Huwenbo Shi

List of Publications by Year
in descending order

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

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19	3,584	566801	794141
papers	citations	15 h-index	19 g-index

27	27	27	7119
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Integrative approaches for large-scale transcriptome-wide association studies. Nature Genetics, 2016, 48, 245-252.	9.4	1,618
2	Contrasting the Genetic Architecture of 30 Complex Traits from Summary Association Data. American Journal of Human Genetics, 2016, 99, 139-153.	2.6	348
3	Probabilistic fine-mapping of transcriptome-wide association studies. Nature Genetics, 2019, 51, 675-682.	9.4	275
4	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
5	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
6	Fast and accurate imputation of summary statistics enhances evidence of functional enrichment. Bioinformatics, 2014, 30, 2906-2914.	1.8	173
7	Leveraging fine-mapping and multipopulation training data to improve cross-population polygenic risk scores. Nature Genetics, 2022, 54, 450-458.	9.4	109
8	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
9	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
10	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
11	Accurate estimation of SNP-heritability from biobank-scale data irrespective of genetic architecture. Nature Genetics, 2019, 51, 1244-1251.	9.4	69
12	Population-specific causal disease effect sizes in functionally important regions impacted by selection. Nature Communications, 2021, 12, 1098.	5.8	68
13	Combining SNP-to-gene linking strategies to identify disease genes and assess disease omnigenicity. Nature Genetics, 2022, 54, 827-836.	9.4	61
14	Technology dictates algorithms: recent developments in read alignment. Genome Biology, 2021, 22, 249.	3.8	51
15	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
16	Leveraging gene co-regulation to identify gene sets enriched for disease heritability. American Journal of Human Genetics, 2022, 109, 393-404.	2.6	10
17	A unifying framework for joint trait analysis under a non-infinitesimal model. Bioinformatics, 2018, 34, i195-i201.	1.8	5
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	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