Boyang Li

List of Publications by Year
in descending order

22 papers	1,551 citations	516710 16 h-index	677142 22 g-index
27 all docs	27 docs citations	27 times ranked	3308 citing authors

#	Article	IF	Citations
1	A statistical framework for cross-tissue transcriptome-wide association analysis. Nature Genetics, 2019, 51, 568-576.	21.4	262
2	Genome-wide meta-analysis of problematic alcohol use in 435,563 individuals yields insights into biology and relationships with other traits. Nature Neuroscience, 2020, 23, 809-818.	14.8	242
3	Genome-wide association study of post-traumatic stress disorder reexperiencing symptoms in >165,000 US veterans. Nature Neuroscience, 2019, 22, 1394-1401.	14.8	145
4	A Powerful Approach to Estimating Annotation-Stratified Genetic Covariance via GWAS Summary Statistics. American Journal of Human Genetics, 2017, 101, 939-964.	6.2	141
5	Systematic tissue-specific functional annotation of the human genome highlights immune-related DNA elements for late-onset Alzheimer's disease. PLoS Genetics, 2017, 13, e1006933.	3.5	96
6	Mutations disrupting neuritogenesis genes confer risk for cerebral palsy. Nature Genetics, 2020, 52, 1046-1056.	21.4	96
7	Exome sequencing implicates genetic disruption of prenatal neuro-gliogenesis in sporadic congenital hydrocephalus. Nature Medicine, 2020, 26, 1754-1765.	30.7	84
8	Genome-wide Association Study of Maximum Habitual Alcohol Intake in >140,000 U.S. European and African American Veterans Yields Novel Risk Loci. Biological Psychiatry, 2019, 86, 365-376.	1.3	82
9	Characterization and identification of long non-coding RNAs based on feature relationship. Bioinformatics, 2019, 35, 2949-2956.	4.1	64
10	Genome-wide association study of smoking trajectory and meta-analysis of smoking status in 842,000 individuals. Nature Communications, 2020, 11, 5302.	12.8	59
11	SUPERGNOVA: local genetic correlation analysis reveals heterogeneous etiologic sharing of complex traits. Genome Biology, 2021, 22, 262.	8.8	56
12	Genome-Wide Association Studies of Schizophrenia and Bipolar Disorder in a Diverse Cohort of US Veterans. Schizophrenia Bulletin, 2021, 47, 517-529.	4.3	48
13	*DIAPH1* Variants in Non–East Asian Patients With Sporadic Moyamoya Disease. JAMA Neurology, 2021, 78, 993.	9.0	33
14	DNA methylation signatures of illicit drug injection and hepatitis C are associated with HIV frailty. Nature Communications, 2017, 8, 2243.	12.8	32
15	Exome Sequencing Implicates Impaired GABA Signaling and Neuronal Ion Transport in Trigeminal Neuralgia. IScience, 2020, 23, 101552.	4.1	32
16	Genome-wide association study of cognitive performance in U.S. veterans with schizophrenia or bipolar disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2020, 183, 181-194.	1.7	17
17	Using DNA methylation to validate an electronic medical record phenotype for smoking. Addiction Biology, 2019, 24, 1056-1065.	2.6	11
18	The impact of removing former drinkers from genome-wide association studies of AUDIT-C. Addiction, 2021, 116, 3044-3054.	3.3	11

#	Article	IF	Citations
19	An evaluation of noncoding genome annotation tools through enrichment analysis of 15 genome-wide association studies. Briefings in Bioinformatics, 2019, 20, 995-1003.	6.5	3
20	Incorporating local ancestry improves identification of ancestry-associated methylation signatures and meQTLs in African Americans. Communications Biology, 2022, 5, 401.	4.4	3
21	Quantifying concordant genetic effects of de novo mutations on multiple disorders. ELife, 0, 11, .	6.0	3
22	Whole-exome sequencing reveals damaging gene variants associated with hypoalphalipoproteinemia. Journal of Lipid Research, 2022, 63, 100209.	4.2	2