Yen-Feng Chiu

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4000957/publications.pdf

Version: 2024-02-01

46 papers

1,241 citations

16 h-index 32 g-index

48 all docs

48 docs citations

48 times ranked

2547 citing authors

#	Article	IF	CITATIONS
1	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
2	Cross-sectional and longitudinal comparisons of metabolic profiles between vegetarian and non-vegetarian subjects: a matched cohort study. British Journal of Nutrition, 2015, 114, 1313-1320.	2.3	114
3	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
4	A meta-analysis of genome-wide association studies for adiponectin levels in East Asians identifies a novel locus near WDR11-FGFR2. Human Molecular Genetics, 2014, 23, 1108-1119.	2.9	68
5	A Robust Identity-by-Descent Procedure Using Affected Sib Pairs: Multipoint Mapping for Complex Diseases. Human Heredity, 2001, 51, 64-78.	0.8	67
6	Taiwanese Vegetarians and Omnivores: Dietary Composition, Prevalence of Diabetes and IFG. PLoS ONE, 2014, 9, e88547.	2.5	67
7	Vegetarian diet reduces the risk of hypertension independent of abdominal obesity and inflammation. Journal of Hypertension, 2016, 34, 2164-2171.	0.5	47
8	Multipoint affected sibpair linkage methods for localizing susceptibility genes of complex diseases. Genetic Epidemiology, 2003, 24, 107-117.	1.3	33
9	Independent association between subjective cognitive decline and frailty in the elderly. PLoS ONE, 2018, 13, e0201351.	2.5	33
10	Genetics of Coronary Artery Disease in Taiwan: A Cardiometabochip Study by the Taichi Consortium. PLoS ONE, 2016, 11, e0138014.	2.5	33
11	Prevalence of and risk factors for minor and major depression among community-dwelling older adults in Taiwan. International Psychogeriatrics, 2017, 29, 1113-1121.	1.0	31
12	An Autosomal Genome-wide Scan for Loci Linked to Pre-Diabetic Phenotypes in Nondiabetic Chinese Subjects From the Stanford Asia-Pacific Program of Hypertension and Insulin Resistance Family Study. Diabetes, 2005, 54, 1200-1206.	0.6	29
13	Cohort Profile: The Healthy Aging Longitudinal Study in Taiwan (HALST). International Journal of Epidemiology, 2017, 46, 1106-1106j.	1.9	26
14	SVMâ€Based Generalized Multifactor Dimensionality Reduction Approaches for Detecting Geneâ€Gene Interactions in Family Studies. Genetic Epidemiology, 2012, 36, 88-98.	1.3	22
15	Longitudinal analytical approaches to genetic data. BMC Genetics, 2016, 17, 4.	2.7	19
16	Adiponectin gene (ADIPOQ) polymorphisms correlate with the progression of nephropathy in Taiwanese male patients with type 2 diabetes. Diabetes Research and Clinical Practice, 2014, 105, 261-270.	2.8	17
17	The Role of Consolidation Chemoradiotherapy in Locally Advanced Pancreatic Cancer Receiving Chemotherapy: An Updated Systematic Review and Meta-Analysis. Cancer Research and Treatment, 2018, 50, 562-574.	3.0	16
18	SLC2A10 genetic polymorphism predicts development of peripheral arterial disease in patients with type 2 diabetes. SLC2A10and PAD in type 2 diabetes. BMC Medical Genetics, 2010, 11, 126.	2.1	15

