

Pei-Chien Tsai

List of Publications by Citations

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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.

47
papers

3,595
citations

22
h-index

51
g-index

51
ext. papers

4,706
ext. citations

9.4
avg, IF

4.58
L-index

#	Paper	IF	Citations
47	DNA methylation-based measures of biological age: meta-analysis predicting time to death. <i>Aging</i> , 2016 , 8, 1844-1865	5.6	531
46	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. <i>Nature</i> , 2017 , 541, 81-86	50.4	511
45	Epigenome-wide scans identify differentially methylated regions for age and age-related phenotypes in a healthy ageing population. <i>PLoS Genetics</i> , 2012 , 8, e1002629	6	501
44	Obesity accelerates epigenetic aging of human liver. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 15538-43	11.5	456
43	Metabolomic markers reveal novel pathways of ageing and early development in human populations. <i>International Journal of Epidemiology</i> , 2013 , 42, 1111-9	7.8	166
42	Significant predictive factors for prognosis of primary upper urinary tract cancer after radical nephroureterectomy in Taiwanese patients. <i>European Urology</i> , 2008 , 54, 1127-34	10.2	154
41	Power and sample size estimation for epigenome-wide association scans to detect differential DNA methylation. <i>International Journal of Epidemiology</i> , 2015 , 44, 1429-1441	7.8	121
40	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. <i>Nature Communications</i> , 2018 , 9, 387	17.4	106
39	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , 2017 , 101, 888-902	11	83
38	Regulatory variants at KLF14 influence type 2 diabetes risk via a female-specific effect on adipocyte size and body composition. <i>Nature Genetics</i> , 2018 , 50, 572-580	36.3	82
37	coMET: visualisation of regional epigenome-wide association scan results and DNA co-methylation patterns. <i>BMC Bioinformatics</i> , 2015 , 16, 131	3.6	79
36	Epigenetic associations of type 2 diabetes and BMI in an Arab population. <i>Clinical Epigenetics</i> , 2016 , 8, 13	7.7	76
35	Huge gap between clinical efficacy and community effectiveness in the treatment of chronic hepatitis C: a nationwide survey in Taiwan. <i>Medicine (United States)</i> , 2015 , 94, e690	1.8	71
34	DNA methylation-based estimator of telomere length. <i>Aging</i> , 2019 , 11, 5895-5923	5.6	69
33	Smoking induces coordinated DNA methylation and gene expression changes in adipose tissue with consequences for metabolic health. <i>Clinical Epigenetics</i> , 2018 , 10, 126	7.7	56
32	Meta-analysis of epigenome-wide association studies of cognitive abilities. <i>Molecular Psychiatry</i> , 2018 , 23, 2133-2144	15.1	46
31	Age-dependent changes in mean and variance of gene expression across tissues in a twin cohort. <i>Human Molecular Genetics</i> , 2018 , 27, 732-741	5.6	43

