

Huwenbo Shi

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2340299/publications.pdf>

Version: 2024-02-01

19
papers

3,584
citations

566801

15
h-index

794141

19
g-index

27
all docs

27
docs citations

27
times ranked

7119
citing authors

#	ARTICLE	IF	CITATIONS
1	Leveraging gene co-regulation to identify gene sets enriched for disease heritability. American Journal of Human Genetics, 2022, 109, 393-404.	2.6	10
2	Leveraging fine-mapping and multipopulation training data to improve cross-population polygenic risk scores. Nature Genetics, 2022, 54, 450-458.	9.4	109
3	Partitioning gene-level contributions to complex-trait heritability by allele frequency identifies disease-relevant genes. American Journal of Human Genetics, 2022, 109, 692-709.	2.6	2
4	Combining SNP-to-gene linking strategies to identify disease genes and assess disease omnigenicity. Nature Genetics, 2022, 54, 827-836.	9.4	61
5	Population-specific causal disease effect sizes in functionally important regions impacted by selection. Nature Communications, 2021, 12, 1098.	5.8	68
6	A large-scale genome-wide association analysis of lung function in the Chinese population identifies novel loci and highlights shared genetic aetiology with obesity. European Respiratory Journal, 2021, 58, 2100199.	3.1	30
7	Technology dictates algorithms: recent developments in read alignment. Genome Biology, 2021, 22, 249.	3.8	51
8	Localizing Components of Shared Transethnic Genetic Architecture of Complex Traits from GWAS Summary Data. American Journal of Human Genetics, 2020, 106, 805-817.	2.6	71
9	Accurate estimation of SNP-heritability from biobank-scale data irrespective of genetic architecture. Nature Genetics, 2019, 51, 1244-1251.	9.4	69
10	Shared genetics of asthma and mental health disorders: a large-scale genome-wide cross-trait analysis. European Respiratory Journal, 2019, 54, 1901507.	3.1	106
11	Probabilistic fine-mapping of transcriptome-wide association studies. Nature Genetics, 2019, 51, 675-682.	9.4	275
12	Phenotype-Specific Enrichment of Mendelian Disorder Genes near GWAS Regions across 62 Complex Traits. American Journal of Human Genetics, 2018, 103, 535-552.	2.6	90
13	A unifying framework for joint trait analysis under a non-infinitesimal model. Bioinformatics, 2018, 34, i195-i201.	1.8	5
14	Integrating Gene Expression with Summary Association Statistics to Identify Genes Associated with 30 Complex Traits. American Journal of Human Genetics, 2017, 100, 473-487.	2.6	248
15	Local Genetic Correlation Gives Insights into the Shared Genetic Architecture of Complex Traits. American Journal of Human Genetics, 2017, 101, 737-751.	2.6	220
16	Contrasting the Genetic Architecture of 30 Complex Traits from Summary Association Data. American Journal of Human Genetics, 2016, 99, 139-153.	2.6	348
17	Integrative approaches for large-scale transcriptome-wide association studies. Nature Genetics, 2016, 48, 245-252.	9.4	1,618
18	A multivariate Bernoulli model to predict DNaseI hypersensitivity status from haplotype data. Bioinformatics, 2015, 31, 3514-3521.	1.8	2

#	ARTICLE	IF	CITATIONS
19	Fast and accurate imputation of summary statistics enhances evidence of functional enrichment. <i>Bioinformatics</i> , 2014, 30, 2906-2914.	1.8	173