

# Yang Wu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2456123/publications.pdf>

Version: 2024-02-01

32  
papers

9,668  
citations

257450

24  
h-index

414414

32  
g-index

37  
all docs

37  
docs citations

37  
times ranked

16454  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018, 50, 668-681.	21.4	2,224
2	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. <i>Nature Genetics</i> , 2018, 50, 1112-1121.	21.4	1,835
3	Genetic mechanisms of critical illness in COVID-19. <i>Nature</i> , 2021, 591, 92-98.	27.8	1,014
4	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. <i>Nature</i> , 2022, 604, 502-508.	27.8	929
5	Causal associations between risk factors and common diseases inferred from GWAS summary data. <i>Nature Communications</i> , 2018, 9, 224.	12.8	629
6	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. <i>Nature Communications</i> , 2018, 9, 2941.	12.8	570
7	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. <i>Nature Genetics</i> , 2019, 51, 245-257.	21.4	536
8	Signatures of negative selection in the genetic architecture of human complex traits. <i>Nature Genetics</i> , 2018, 50, 746-753.	21.4	304
9	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. <i>Nature Communications</i> , 2018, 9, 2282.	12.8	294
10	Integrative analysis of omics summary data reveals putative mechanisms underlying complex traits. <i>Nature Communications</i> , 2018, 9, 918.	12.8	250
11	Whole-genome sequencing reveals host factors underlying critical COVID-19. <i>Nature</i> , 2022, 607, 97-103.	27.8	174
12	Genotype-by-environment interactions inferred from genetic effects on phenotypic variability in the UK Biobank. <i>Science Advances</i> , 2019, 5, eaaw3538.	10.3	123
13	The Genetic Architecture of Depression in Individuals of East Asian Ancestry. <i>JAMA Psychiatry</i> , 2021, 78, 1258.	11.0	88
14	Quantifying the mapping precision of genome-wide association studies using whole-genome sequencing data. <i>Genome Biology</i> , 2017, 18, 86.	8.8	84
15	Global genetic differentiation of complex traits shaped by natural selection in humans. <i>Nature Communications</i> , 2018, 9, 1865.	12.8	70
16	Dissection of genetic variation and evidence for pleiotropy in male pattern baldness. <i>Nature Communications</i> , 2018, 9, 5407.	12.8	65
17	Cross-disorder analysis of schizophrenia and 19 immune-mediated diseases identifies shared genetic risk. <i>Human Molecular Genetics</i> , 2019, 28, 3498-3513.	2.9	65
18	Genome-wide association study identifies loci and candidate genes for meat quality traits in Simmental beef cattle. <i>Mammalian Genome</i> , 2016, 27, 246-255.	2.2	50

#	ARTICLE	IF	CITATIONS
19	Widespread signatures of natural selection across human complex traits and functional genomic categories. <i>Nature Communications</i> , 2021, 12, 1164.	12.8	50
20	Genome-Wide Association Studies Using Haplotypes and Individual SNPs in Simmental Cattle. <i>PLoS ONE</i> , 2014, 9, e109330.	2.5	42
21	A genome-wide scan for copy number variations using high-density single nucleotide polymorphism array in Simmental cattle. <i>Animal Genetics</i> , 2015, 46, 289-298.	1.7	39
22	Identifying the Common Genetic Basis of Antidepressant Response. <i>Biological Psychiatry Global Open Science</i> , 2022, 2, 115-126.	2.2	31
23	Improved analyses of GWAS summary statistics by reducing data heterogeneity and errors. <i>Nature Communications</i> , 2021, 12, 7117.	12.8	31
24	Genome-wide detection of selective signatures in Simmental cattle. <i>Journal of Applied Genetics</i> , 2014, 55, 343-351.	1.9	30
25	Pathway-Based Genome-Wide Association Studies for Two Meat Production Traits in Simmental Cattle. <i>Scientific Reports</i> , 2016, 5, 18389.	3.3	28
26	Genetic regulation of methylation in human endometrium and blood and gene targets for reproductive diseases. <i>Clinical Epigenetics</i> , 2019, 11, 49.	4.1	26
27	Detection of candidate genes for growth and carcass traits using genome-wide association strategy in Chinese Simmental beef cattle. <i>Animal Production Science</i> , 2018, 58, 224.	1.3	22
28	Forward LASSO analysis for high-order interactions in genome-wide association study. <i>Briefings in Bioinformatics</i> , 2014, 15, 552-561.	6.5	15
29	The Impact of Variable Degrees of Freedom and Scale Parameters in Bayesian Methods for Genomic Prediction in Chinese Simmental Beef Cattle. <i>PLoS ONE</i> , 2016, 11, e0154118.	2.5	14
30	Functional characterisation of the amyotrophic lateral sclerosis risk locus GPX3/TNIP1. <i>Genome Medicine</i> , 2022, 14, 7.	8.2	12
31	Promoter-anchored chromatin interactions predicted from genetic analysis of epigenomic data. <i>Nature Communications</i> , 2020, 11, 2061.	12.8	8
32	Cox regression model for dissecting genetic architecture of survival time. <i>Genomics</i> , 2014, 104, 472-476.	2.9	6