

# Guimin Gao

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/266213/publications.pdf>

Version: 2024-02-01

11  
papers

189  
citations

1307594

7  
h-index

1372567

10  
g-index

11  
all docs

11  
docs citations

11  
times ranked

687  
citing authors

#	ARTICLE	IF	CITATIONS
1	Evaluating Polygenic Risk Scores for Breast Cancer in Women of African Ancestry. <i>Journal of the National Cancer Institute</i> , 2021, 113, 1168-1176.	6.3	41
2	WHSC1L1 drives cell cycle progression through transcriptional regulation of CDC6 and CDK2 in squamous cell carcinoma of the head and neck. <i>Oncotarget</i> , 0, 7, 42527-42538.	1.8	33
3	Cross-ancestry GWAS meta-analysis identifies six breast cancer loci in African and European ancestry women. <i>Nature Communications</i> , 2021, 12, 4198.	12.8	24
4	Daily Aspirin Use Does Not Impact Clinical Outcomes in Patients With Inflammatory Bowel Disease. <i>Inflammatory Bowel Diseases</i> , 2021, 27, 236-241.	1.9	18
5	Germline variants and somatic mutation signatures of breast cancer across populations of African and European ancestry in the US and Nigeria. <i>International Journal of Cancer</i> , 2019, 145, 3321-3333.	5.1	16
6	Associating Multivariate Quantitative Phenotypes with Genetic Variants in Family Samples with a Novel Kernel Machine Regression Method. <i>Genetics</i> , 2015, 201, 1329-1339.	2.9	14
7	Trans-ethnic predicted expression genome-wide association analysis identifies a gene for estrogen receptor-negative breast cancer. <i>PLoS Genetics</i> , 2017, 13, e1006727.	3.5	14
8	Plasma metabolites and lipids associate with kidney function and kidney volume in hypertensive ADPKD patients early in the disease course. <i>BMC Nephrology</i> , 2019, 20, 66.	1.8	14
9	Novel strategy for disease risk prediction incorporating predicted gene expression and DNA methylation data: a multi-phased study of prostate cancer. <i>Cancer Communications</i> , 2021, 41, 1387-1397.	9.2	6
10	Penalized Fieller's confidence interval for the ratio of bivariate normal means. <i>Biometrics</i> , 2021, 77, 1355-1368.	1.4	5
11	STEPS: an efficient prospective likelihood approach to genetic association analyses of secondary traits in extreme phenotype sequencing. <i>Biostatistics</i> , 2020, 21, 33-49.	1.5	4