

Hsin-Chou Yang

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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

#	Paper	IF	Citations
63	Identification of Serum Oxylipins Associated with the Development of Coronary Artery Disease: A Nested Case-Control Study. <i>Metabolites</i> , 2022 , 12, 495	5.6	
62	Family-based gene-environment interaction using sequence kernel association test (FGE-SKAT) for complex quantitative traits. <i>Scientific Reports</i> , 2021 , 11, 7431	4.9	
61	Genetic ancestry plays a central role in population pharmacogenomics. <i>Communications Biology</i> , 2021 , 4, 171	6.7	3
60	PRAP1 is a novel lipid-binding protein that promotes lipid absorption by facilitating MTP-mediated lipid transport. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100052	5.4	4
59	The causal role of elevated uric acid and waist circumference on the risk of metabolic syndrome components. <i>International Journal of Obesity</i> , 2020 , 44, 865-874	5.5	7
58	Analysis of genomic distributions of SARS-CoV-2 reveals a dominant strain type with strong allelic associations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 30679-30686	11.5	39
57	OPATs: Omnibus P-value association tests. <i>Briefings in Bioinformatics</i> , 2019 , 20, 1-14	13.4	13
56	Integrated omics-based pathway analyses uncover CYP epoxigenase-associated networks as theranostic targets for metastatic triple negative breast cancer. <i>Journal of Experimental and Clinical Cancer Research</i> , 2019 , 38, 187	12.8	8
55	Is Hyperuricemia, an Early-Onset Metabolic Disorder, Causally Associated with Cardiovascular Disease Events in Han Chinese?. <i>Journal of Clinical Medicine</i> , 2019 , 8,	5.1	19
54	Genome-wide association study of morbid obesity in Han Chinese. <i>BMC Genetics</i> , 2019 , 20, 97	2.6	9
53	Vegetable Signatures Derived from Human Urinary Metabolomic Data in Controlled Feeding Studies. <i>Journal of Proteome Research</i> , 2019 , 18, 159-168	5.6	2
52	A Two-Stage Whole-Genome Gene Expression Association Study of Young-Onset Hypertension in Han Chinese Population of Taiwan. <i>Scientific Reports</i> , 2018 , 8, 1800	4.9	4
51	Postprandial Metabolomics Response to Various Cooking Oils in Humans. <i>Journal of Agricultural and Food Chemistry</i> , 2018 , 66, 4977-4984	5.7	5
50	Homozygosity disequilibrium associated with treatment response and its methylation regulation. <i>BMC Proceedings</i> , 2018 , 12, 45	2.3	2
49	Interethnic DNA methylation difference and its implications in pharmacoepigenetics. <i>Epigenomics</i> , 2017 , 9, 1437-1454	4.4	13
48	Using an Event-History with Risk-Free Model to Study the Genetics of Alcoholism. <i>Scientific Reports</i> , 2017 , 7, 1975	4.9	5
47	Morbid obesity in Taiwan: Prevalence, trends, associated social demographics, and lifestyle factors. <i>PLoS ONE</i> , 2017 , 12, e0169577	3.7	58

46	Pharmacogenomics study on cadherin 2 network with regard to HIV infection and methadone treatment outcome. <i>PLoS ONE</i> , 2017 , 12, e0174647	3.7	3
45	Homozygosity disequilibrium and its gene regulation. <i>BMC Proceedings</i> , 2016 , 10, 159-163	2.3	2
44	Genetic signatures of heroin addiction. <i>Medicine (United States)</i> , 2016 , 95, e4473	1.8	7
43	SMART: Statistical Metabolomics Analysis-An R Tool. <i>Analytical Chemistry</i> , 2016 , 88, 6334-41	7.8	21
42	An integrated analysis tool for analyzing hybridization intensities and genotypes using new-generation population-optimized human arrays. <i>BMC Genomics</i> , 2016 , 17, 266	4.5	2
41	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. <i>PLoS Genetics</i> , 2016 , 12, e0160310	6	34
40	THE USE OF CAPTURE-RECAPTURE METHODOLOGY IN EPIDEMIOLOGICAL SURVEILLANCE AND ECOLOGICAL SURVEYS 2015 , 425-467		
39	Association of circadian genes with diurnal blood pressure changes and non-dipper essential hypertension: a genetic association with young-onset hypertension. <i>Hypertension Research</i> , 2015 , 38, 155-62	4.7	29
38	Analysis of homozygosity disequilibrium using whole-genome sequencing data. <i>BMC Proceedings</i> , 2014 , 8, S15	2.3	7
37	Applying genome-wide gene-based expression quantitative trait locus mapping to study population ancestry and pharmacogenetics. <i>BMC Genomics</i> , 2014 , 15, 319	4.5	6
36	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. <i>PLoS ONE</i> , 2014 , 9, e97919	3.7	9
35	A three-stage genome-wide association study combining multilocus test and gene expression analysis for young-onset hypertension in Taiwan Han Chinese. <i>American Journal of Hypertension</i> , 2014 , 27, 819-27	2.3	10
34	The DAO gene is associated with schizophrenia and interacts with other genes in the Taiwan Han Chinese population. <i>PLoS ONE</i> , 2013 , 8, e60099	3.7	12
33	Fine-mapping angiotensin-converting enzyme gene: separate QTLs identified for hypertension and for ACE activity. <i>PLoS ONE</i> , 2013 , 8, e56119	3.7	16
32	Androgenic alopecia is associated with less dietary soy, lower [corrected] blood vanadium and rs1160312 1 polymorphism in Taiwanese communities. <i>PLoS ONE</i> , 2013 , 8, e79789	3.7	12
31	Integrative analysis of single nucleotide polymorphisms and gene expression efficiently distinguishes samples from closely related ethnic populations. <i>BMC Genomics</i> , 2012 , 13, 346	4.5	9
30	A genome-wide homozygosity association study identifies runs of homozygosity associated with rheumatoid arthritis in the human major histocompatibility complex. <i>PLoS ONE</i> , 2012 , 7, e34840	3.7	28
29	Identification of IGF1, SLC4A4, WWOX, and SFMBT1 as hypertension susceptibility genes in Han Chinese with a genome-wide gene-based association study. <i>PLoS ONE</i> , 2012 , 7, e32907	3.7	38

