

Liang He

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

3,225
citations

567281

15
h-index

377865

34
g-index

42
all docs

42
docs citations

42
times ranked

7879
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-cell transcriptomic analysis of Alzheimer's disease. <i>Nature</i> , 2019, 570, 332-337.	27.8	1,528
2	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	27.8	544
3	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2018, 50, 26-41.	21.4	286
4	<i>APOE4</i> disrupts intracellular lipid homeostasis in human iPSC-derived glia. <i>Science Translational Medicine</i> , 2021, 13, .	12.4	141
5	High-resolution genome-wide functional dissection of transcriptional regulatory regions and nucleotides in human. <i>Nature Communications</i> , 2018, 9, 5380.	12.8	117
6	Genome-wide association study on detailed profiles of smoking behavior and nicotine dependence in a twin sample. <i>Molecular Psychiatry</i> , 2014, 19, 615-624.	7.9	64
7	Discovery of high-confidence human protein-coding genes and exons by whole-genome PhyloCSF helps elucidate 118 GWAS loci. <i>Genome Research</i> , 2019, 29, 2073-2087.	5.5	52
8	NEBULA is a fast negative binomial mixed model for differential or co-expression analysis of large-scale multi-subject single-cell data. <i>Communications Biology</i> , 2021, 4, 629.	4.4	50
9	Pleiotropic Meta-Analyses of Longitudinal Studies Discover Novel Genetic Variants Associated with Age-Related Diseases. <i>Frontiers in Genetics</i> , 2016, 7, 179.	2.3	40
10	Pleiotropic Associations of Allelic Variants in a 2q22 Region with Risks of Major Human Diseases and Mortality. <i>PLoS Genetics</i> , 2016, 12, e1006314.	3.5	39
11	The Durations of Past Sickness Absences Predict Future Absence Episodes. <i>Journal of Occupational and Environmental Medicine</i> , 2013, 55, 87-92.	1.7	36
12	Apolipoprotein E region molecular signatures of Alzheimer's disease. <i>Aging Cell</i> , 2018, 17, e12779.	6.7	32
13	Fast Algorithms for Conducting Large-Scale GWAS of Age-at-Onset Traits Using Cox Mixed-Effects Models. <i>Genetics</i> , 2020, 215, 41-58.	2.9	29
14	Specific probiotics and virological findings in symptomatic conscripts attending military service in Finland. <i>Journal of Clinical Virology</i> , 2014, 60, 276-281.	3.1	27
15	Impact of classical risk factors of type 2 diabetes among Asian Indian, Chinese and Japanese populations. <i>Diabetes and Metabolism</i> , 2015, 41, 401-409.	2.9	19
16	Causal effects of cardiovascular risk factors on onset of major age-related diseases: A time-to-event Mendelian randomization study. <i>Experimental Gerontology</i> , 2018, 107, 74-86.	2.8	16
17	Genome-wide time-to-event analysis on smoking progression stages in a family-based study. <i>Brain and Behavior</i> , 2016, 6, e00462.	2.2	14
18	Estimating Modifying Effect of Age on Genetic and Environmental Variance Components in Twin Models. <i>Genetics</i> , 2016, 202, 1313-1328.	2.9	14

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19	Probiotics and respiratory and gastrointestinal tract infections in Finnish military conscripts â€” a randomised placebo-controlled double-blinded study. <i>Beneficial Microbes</i> , 2016, 7, 463-471.	2.4	13
20	Haplotype architecture of the Alzheimer's risk in the <i>APOE</i> region via co-skewness. <i>Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring</i> , 2020, 12, e12129.	2.4	13
21	Exome-wide age-of-onset analysis reveals exonic variants in ERN1 and SPPL2C associated with Alzheimer's disease. <i>Translational Psychiatry</i> , 2021, 11, 146.	4.8	13
22	Genetic and regulatory architecture of Alzheimer's disease in the <i>APOE</i> region. <i>Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring</i> , 2020, 12, e12008.	2.4	12
23	Allele-specific analysis reveals exon- and cell-type-specific regulatory effects of Alzheimer's disease-associated genetic variants. <i>Translational Psychiatry</i> , 2022, 12, 163.	4.8	10
24	Hierarchical Bayesian Model for Rare Variant Association Analysis Integrating Genotype Uncertainty in Human Sequence Data. <i>Genetic Epidemiology</i> , 2015, 39, 89-100.	1.3	9
25	Neuregulin signaling pathway in smoking behavior. <i>Translational Psychiatry</i> , 2017, 7, e1212-e1212.	4.8	8
26	Protective association of the $\epsilon 2/\epsilon 3$ heterozygote with Alzheimer's disease is strengthened by TOMM40 <i>APOE</i> variants in men. <i>Alzheimer's and Dementia</i> , 2021, 17, 1779-1787.	0.8	8
27	Genome-wide analysis identified abundant genetic modulators of contributions of the apolipoprotein E alleles to Alzheimer's disease risk. <i>Alzheimer's and Dementia</i> , 2022, , .	0.8	4
28	Parity and mortality in cases of childhood-onset diabetes mellitus. <i>Diabetes/Metabolism Research and Reviews</i> , 2016, 32, 607-614.	4.0	3
29	A genetic stochastic process model for genome-wide joint analysis of biomarker dynamics and disease susceptibility with longitudinal data. <i>Genetic Epidemiology</i> , 2017, 41, 620-635.	1.3	3
30	Association between fruit, vegetable, seafood, and dairy intake and a reduction in the prevalence of type 2 diabetes in Qingdao, China. <i>Asia Pacific Journal of Clinical Nutrition</i> , 2017, 26, 255-261.	0.4	3
31	Family-based Bayesian collapsing method for rare-variant association study. <i>BMC Proceedings</i> , 2014, 8, S37.	1.6	2
32	ACEt: An R Package for Estimating Dynamic Heritability and Comparing Twin Models. <i>Behavior Genetics</i> , 2017, 47, 620-641.	2.1	2
33	Inter- and intra-chromosomal modulators of the <i>APOE</i> $\epsilon 2$ and $\epsilon 4$ effects on the Alzheimer's disease risk. <i>GeroScience</i> , 0, , .	4.6	2
34	Bayesian Latent Variable Collapsing Model for Detecting Rare Variant Interaction Effect in Twin Study. <i>Genetic Epidemiology</i> , 2014, 38, 310-324.	1.3	1