# Qiongshi Lu

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4556688/publications.pdf

Version: 2024-02-01

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|---|---|---|---|
| 68<br>papers | 3,459<br>citations | 257101<br>24<br>h-index | 182168<br>51<br>g-index |
| 116<br>all docs | 116<br>docs citations | 116<br>times ranked | 7170<br>citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | The Socioeconomic Gradient in Epigenetic Ageing Clocks: Evidence from the Multi-Ethnic Study of Atherosclerosis and the Health and Retirement Study. Epigenetics, 2022, 17, 589-611. | 1.3 | 47 |
| 2 | Higher educational attainment is associated with longer telomeres in midlife: Evidence from sibling comparisons in the UK Biobank. SSM - Population Health, 2022, 17, 101018. | 1.3 | 5 |
| 3 | Detecting genetic heterogeneities in response to trauma: The case of 9/11. SSM Mental Health, 2022, 2, 100044. | 0.9 | 0 |
| 4 | Computational Genomics in the Era of Precision Medicine: Applications to Variant Analysis and Gene Therapy. Journal of Personalized Medicine, 2022, 12, 175. | 1.1 | 4 |
| 5 | GWAS on birth year infant mortality rates provides evidence of recent natural selection. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2117312119. | 3.3 | 9 |
| 6 | Principal components from untargeted cerebrospinal fluid metabolomics associated with Alzheimer's disease biomarkers. Neurobiology of Aging, 2022, 117, 12-23. | 1.5 | 7 |
| 7 | Sex differences in the genetic architecture of cognitive resilience to Alzheimerâ€™s disease. Brain, 2022, 145, 2541-2554. | 3.7 | 26 |
| 8 | Genome-Wide Association Studies of Schizophrenia and Bipolar Disorder in a Diverse Cohort of US Veterans. Schizophrenia Bulletin, 2021, 47, 517-529. | 2.3 | 48 |
| 9 | Cerebrospinal fluid metabolomics identifies 19 brain-related phenotype associations. Communications Biology, 2021, 4, 63. | 2.0 | 28 |
| 10 | Comparison of methods for estimating genetic correlation between complex traits using GWAS summary statistics. Briefings in Bioinformatics, 2021, 22, . | 3.2 | 24 |
| 11 | Transcriptome-wide transmission disequilibrium analysis identifies novel risk genes for autism spectrum disorder. PLoS Genetics, 2021, 17, e1009309. | 1.5 | 14 |
| 12 | Metabolites Associated with Early Cognitive Changes Implicated in Alzheimerâ€™s Disease. Journal of Alzheimer's Disease, 2021, 79, 1041-1054. | 1.2 | 4 |
| 13 | The impact of late-career job loss and genetic risk on body mass index: Evidence from variance polygenic scores. Scientific Reports, 2021, 11, 7647. | 1.6 | 11 |
| 14 | The impact of parenting a child with serious mental illness: Accounting for the parentâ€™s genetic vulnerability to mental illness.. Journal of Family Psychology, 2021, 35, 417-422. | 1.0 | 1 |
| 15 | Detecting local genetic correlations with scan statistics. Nature Communications, 2021, 12, 2033. | 5.8 | 23 |
| 16 | Estimating genetic nurture with summary statistics of multigenerational genome-wide association studies. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, . | 3.3 | 31 |
| 17 | The effects of education on cognition in older age: Evidence from genotyped Siblings. Social Science and Medicine, 2021, 280, 114044. | 1.8 | 23 |
| 18 | DIAPH1 Variants in Nonâ€“East Asian Patients With Sporadic Moyamoya Disease. JAMA Neurology, 2021, 78, 993. | 4.5 | 33 |

