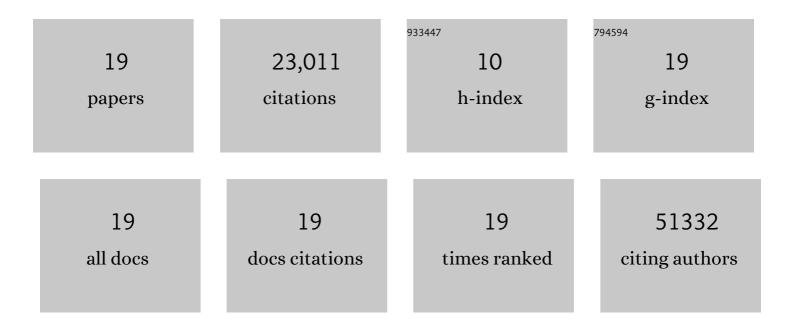
## Tao Wang

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7459028/publications.pdf Version: 2024-02-01



TAOMANO

#	Article	IF	CITATIONS
1	Clinical Characteristics of Coronavirus Disease 2019 in China. New England Journal of Medicine, 2020, 382, 1708-1720.	27.0	22,372
2	Use of >100,000 NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium whole genome sequences improves imputation quality and detection of rare variant associations in admixed African and Hispanic/Latino populations. PLoS Genetics, 2019, 15, e1008500.	3.5	203
3	A Prospective Study of Inflammation Markers and Endometrial Cancer Risk in Postmenopausal Hormone Nonusers. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 971-977.	2.5	83
4	Circulating Adipokines and Inflammatory Markers and Postmenopausal Breast Cancer Risk. Journal of the National Cancer Institute, 2015, 107, .	6.3	83
5	Hsaâ€miRâ€375 is differentially expressed during breast lobular neoplasia and promotes loss of mammary acinar polarity. Journal of Pathology, 2012, 226, 108-119.	4.5	64
6	The clinical significance of inflammatory cytokines in primary cell culture in endometrial carcinoma. Molecular Oncology, 2013, 7, 41-54.	4.6	49
7	Treatment of Severe COVID-19 with Convalescent Plasma in Bronx, NYC. JCI Insight, 2021, 6, .	5.0	36
8	Resequencing of pooled DNA for detecting disease associations with rare variants. Genetic Epidemiology, 2010, 34, 492-501.	1.3	23
9	Differential expression of circulating microRNAs according to severity of colorectal neoplasia. Translational Research, 2015, 166, 225-232.	5.0	18
10	Evaluation and Adaptation of a Laboratory-Based cDNA Library Preparation Protocol for Retrospective Sequencing of Archived MicroRNAs from up to 35-Year-Old Clinical FFPE Specimens. International Journal of Molecular Sciences, 2017, 18, 627.	4.1	15
11	Opposite Genetic Effects of CMIP Polymorphisms on the Risk of Type 2 Diabetes and Obesity: A Family-Based Study in China. International Journal of Molecular Sciences, 2018, 19, 1011.	4.1	12
12	Transcriptome-Wide Association Study of Blood Cell Traits in African Ancestry and Hispanic/Latino Populations. Genes, 2021, 12, 1049.	2.4	11
13	Differences in Vaginal Microbiota, Host Transcriptome, and Proteins in Women With Bacterial Vaginosis Are Associated With Metronidazole Treatment Response. Journal of Infectious Diseases, 2021, 224, 2094-2104.	4.0	10
14	Estimating Allele Frequency from Next-Generation Sequencing of Pooled Mitochondrial DNA Samples. Frontiers in Genetics, 2011, 2, 51.	2.3	9
15	Classical monocyte transcriptomes reveal significant anti-inflammatory statin effect in women with chronic HIV. Cardiovascular Research, 2021, 117, 1166-1177.	3.8	8
16	A Robust Method for Genomeâ€Wide Association Metaâ€Analysis With the Application to Circulating Insulinâ€Like Growth Factor I Concentrations. Genetic Epidemiology, 2014, 38, 162-171.	1.3	5
17	Adjustment for covariates using summary statistics of genomeâ€wide association studies. Genetic Epidemiology, 2018, 42, 812-825.	1.3	5
18	Design and Statistical Analysis of Pooled Next Generation Sequencing for Rare Variants. Journal of Probability and Statistics, 2012, 2012, 1-19.	0.7	4

#	Article	IF	CITATIONS
19	Molecular markers of risk of subsequent invasive breast cancer in women with ductal carcinoma in situ: protocol for a population-based cohort study. BMJ Open, 2021, 11, e053397.	1.9	1