30	Using epigenome-wide association scans of DNA methylation in age-related complex human traits. <i>Epigenomics</i> , 2012 , 4, 511-26	4.4	39
29	Epigenome-wide Association of DNA Methylation in Whole Blood With Bone Mineral Density. <i>Journal of Bone and Mineral Research</i> , 2017 , 32, 1644-1650	6.3	33
28	Exploring the molecular basis of age-related disease comorbidities using a multi-omics graphical model. <i>Scientific Reports</i> , 2016 , 6, 37646	4.9	33
27	Unexpected early tumor recurrence in patients with hepatitis C virus-related hepatocellular carcinoma undergoing interferon-free therapy: Issue of the interval between HCC treatment and antiviral therapy. <i>Journal of Hepatology</i> , 2017 , 66, 464	13.4	33
26	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. <i>Nature Communications</i> , 2019 , 10, 2581	17.4	31
25	Association of dietary folate and vitamin B-12 intake with genome-wide DNA methylation in blood: a large-scale epigenome-wide association analysis in 5841 individuals. <i>American Journal of Clinical Nutrition</i> , 2019 , 110, 437-450	7	22
24	Deep molecular phenotypes link complex disorders and physiological insult to CpG methylation. <i>Human Molecular Genetics</i> , 2018 , 27, 1106-1121	5.6	21
23	Improved nondominant hand performance on a laparoscopic virtual reality simulator after playing the Nintendo Wii. <i>Surgical Endoscopy and Other Interventional Techniques</i> , 2013 , 27, 4224-31	5.2	21
22	Metabolomics profiling reveals novel markers for leukocyte telomere length. <i>Aging</i> , 2016 , 8, 77-94	5.6	21
21	Hepatocellular carcinoma recurrence after direct-acting antiviral therapy: an individual patient data meta-analysis. <i>Gut</i> , 2021 ,	19.2	21
20	DNA Methylation Changes in the IGF1R Gene in Birth Weight Discordant Adult Monozygotic Twins. <i>Twin Research and Human Genetics</i> , 2015 , 18, 635-46	2.2	20
19	Heritability of skewed X-inactivation in female twins is tissue-specific and associated with age. <i>Nature Communications</i> , 2019 , 10, 5339	17.4	19
18	Epigenetic findings in periodontitis in UK twins: a cross-sectional study. <i>Clinical Epigenetics</i> , 2019 , 11, 27	7.7	17
17	Genetic and environmental impacts on DNA methylation levels in twins. <i>Epigenomics</i> , 2016 , 8, 105-17	4.4	17
16	Epigenome-wide DNA methylation in hearing ability: new mechanisms for an old problem. <i>PLoS ONE</i> , 2014 , 9, e105729	3.7	15
15	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021 , 22, 194	18.3	14
14	A real-world impact of cost-effectiveness of pegylated interferon/ribavarin regimens on treatment-naïve chronic hepatitis C patients in Taiwan. <i>Kaohsiung Journal of Medical Sciences</i> , 2017 , 33, 44-49	2.4	10
13	Epigenetic Signatures at AQP3 and SOCS3 Engage in Low-Grade Inflammation across Different Tissues. <i>PLoS ONE</i> , 2016 , 11, e0166015	3.7	10

12	Epigenome-wide association meta-analysis of DNA methylation with coffee and tea consumption. <i>Nature Communications</i> , 2021 , 12, 2830	17.4	9
11	Genome-wide association studies identify 137 loci for DNA methylation biomarkers of ageing		8
10	Blood DNA methylation sites predict death risk in a longitudinal study of 12, 300 individuals. <i>Aging</i> , 2020 , 12, 14092-14124	5.6	6
9	Identical twins carry a persistent epigenetic signature of early genome programming. <i>Nature Communications</i> , 2021 , 12, 5618	17.4	6
8	Age-dependent changes in mean and variance of gene expression across tissues in a twin cohort		4
7	Identification of groups with poor cost-effectiveness of peginterferon plus ribavirin for naïve hepatitis C patients with a real-world cohort and database. <i>Medicine (United States)</i> , 2017 , 96, e6984	1.8	3
6	Identification of treatment-experienced hepatitis C patients with poor cost-effectiveness of pegylated interferon plus ribavirin from a real-world cohort. <i>Journal of the Formosan Medical Association</i> , 2018 , 117, 54-62	3.2	2
5	Smoking induces coordinated DNA methylation and gene expression changes in adipose tissue with consequences for metabolic health		2
4	GWAS of epigenetic ageing rates in blood reveals a critical role for TERT		1
3	Genetic loci determining total immunoglobulin E levels from birth through adulthood. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2019 , 74, 621-625	9.3	1
2	DNA methylation signature of chronic low-grade inflammation and its role in cardio-respiratory diseases.. <i>Nature Communications</i> , 2022 , 13, 2408	17.4	1
1	Reply to "cost effectiveness of hepatitis C treatments: Need for a comprehensive evaluation". <i>Kaohsiung Journal of Medical Sciences</i> , 2017 , 33, 586	2.4	