

Boyang Li

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8526020/publications.pdf>

Version: 2024-02-01

22
papers

1,551
citations

516681

16
h-index

677123

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. <i>Nature Genetics</i> , 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. <i>Nature Neuroscience</i> , 2020, 23, 809-818.	14.8	242
3	Genome-wide association study of post-traumatic stress disorder reexperiencing symptoms in >165,000 US veterans. <i>Nature Neuroscience</i> , 2019, 22, 1394-1401.	14.8	145
4	A Powerful Approach to Estimating Annotation-Stratified Genetic Covariance via GWAS Summary Statistics. <i>American Journal of Human Genetics</i> , 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. <i>PLoS Genetics</i> , 2017, 13, e1006933.	3.5	96
6	Mutations disrupting neuritogenesis genes confer risk for cerebral palsy. <i>Nature Genetics</i> , 2020, 52, 1046-1056.	21.4	96
7	Exome sequencing implicates genetic disruption of prenatal neuro-gliogenesis in sporadic congenital hydrocephalus. <i>Nature Medicine</i> , 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. <i>Biological Psychiatry</i> , 2019, 86, 365-376.	1.3	82
9	Characterization and identification of long non-coding RNAs based on feature relationship. <i>Bioinformatics</i> , 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. <i>Nature Communications</i> , 2020, 11, 5302.	12.8	59
11	SUPERGNOVA: local genetic correlation analysis reveals heterogeneous etiologic sharing of complex traits. <i>Genome Biology</i> , 2021, 22, 262.	8.8	56
12	Genome-Wide Association Studies of Schizophrenia and Bipolar Disorder in a Diverse Cohort of US Veterans. <i>Schizophrenia Bulletin</i> , 2021, 47, 517-529.	4.3	48
13	DIAPH1 Variants in Non-East Asian Patients With Sporadic Moyamoya Disease. <i>JAMA Neurology</i> , 2021, 78, 993.	9.0	33
14	DNA methylation signatures of illicit drug injection and hepatitis C are associated with HIV frailty. <i>Nature Communications</i> , 2017, 8, 2243.	12.8	32
15	Exome Sequencing Implicates Impaired GABA Signaling and Neuronal Ion Transport in Trigeminal Neuralgia. <i>iScience</i> , 2020, 23, 101552.	4.1	32
16	Genome-wide association study of cognitive performance in U.S. veterans with schizophrenia or bipolar disorder. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2020, 183, 181-194.	1.7	17
17	Using DNA methylation to validate an electronic medical record phenotype for smoking. <i>Addiction Biology</i> , 2019, 24, 1056-1065.	2.6	11
18	The impact of removing former drinkers from genome-wide association studies of AUDIT. <i>Addiction</i> , 2021, 116, 3044-3054.	3.3	11

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