Hsin-Chou Yang

List of Publications by Citations

63	987	17	27
papers	citations	h-index	g-index
68	1,171	4.5	4.08
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
63	A genome-wide association study reveals a quantitative trait locus of adiponectin on CDH13 that predicts cardiometabolic outcomes. *Diabetes*, **2011**, 60, 2417-23	0.9	91
62	Breast cancer risk associated with genotypic polymorphism of the mitosis-regulating gene Aurora-A/STK15/BTAK. *International Journal of Cancer*, **2005**, 115, 276-83	7.5	60
61	Morbid obesity in Taiwan: Prevalence, trends, associated social demographics, and lifestyle factors. *PLoS ONE*, **2017**, 12, e0169577	3.7	58
60	Genome-wide association study of young-onset hypertension in the Han Chinese population of Taiwan. *PLoS ONE*, **2009**, 4, e5459	3.7	51
59	A comparison of major histocompatibility complex SNPs in Han Chinese residing in Taiwan and Caucasians. *Journal of Biomedical Science*, **2006**, 13, 489-98	13.3	42
58	Analysis of genomic distributions of SARS-CoV-2 reveals a dominant strain type with strong allelic associations. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 30679-30686	11.5	39
57	Identification of IGF1, SLC4A4, WWOX, and SFMBT1 as hypertension susceptibility genes in Han Chinese with a genome-wide gene-based association study. *PLoS ONE*, **2012**, 7, e32907	3.7	38
56	Genome-Wide Pharmacogenomic Study on Methadone Maintenance Treatment Identifies SNP rs17180299 and Multiple Haplotypes on CYP2B6, SPON1, and GSG1L Associated with Plasma Concentrations of Methadone R- and S-enantiomers in Heroin-Dependent Patients. *PLoS Genetics*, **2016**, 12, e1005910	6	34
55	Modeling animalsTbehavioral response by Markov chain models for capture-recapture experiments. *Biometrics*, **2005**, 61, 1010-7	1.8	31
54	Association of circadian genes with diurnal blood pressure changes and non-dipper essential hypertension: a genetic association with young-onset hypertension. *Hypertension Research*, **2015**, 38, 155-62	4.7	29
53	A genome-wide homozygosity association study identifies runs of homozygosity associated with rheumatoid arthritis in the human major histocompatibility complex. *PLoS ONE*, **2012**, 7, e34840	3.7	28
52	Kernel-based association test. *Genetics*, **2008**, 179, 1057-68	4	22
51	SMART: Statistical Metabolomics Analysis-An R Tool. *Analytical Chemistry*, **2016**, 88, 6334-41	7.8	21
50	Is Hyperuricemia, an Early-Onset Metabolic Disorder, Causally Associated with Cardiovascular Disease Events in Han Chinese?. *Journal of Clinical Medicine*, **2019**, 8,	5.1	19
49	PoooL: an efficient method for estimating haplotype frequencies from large DNA pools. *Bioinformatics*, **2008**, 24, 1942-8	7.2	18
48	A sliding-window weighted linkage disequilibrium test. *Genetic Epidemiology*, **2006**, 30, 531-45	2.6	18
47	New adjustment factors and sample size calculation in a DNA-pooling experiment with preferential amplification. *Genetics*, **2005**, 169, 399-410	4	18

46	PDA: Pooled DNA analyzer. *BMC Bioinformatics*, **2006**, 7, 233	3.6	17
45	A genome-wide scanning and fine mapping study of COGA data. *BMC Genetics*, **2005**, 6 Suppl 1, S30	2.6	17
44	Fine-mapping angiotensin-converting enzyme gene: separate QTLs identified for hypertension and for ACE activity. *PLoS ONE*, **2013**, 8, e56119	3.7	16
43	A genome-wide study of preferential amplification/hybridization in microarray-based pooled DNA experiments. *Nucleic Acids Research*, **2006**, 34, e106	20.1	16
42	Genome-wide gene-based association study. *BMC Proceedings*, **2009**, 3 Suppl 7, S135	2.3	15
41	Risk of asthma associated with energy-dense but nutrient-poor dietary pattern in Taiwanese children. *Asia Pacific Journal of Clinical Nutrition*, **2012**, 21, 73-81	1	15
40	Interethnic DNA methylation difference and its implications in pharmacoepigenetics. *Epigenomics*, **2017**, 9, 1437-1454	4.4	13
39	OPATs: Omnibus P-value association tests. *Briefings in Bioinformatics*, **2019**, 20, 1-14	13.4	13
38	The DAO gene is associated with schizophrenia and interacts with other genes in the Taiwan Han Chinese population. *PLoS ONE*, **2013**, 8, e60099	3.7	12
37	Androgenic alopecia is associated with less dietary soy, lower [corrected] blood vanadium and rs1160312 1 polymorphism in Taiwanese communities. *PLoS ONE*, **2013**, 8, e79789	3.7	12
36	LOHAS: loss-of-heterozygosity analysis suite. *Genetic Epidemiology*, **2011**, 35, 247-60	2.6	11
35	Population size estimation using local sample coverage for open populations. *Journal of Statistical Planning and Inference*, **2003**, 113, 699-714	0.8	11
34	Genomic, geographic and temporal distributions of SARS-CoV-2 mutations		11
33	A three-stage genome-wide association study combining multilocus test and gene expression analysis for young-onset hypertension in Taiwan Han Chinese. *American Journal of Hypertension*, **2014**, 27, 819-27	2.3	10
32	MPDA: microarray pooled DNA analyzer. *BMC Bioinformatics*, **2008**, 9, 196	3.6	10
31	Nonparametric estimation of LOH using Affymetrix SNP genotyping arrays for unpaired samples. *Journal of Human Genetics*, **2008**, 53, 983-990	4.3	10
30	A novel SNP associated with nighttime pulse pressure in young-onset hypertension patients could be a genetic prognostic factor for cardiovascular events in a general cohort in Taiwan. *PLoS ONE*, **2014**, 9, e97919	3.7	9
29	Integrative analysis of single nucleotide polymorphisms and gene expression efficiently distinguishes samples from closely related ethnic populations. *BMC Genomics*, **2012**, 13, 346	4.5	9

