Liang He

List of Publications by Year
in descending order

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	Genomeâ€wide analysis identified abundant genetic modulators of contributions of the apolipoprotein E alleles to Alzheimer's disease risk. Alzheimer's and Dementia, 2022, , .	0.8	4
2	Allele-specific analysis reveals exon- and cell-type-specific regulatory effects of Alzheimerâ€™s disease-associated genetic variants. Translational Psychiatry, 2022, 12, 163.	4.8	10
3	Exome-wide age-of-onset analysis reveals exonic variants in ERN1 and SPPL2C associated with Alzheimerâ€™s disease. Translational Psychiatry, 2021, 11, 146.	4.8	13
4	APOE4 disrupts intracellular lipid homeostasis in human iPSC-derived glia. Science Translational Medicine, 2021, 13, .	12.4	141
5	NEBULA is a fast negative binomial mixed model for differential or co-expression analysis of large-scale multi-subject single-cell data. Communications Biology, 2021, 4, 629.	4.4	50
6	Protective association of the Îµ2/Îµ3 heterozygote with Alzheimer's disease is strengthened by TOMM40â€“APOE variants in men. Alzheimer's and Dementia, 2021, 17, 1779-1787.	0.8	8
7	Haplotype architecture of the Alzheimer's risk in the APOE region via coâ€skewness. Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2020, 12, e12129.	2.4	13
8	Genetic and regulatory architecture of Alzheimer's disease in the APOE region. Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2020, 12, e12008.	2.4	12
9	Fast Algorithms for Conducting Large-Scale GWAS of Age-at-Onset Traits Using Cox Mixed-Effects Models. Genetics, 2020, 215, 41-58.	2.9	29
10	Single-cell transcriptomic analysis of Alzheimerâ€™s disease. Nature, 2019, 570, 332-337.	27.8	1,528
11	Discovery of high-confidence human protein-coding genes and exons by whole-genome PhyloCSF helps elucidate 118 GWAS loci. Genome Research, 2019, 29, 2073-2087.	5.5	52
12	Causal effects of cardiovascular risk factors on onset of major age-related diseases: A time-to-event Mendelian randomization study. Experimental Gerontology, 2018, 107, 74-86.	2.8	16
13	High-resolution genome-wide functional dissection of transcriptional regulatory regions and nucleotides in human. Nature Communications, 2018, 9, 5380.	12.8	117
14	Apolipoprotein E region molecular signatures of Alzheimer's disease. Aging Cell, 2018, 17, e12779.	6.7	32
15	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
16	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
17	ACEt: An R Package for Estimating Dynamic Heritability and Comparing Twin Models. Behavior Genetics, 2017, 47, 620-641.	2.1	2
18	Neuregulin signaling pathway in smoking behavior. Translational Psychiatry, 2017, 7, e1212-e1212.	4.8	8

#	Article	IF	Citations
19	A genetic stochastic process model for genomeâ€wide joint analysis of biomarker dynamics and disease susceptibility with longitudinal data. Genetic Epidemiology, 2017, 41, 620-635.	1.3	3
20	Association between fruit, vegetable, seafood, and dairy intake and a reduction in the prevalence of type 2 diabetes in Qingdao, China. Asia Pacific Journal of Clinical Nutrition, 2017, 26, 255-261.	0.4	3
21	Pleiotropic Meta-Analyses of Longitudinal Studies Discover Novel Genetic Variants Associated with Age-Related Diseases. Frontiers in Genetics, 2016, 7, 179.	2.3	40
22	Genomeâ€wide timeâ€toâ€event analysis on smoking progression stages in a familyâ€based study. Brain and Behavior, 2016, 6, e00462.	2.2	14
23	Parity and mortality in cases of childhoodâ€onset diabetes mellitus. Diabetes/Metabolism Research and Reviews, 2016, 32, 607-614.	4.0	3
24	Probiotics and respiratory and gastrointestinal tract infections in Finnish military conscripts â€“ a randomised placebo-controlled double-blinded study. Beneficial Microbes, 2016, 7, 463-471.	2.4	13
25	Estimating Modifying Effect of Age on Genetic and Environmental Variance Components in Twin Models. Genetics, 2016, 202, 1313-1328.	2.9	14
26	Pleiotropic Associations of Allelic Variants in a 2q22 Region with Risks of Major Human Diseases and Mortality. PLoS Genetics, 2016, 12, e1006314.	3.5	39
27	Hierarchical Bayesian Model for Rare Variant Association Analysis Integrating Genotype Uncertainty in Human Sequence Data. Genetic Epidemiology, 2015, 39, 89-100.	1.3	9
28	Impact of classical risk factors of type 2 diabetes among Asian Indian, Chinese and Japanese populations. Diabetes and Metabolism, 2015, 41, 401-409.	2.9	19
29	Genome-wide association study on detailed profiles of smoking behavior and nicotine dependence in a twin sample. Molecular Psychiatry, 2014, 19, 615-624.	7.9	64
30	Bayesian Latent Variable Collapsing Model for Detecting Rare Variant Interaction Effect in Twin Study. Genetic Epidemiology, 2014, 38, 310-324.	1.3	1
31	Specific probiotics and virological findings in symptomatic conscripts attending military service in Finland. Journal of Clinical Virology, 2014, 60, 276-281.	3.1	27
32	Family-based Bayesian collapsing method for rare-variant association study. BMC Proceedings, 2014, 8, S37.	1.6	2
33	The Durations of Past Sickness Absences Predict Future Absence Episodes. Journal of Occupational and Environmental Medicine, 2013, 55, 87-92.	1.7	36
34	Inter- and intra-chromosomal modulators of the APOE É›2 and É›4 effects on the Alzheimerâ€™s disease risk. GeroScience, 0, , .	4.6	2