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19	Interleukin-6 gene polymorphisms correlate with the progression of nephropathy in Chinese patients with type 2 diabetes: A prospective cohort study. Diabetes Research and Clinical Practice, 2016, 120, 15-23.	2.8	15
20	Genomeâ€wide scan for circulating vascular adhesion proteinâ€1 levels: <i><scp>MACROD</scp>2</i> as a potential transcriptional regulator of adipogenesis. Journal of Diabetes Investigation, 2018, 9, 1067-1074.	2.4	13
21	The paradox of aging and health-related quality of life in Asian Chinese: results from the Healthy Aging Longitudinal Study in Taiwan. BMC Geriatrics, 2020, 20, 91.	2.7	12
22	A phase II randomised trial of induction chemotherapy followed by concurrent chemoradiotherapy in locally advanced pancreatic cancer: the Taiwan Cooperative Oncology Group T2212 study. British Journal of Cancer, 2022, 126, 1018-1026.	6.4	11
23	Multi-omics analysis identifies CpGs near G6PC2 mediating the effects of genetic variants on fasting glucose. Diabetologia, 2021, 64, 1613-1625.	6.3	9
24	Assessment of incident frailty hazard associated with depressive symptoms in a Taiwanese longitudinal study. International Psychogeriatrics, 2022, 34, 61-70.	1.0	9
25	Multipoint linkage mapping using sibpairs: Non-parametric estimation of trait effects with quantitative covariates. Genetic Epidemiology, 2005, 28, 58-69.	1.3	8
26	Multipoint linkage disequilibrium mapping using case-control designs. Genetic Epidemiology, 2005, 29, 365-376.	1.3	8
27	Genome-wide copy number variation analysis identified deletions in SFMBT1 associated with fasting plasma glucose in a Han Chinese population. BMC Genomics, 2017, 18, 591.	2.8	8
28	Sedative–hypnotic drug use among community-dwelling elderly in Taiwan. International Psychogeriatrics, 2018, 30, 957-965.	1.0	7
29	Generalization of Rare Variant Association Tests for Longitudinal Family Studies. Genetic Epidemiology, 2016, 40, 101-112.	1.3	6
30	Regionâ€based association tests for sequencing data on survival traits. Genetic Epidemiology, 2017, 41, 511-522.	1.3	6
31	Moderating effect of depression on the association between pain and activities of daily living in older adults. Psychogeriatrics, 2018, 18, 379-387.	1.2	6
32	A comparison in association and linkage genome-wide scans for alcoholism susceptibility genes using single-nucleotide polymorphisms. BMC Genetics, 2005, 6, S89.	2.7	5
33	Identification of rare variants for hypertension with incorporation of linkage information. BMC Proceedings, 2014, 8, S109.	1.6	5
34	Incorporation of covariates into multipoint linkage disequilibrium mapping in caseâ€control studies. Genetic Epidemiology, 2008, 32, 143-151.	1.3	4
35	Incorporating Covariates into Multipoint Association Mapping in the Case-Parent Design. Human Heredity, 2010, 69, 229-241.	0.8	4
36	A Novel Support Vector Machine-Based Approach for Rare Variant Detection. PLoS ONE, 2013, 8, e71114.	2.5	4

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37	Assessment of gene-covariate interactions by incorporating covariates into association mapping. BMC Proceedings, 2009, 3, S85.	1.6	3
38	Multipoint association mapping for longitudinal family data: an application to hypertension phenotypes. BMC Proceedings, 2016, 10, 315-320.	1.6	3
39	Assessment of fenofibrate-methylation interactions on triglycerides using longitudinal family data. BMC Proceedings, 2018, 12, 48.	1.6	3
40	<i>IGF1</i> Gene Is Associated With Triglyceride Levels In Subjects With Family History Of Hypertension From The SAPPHIRe And TWB Projects. International Journal of Medical Sciences, 2018, 15, 1035-1042.	2.5	3
41	Incorporating quantitative variables into linkage analysis using affected sib pairs. BMC Proceedings, 2007, 1, S98.	1.6	2
42	Incorporation of covariates in simultaneous localization of two linked loci using affected relative pairs. BMC Genetics, 2010, 11, 67.	2.7	2
43	Analysis of Family―and Populationâ€Based Samples Using Multiple Linkage Disequilibrium Mapping. Annals of Human Genetics, 2013, 77, 251-267.	0.8	2
44	Longitudinal changes in physical and mental health of older adults with chronic hepatitis B infection: Trajectories and predictors. Preventive Medicine Reports, 2021, 23, 101432.	1.8	1
45	Simultaneous estimation of the locations and effects of multiple disease loci in case-control studies. Biostatistics, 2015, 16, 222-239.	1.5	0
46	General retrospective megaâ€analysis framework for rare variant association tests. Genetic Epidemiology, 2018, 42, 621-635.	1.3	0