28	Genome-wide association study of morbid obesity in Han Chinese. *BMC Genetics*, **2019**, 20, 97	2.6	9
27	Integrated omics-based pathway analyses uncover CYP epoxygenase-associated networks as theranostic targets for metastatic triple negative breast cancer. *Journal of Experimental and Clinical Cancer Research*, **2019**, 38, 187	12.8	8
26	Region-based and pathway-based QTL mapping using a p-value combination method. *BMC Proceedings*, **2011**, 5 Suppl 9, S43	2.3	8
25	Genome-wide scan for quantitative ACE activity in Taiwan young-onset hypertension study. *Human Heredity*, **2008**, 65, 85-90	1.1	8
24	Genetic signatures of heroin addiction. *Medicine (United States)*, **2016**, 95, e4473	1.8	7
23	Analysis of homozygosity disequilibrium using whole-genome sequencing data. *BMC Proceedings*, **2014**, 8, S15	2.3	7
22	A comparison of individual genotyping and pooled DNA analysis for polymorphism validation prior to large-scale genetic studies. *Annals of Human Genetics*, **2006**, 70, 350-9	2.2	7
21	Receptor mediated effect of serotonergic transmission in patients with bipolar affective disorder. *Journal of Medical Genetics*, **2003**, 40, 781-6	5.8	7
20	The causal role of elevated uric acid and waist circumference on the risk of metabolic syndrome components. *International Journal of Obesity*, **2020**, 44, 865-874	5.5	7
19	Applying genome-wide gene-based expression quantitative trait locus mapping to study population ancestry and pharmacogenetics. *BMC Genomics*, **2014**, 15, 319	4.5	6
18	A new analysis tool for individual-level allele frequency for genomic studies. *BMC Genomics*, **2010**, 11, 415	4.5	6
17	Estimation of the size of an open population using local estimating equations II: a partially parametric approach. *Biometrics*, **2003**, 59, 365-74	1.8	6
16	Postprandial Metabolomics Response to Various Cooking Oils in Humans. *Journal of Agricultural and Food Chemistry*, **2018**, 66, 4977-4984	5.7	5
15	Using an Event-History with Risk-Free Model to Study the Genetics of Alcoholism. *Scientific Reports*, **2017**, 7, 1975	4.9	5
14	A Two-Stage Whole-Genome Gene Expression Association Study of Young-Onset Hypertension in Han Chinese Population of Taiwan. *Scientific Reports*, **2018**, 8, 1800	4.9	4
13	SAQC: SNP array quality control. *BMC Bioinformatics*, **2011**, 12, 100	3.6	4
12	Association mapping using pooled DNA. *Methods in Molecular Biology*, **2007**, 376, 161-75	1.4	4
11	PRAP1 is a novel lipid-binding protein that promotes lipid absorption by facilitating MTTP-mediated lipid transport. *Journal of Biological Chemistry*, **2021**, 296, 100052	5.4	4

List of Publications

10	Using the longest significance run to estimate region-specific p-values in genetic association mapping studies. *BMC Bioinformatics*, **2008**, 9, 246	3.6	3
9	Pharmacogenomics study on cadherin 2 network with regard to HIV infection and methadone treatment outcome. *PLoS ONE*, **2017**, 12, e0174647	3.7	3
8	Genetic ancestry plays a central role in population pharmacogenomics. *Communications Biology*, **2021**, 4, 171	6.7	3
7	Homozygosity disequilibrium and its gene regulation. *BMC Proceedings*, **2016**, 10, 159-163	2.3	2
6	An integrated analysis tool for analyzing hybridization intensities and genotypes using new-generation population-optimized human arrays. *BMC Genomics*, **2016**, 17, 266	4.5	2
5	Homozygosity disequilibrium associated with treatment response and its methylation regulation. *BMC Proceedings*, **2018**, 12, 45	2.3	2
4	Vegetable Signatures Derived from Human Urinary Metabolomic Data in Controlled Feeding Studies. *Journal of Proteome Research*, **2019**, 18, 159-168	5.6	2
3	THE USE OF CAPTURE-RECAPTURE METHODOLOGY IN EPIDEMIOLOGICAL SURVEILLANCE AND ECOLOGICAL SURVEYS **2015**, 425-467		
2	Family-based gene-environment interaction using sequence kernel association test (FGE-SKAT) for complex quantitative traits. *Scientific Reports*, **2021**, 11, 7431	4.9	
1	Identification of Serum Oxylipins Associated with the Development of Coronary Artery Disease: A Nested Case-Control Study. *Metabolites*, **2022**, 12, 495	5.6	