28	Risk of asthma associated with energy-dense but nutrient-poor dietary pattern in Taiwanese children. <i>Asia Pacific Journal of Clinical Nutrition</i> , 2012 , 21, 73-81	1	15
27	Region-based and pathway-based QTL mapping using a p-value combination method. <i>BMC Proceedings</i> , 2011 , 5 Suppl 9, S43	2.3	8
26	SAQC: SNP array quality control. <i>BMC Bioinformatics</i> , 2011 , 12, 100	3.6	4
25	LOHAS: loss-of-heterozygosity analysis suite. <i>Genetic Epidemiology</i> , 2011 , 35, 247-60	2.6	11
24	A genome-wide association study reveals a quantitative trait locus of adiponectin on CDH13 that predicts cardiometabolic outcomes. <i>Diabetes</i> , 2011 , 60, 2417-23	0.9	91
23	A new analysis tool for individual-level allele frequency for genomic studies. <i>BMC Genomics</i> , 2010 , 11, 415	4.5	6
22	Genome-wide association study of young-onset hypertension in the Han Chinese population of Taiwan. <i>PLoS ONE</i> , 2009 , 4, e5459	3.7	51
21	Genome-wide gene-based association study. <i>BMC Proceedings</i> , 2009 , 3 Suppl 7, S135	2.3	15
20	MPDA: microarray pooled DNA analyzer. <i>BMC Bioinformatics</i> , 2008 , 9, 196	3.6	10
19	Using the longest significance run to estimate region-specific p-values in genetic association mapping studies. <i>BMC Bioinformatics</i> , 2008 , 9, 246	3.6	3
18	PoooL: an efficient method for estimating haplotype frequencies from large DNA pools. <i>Bioinformatics</i> , 2008 , 24, 1942-8	7.2	18
17	Kernel-based association test. <i>Genetics</i> , 2008 , 179, 1057-68	4	22
16	Genome-wide scan for quantitative ACE activity in Taiwan young-onset hypertension study. <i>Human Heredity</i> , 2008 , 65, 85-90	1.1	8
15	Nonparametric estimation of LOH using Affymetrix SNP genotyping arrays for unpaired samples. <i>Journal of Human Genetics</i> , 2008 , 53, 983-990	4.3	10
14	Association mapping using pooled DNA. <i>Methods in Molecular Biology</i> , 2007 , 376, 161-75	1.4	4
13	A comparison of individual genotyping and pooled DNA analysis for polymorphism validation prior to large-scale genetic studies. <i>Annals of Human Genetics</i> , 2006 , 70, 350-9	2.2	7
12	A comparison of major histocompatibility complex SNPs in Han Chinese residing in Taiwan and Caucasians. <i>Journal of Biomedical Science</i> , 2006 , 13, 489-98	13.3	42
11	PDA: Pooled DNA analyzer. <i>BMC Bioinformatics</i> , 2006 , 7, 233	3.6	17

10	A sliding-window weighted linkage disequilibrium test. <i>Genetic Epidemiology</i> , 2006 , 30, 531-45	2.6	18
9	A genome-wide study of preferential amplification/hybridization in microarray-based pooled DNA experiments. <i>Nucleic Acids Research</i> , 2006 , 34, e106	20.1	16
8	Modeling animals behavioral response by Markov chain models for capture-recapture experiments. <i>Biometrics</i> , 2005 , 61, 1010-7	1.8	31
7	Breast cancer risk associated with genotypic polymorphism of the mitosis-regulating gene Aurora-A/STK15/BTAK. <i>International Journal of Cancer</i> , 2005 , 115, 276-83	7.5	60
6	A genome-wide scanning and fine mapping study of COGA data. <i>BMC Genetics</i> , 2005 , 6 Suppl 1, S30	2.6	17
5	New adjustment factors and sample size calculation in a DNA-pooling experiment with preferential amplification. <i>Genetics</i> , 2005 , 169, 399-410	4	18
4	Receptor mediated effect of serotonergic transmission in patients with bipolar affective disorder. <i>Journal of Medical Genetics</i> , 2003 , 40, 781-6	5.8	7
3	Population size estimation using local sample coverage for open populations. <i>Journal of Statistical Planning and Inference</i> , 2003 , 113, 699-714	0.8	11
2	Estimation of the size of an open population using local estimating equations II: a partially parametric approach. <i>Biometrics</i> , 2003 , 59, 365-74	1.8	6
1	Genomic, geographic and temporal distributions of SARS-CoV-2 mutations		11