obstructive sleep apnea in Hispanic/Latino Americans. Human Molecular Genetics, 2019, 28, 675-687.	1.4	41
27	Incorporating Gene-Environment Interaction in Testing for Association with Rare Genetic Variants. Human Heredity, 2014, 78, 81-90.	0.4	35
28	Comparison of Heritability Estimation and Linkage Analysis for Multiple Traits Using Principal Component Analyses. Genetic Epidemiology, 2016, 40, 222-232.	0.6	32
29	Whole exome sequencing analysis in severe chronic obstructive pulmonary disease. Human Molecular Genetics, 2018, 27, 3801-3812.	1.4	32
30	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
31	Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 379-384.	3.3	28
32	Associations of variants In the hexokinase 1 and interleukin 18 receptor regions with oxyhemoglobin saturation during sleep. PLoS Genetics, 2019, 15, e1007739.	1.5	28
33	Epigenome-wide association analysis of daytime sleepiness in the Multi-Ethnic Study of Atherosclerosis reveals African-American-specific associations. Sleep, 2019, 42, .	0.6	27
34	No Interactions Between Previously Associated 2-Hour Glucose Gene Variants and Physical Activity or BMI on 2-Hour Glucose Levels. Diabetes, 2012, 61, 1291-1296.	0.3	23
35	Variants in angiopoietin-2 (ANGPT2) contribute to variation in nocturnal oxyhaemoglobin saturation level. Human Molecular Genetics, 2016, 25, ddw324.	1.4	21
36	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. Human Molecular Genetics, 2016, 25, 2070-2081.	1.4	21

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37	Genome-wide gene by lead exposure interaction analysis identifies UNC5D as a candidate gene for neurodevelopment. Environmental Health, 2017, 16, 81.	1.7	20
38	Strategies to Design and Analyze Targeted Sequencing Data. Circulation: Cardiovascular Genetics, 2014, 7, 335-343.	5.1	18
39	GEM: scalable and flexible geneâ€“environment interaction analysis in millions of samples. Bioinformatics, 2021, 37, 3514-3520.	1.8	17
40	Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. Genome Medicine, 2021, 13, 136.	3.6	16
41	A powerful and dataâ€adaptive test for rareâ€variantâ€“based geneâ€environment interaction analysis. Statistics in Medicine, 2019, 38, 1230-1244.	0.8	15
42	Efficient geneâ€“environment interaction tests for large biobankâ€scale sequencing studies. Genetic Epidemiology, 2020, 44, 908-923.	0.6	15
43	Multi-ancestry genome-wide geneâ€“sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	4.1	13
44	Coâ€occurring defect analysis: A platform for analyzing birth defect coâ€occurrence in registries. Birth Defects Research, 2019, 111, 1356-1364.	0.8	12
45	Role of Rare and Low-Frequency Variants in Gene-Alcohol Interactions on Plasma Lipid Levels. Circulation Genomic and Precision Medicine, 2020, 13, e002772.	1.6	11
46	Genome-wide geneâ€“diet interaction analysis in the UK Biobank identifies novel effects on hemoglobin A1c. Human Molecular Genetics, 2021, 30, 1773-1783.	1.4	11
47	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.	2.6	10
48	Comparison of statistical approaches to rare variant analysis for quantitative traits. BMC Proceedings, 2011, 5, S113.	1.8	9
49	Birth defects that coâ€occur with nonâ€syndromic gastroschisis and omphalocele. American Journal of Medical Genetics, Part A, 2020, 182, 2581-2593.	0.7	9
50	Management and reproductive counseling in cervical, caesarean scar and interstitial ectopic pregnancies over 11Âyears: identifying the need for a modern management algorithm. Human Reproduction Open, 2019, 2019, hoz028.	2.3	8
51	A unified method for rare variant analysis of geneâ€environment interactions. Statistics in Medicine, 2020, 39, 801-813.	0.8	8
52	Genome-wide association study of neck circumference identifies sex-specific loci independent of generalized adiposity. International Journal of Obesity, 2021, 45, 1532-1541.	1.6	8
53	Birth defect co-occurrence patterns in the Texas Birth Defects Registry. Pediatric Research, 2022, 91, 1278-1285.	1.1	8
54	Testing Genetic Association With Rare and Common Variants in Family Data. Genetic Epidemiology, 2014, 38, S37-43.	0.6	7

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55	Birth Defect Co-Occurrence Patterns Among Infants With Cleft Lip and/or Palate. Cleft Palate-Craniofacial Journal, 2022, 59, 417-426.	0.5	7
56	Robust, flexible, and scalable tests for Hardyâ€“Weinberg equilibrium across diverse ancestries. Genetics, 2021, 218, .	1.2	6
57	Estimation of total mediation effect for high-dimensional omics mediators. BMC Bioinformatics, 2021, 22, 414.	1.2	6
58	Rare genetic variant analysis on blood pressure in related samples. BMC Proceedings, 2014, 8, S35.	1.8	5
59	Targeted Genome Sequencing Identifies Multiple Rare Variants in Caveolin-1 Associated with Obstructive Sleep Apnea. American Journal of Respiratory and Critical Care Medicine, 0, , .	2.5	5
60	Patterns of co-occurring birth defects among infants with hypospadias. Journal of Pediatric Urology, 2021, 17, 64.e1-64.e8.	0.6	4
61	Identification of novel and rare variants associated with handgrip strength using whole genome sequence data from the NHLBI Trans-Omics in Precision Medicine (TOPMed) Program. PLoS ONE, 2021, 16, e0253611.	1.1	4
62	Exploiting family history in aggregation unit-based genetic association tests. European Journal of Human Genetics, 2022, 30, 1355-1362.	1.4	4
63	A Comprehensive Assessment of Co-occurring Birth Defects among Infants with Non-Syndromic Anophthalmia or Microphthalmia. Ophthalmic Epidemiology, 2021, 28, 428-435.	0.8	4
64	Patterns of congenital anomalies among individuals with trisomy 13 in Texas. American Journal of Medical Genetics, Part A, 2021, 185, 1787-1793.	0.7	2
65	Exome sequence association study of levels and longitudinal change of cardiovascular risk factor phenotypes in European Americans and African Americans from the Atherosclerosis Risk in Communities Study. Genetic Epidemiology, 2021, 45, 651-663.	0.6	2
66	BinomiRare: A robust test for association of a rare genetic variant with a binary outcome for mixed models and any case-control proportion. Human Genetics and Genomics Advances, 2021, 2, 100040.	1.0	2
67	Rare and low-frequency exonic variants and gene-by-smoking interactions in pulmonary function. Scientific Reports, 2021, 11, 19365.	1.6	2
68	Upregulated heme biosynthesis increases obstructive sleep apnea severity: a pathway-based Mendelian randomization study. Scientific Reports, 2022, 12, 1472.	1.6	2
69	Rare Variant Association Analysis: Beyond Collapsing Approaches. , 2015, , 149-167.		1
70	Family history aggregation unit-based tests to detect rare genetic variant associations with application to the Framingham Heart Study. American Journal of Human Genetics, 2022, 109, 738-749.	2.6	1
71	Metabolomic Associations of Asthma in the Hispanic Community Health Study/Study of Latinos. Metabolites, 2022, 12, 359.	1.3	1
72	Genetic analysis of biobank data: Familial history aggregationâ€based tests (FHAT) with application to Alzheimer's disease. Alzheimer's and Dementia, 2020, 16, e038648.	0.4	0

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73	0030 Development and Validation of a Metabolomic Risk Score for Obstructive Sleep Apnea across Race/Ethnicities. Sleep, 2022, 45, A13-A14.	0.6	0