Han-Yang Chen

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6946074/publications.pdf

Version: 2024-02-01

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	Birth Defect Co-Occurrence Patterns Among Infants With Cleft Lip and/or Palate. Cleft Palate-Craniofacial Journal, 2022, 59, 417-426.	0.5	7
2	Birth defect co-occurrence patterns in the Texas Birth Defects Registry. Pediatric Research, 2022, 91, 1278-1285.	1.1	8
3	Exploiting family history in aggregation unit-based genetic association tests. European Journal of Human Genetics, 2022, 30, 1355-1362.	1.4	4
4	Upregulated heme biosynthesis increases obstructive sleep apnea severity: a pathway-based Mendelian randomization study. Scientific Reports, 2022, 12, 1472.	1.6	2
5	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
6	Metabolomic Associations of Asthma in the Hispanic Community Health Study/Study of Latinos. Metabolites, 2022, 12, 359.	1.3	1
7	0030 Development and Validation of a Metabolomic Risk Score for Obstructive Sleep Apnea across Race/Ethnicities. Sleep, 2022, 45, A13-A14.	0.6	0
8	Patterns of co-occurring birth defects among infants with hypospadias. Journal of Pediatric Urology, 2021, 17, 64.e1-64.e8.	0.6	4
9	Robust, flexible, and scalable tests for Hardyâ€“Weinberg equilibrium across diverse ancestries. Genetics, 2021, 218, .	1.2	6
10	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
11	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
12	Multi-ancestry genome-wide geneâ€“sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	4.1	13
13	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
14	GEM: scalable and flexible geneâ€“environment interaction analysis in millions of samples. Bioinformatics, 2021, 37, 3514-3520.	1.8	17
15	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
16	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
17	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
18	Estimation of total mediation effect for high-dimensional omics mediators. BMC Bioinformatics, 2021, 22, 414.	1.2	6

#	Article	IF	Citations
19	Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. Genome Medicine, 2021, 13, 136.	3.6	16
20	Rare and low-frequency exonic variants and gene-by-smoking interactions in pulmonary function. Scientific Reports, 2021, 11, 19365.	1.6	2
21	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
22	A unified method for rare variant analysis of geneâ€environment interactions. Statistics in Medicine, 2020, 39, 801-813.	0.8	8
23	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
24	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
25	Efficient geneâ€“environment interaction tests for large biobankâ€scale sequencing studies. Genetic Epidemiology, 2020, 44, 908-923.	0.6	15
26	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
27	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
28	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
29	Coâ€occurring defect analysis: A platform for analyzing birth defect coâ€occurrence in registries. Birth Defects Research, 2019, 111, 1356-1364.	0.8	12
30	Genetic association testing using the GENESIS R/Bioconductor package. Bioinformatics, 2019, 35, 5346-5348.	1.8	260
31	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
32	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
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	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
35	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
36	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

#	Article	IF	Citations
37	Admixture mapping identifies novel loci for obstructive sleep apnea in Hispanic/Latino Americans. Human Molecular Genetics, 2019, 28, 675-687.	1.4	41
38	A powerful and dataâ€adaptive test for rareâ€variantâ€“based geneâ€environment interaction analysis. Statistics in Medicine, 2019, 38, 1230-1244.	0.8	15
39	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
40	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
41	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
42	Whole exome sequencing analysis in severe chronic obstructive pulmonary disease. Human Molecular Genetics, 2018, 27, 3801-3812.	1.4	32
43	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.3	615
44	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
45	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
46	Genome-wide gene by lead exposure interaction analysis identifies UNC5D as a candidate gene for neurodevelopment. Environmental Health, 2017, 16, 81.	1.7	20
47	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
48	Comparison of Heritability Estimation and Linkage Analysis for Multiple Traits Using Principal Component Analyses. Genetic Epidemiology, 2016, 40, 222-232.	0.6	32
49	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
50	Test for Rare Variants by Environment Interactions in Sequencing Association Studies. Biometrics, 2016, 72, 156-164.	0.8	68
51	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
52	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
53	Variants in angiopoietin-2 (ANGPT2) contribute to variation in nocturnal oxyhaemoglobin saturation level. Human Molecular Genetics, 2016, 25, ddw324.	1.4	21
54	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

#	Article	IF	Citations
55	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
56	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
57	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	9.4	365
58	Rare Variant Association Analysis: Beyond Collapsing Approaches. , 2015, , 149-167.		1
59	Sequence Kernel Association Test for Survival Traits. Genetic Epidemiology, 2014, 38, 191-197.	0.6	58
60	Testing Genetic Association With Rare and Common Variants in Family Data. Genetic Epidemiology, 2014, 38, S37-43.	0.6	7
61	Rare genetic variant analysis on blood pressure in related samples. BMC Proceedings, 2014, 8, S35.	1.8	5
62	Strategies to Design and Analyze Targeted Sequencing Data. Circulation: Cardiovascular Genetics, 2014, 7, 335-343.	5.1	18
63	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
64	Incorporating Gene-Environment Interaction in Testing for Association with Rare Genetic Variants. Human Heredity, 2014, 78, 81-90.	0.4	35
65	Sequence Kernel Association Test for Quantitative Traits in Family Samples. Genetic Epidemiology, 2013, 37, 196-204.	0.6	193
66	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
67	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
68	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
69	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
70	A Method of Moments Estimator for Random Effect Multivariate Metaâ€Analysis. Biometrics, 2012, 68, 1278-1284.	0.8	159
71	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
72	Comparison of statistical approaches to rare variant analysis for quantitative traits. BMC Proceedings, 2011, 5, S113.	1.8	9

#	Article	IF	Citations
73	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