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|---|---|---|---|
| 19 | PUMAS: fine-tuning polygenic risk scores with GWAS summary statistics. Genome Biology, 2021, 22, 257. | 3.8 | 22 |
| 20 | SUPERGNOVA: local genetic correlation analysis reveals heterogeneous etiologic sharing of complex traits. Genome Biology, 2021, 22, 262. | 3.8 | 56 |
| 21 | CSF metabolites associate with CSF tau and improve prediction of Alzheimer's disease status. Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2021, 13, e12167. | 1.2 | 2 |
| 22 | Integrative modeling of transmitted and de novo variants identifies novel risk genes for congenital heart disease. Quantitative Biology, 2021, 9, 216-227. | 0.3 | 4 |
| 23 | Health policy and genetic endowments: Understanding sources of response to Minimum Legal Drinking Age laws. Health Economics (United Kingdom), 2021, 30, 194-203. | 0.8 | 8 |
| 24 | Whatâ€™s the use?. ELife, 2021, 10, . | 2.8 | 1 |
| 25 | CSF metabolites associated with CSF NeuroToolKit biomarkers. Alzheimer's and Dementia, 2021, 17, . | 0.4 | 1 |
| 26 | Genomeâ€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. | 1.1 | 17 |
| 27 | Multiâ€ethnic analysis shows genetic risk and environmental predictors interact to influence 25(OH)D concentration and optimal vitamin D intake. Genetic Epidemiology, 2020, 44, 208-217. | 0.6 | 1 |
| 28 | Exome sequencing implicates genetic disruption of prenatal neuro-gliogenesis in sporadic congenital hydrocephalus. Nature Medicine, 2020, 26, 1754-1765. | 15.2 | 84 |
| 29 | Mutations disrupting neuritogenesis genes confer risk for cerebral palsy. Nature Genetics, 2020, 52, 1046-1056. | 9.4 | 96 |
| 30 | Exome Sequencing Implicates Impaired GABA Signaling and Neuronal Ion Transport in Trigeminal Neuralgia. IScience, 2020, 23, 101552. | 1.9 | 32 |
| 31 | Genetic variants and functional pathways associated with resilience to Alzheimerâ€™s disease. Brain, 2020, 143, 2561-2575. | 3.7 | 93 |
| 32 | Sex differences in genetic predictors of resilience to Alzheimerâ€™s disease. Alzheimer's and Dementia, 2020, 16, e043259. | 0.4 | 0 |
| 33 | Principal components from untargeted CSF metabolomics associated with tau. Alzheimer's and Dementia, 2020, 16, e046065. | 0.4 | 1 |
| 34 | Leveraging functional annotation to identify genes associated with complex diseases. PLoS Computational Biology, 2020, 16, e1008315. | 1.5 | 16 |
| 35 | Leveraging functional annotation to identify genes associated with complex diseases. , 2020, 16, e1008315. | | 0 |
| 36 | Leveraging functional annotation to identify genes associated with complex diseases. , 2020, 16, e1008315. | | 0 |

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| 37 | Leveraging functional annotation to identify genes associated with complex diseases. , 2020, 16, e1008315. | | 0 |
| 38 | Leveraging functional annotation to identify genes associated with complex diseases. , 2020, 16, e1008315. | | 0 |
| 39 | Leveraging functional annotation to identify genes associated with complex diseases. , 2020, 16, e1008315. | | 0 |
| 40 | Leveraging functional annotation to identify genes associated with complex diseases. , 2020, 16, e1008315. | | 0 |
| 41 | Ancestry-specific polygenic scores and SNP heritability of 25(OH)D in African- and European-ancestry populations. Human Genetics, 2019, 138, 1155-1169. | 1.8 | 6 |
| 42 | Genome-wide association study of post-traumatic stress disorder reexperiencing symptoms in >165,000 US veterans. Nature Neuroscience, 2019, 22, 1394-1401. | 7.1 | 145 |
| 43 | An evaluation of noncoding genome annotation tools through enrichment analysis of 15 genome-wide association studies. Briefings in Bioinformatics, 2019, 20, 995-1003. | 3.2 | 3 |
| 44 | Integrated analysis of genomics, longitudinal metabolomics, and Alzheimer's risk factors among 1,111 cohort participants. Genetic Epidemiology, 2019, 43, 657-674. | 0.6 | 41 |
| 45 | 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. | 0.7 | 82 |
| 46 | Genome-wide association study reveals sex-specific genetic architecture of facial attractiveness. PLoS Genetics, 2019, 15, e1007973. | 1.5 | 5 |
| 47 | A statistical framework for cross-tissue transcriptome-wide association analysis. Nature Genetics, 2019, 51, 568-576. | 9.4 | 262 |
| 48 | Mutations in Chromatin Modifier and Ephrin Signaling Genes in Vein of Galen Malformation. Neuron, 2019, 101, 429-443.e4. | 3.8 | 56 |
| 49 | Validating psychosocial pathways of risk between neuroticism and late life depression using a polygenic score approach.. Journal of Abnormal Psychology, 2019, 128, 200-211. | 2.0 | 13 |
| 50 | O3â€03â€05: INTEGRATIVE NETWORK ANALYSIS IDENTIFIES RELATIONSHIPS BETWEEN METABOLOMICS, GENOMICS, AND RISK FACTORS FOR AD. Alzheimer's and Dementia, 2018, 14, P1016. | 0.4 | 0 |
| 51 | O3â€03â€06: CROSSâ€TISSUE TRANSCRIPTOMEâ€WIDE ASSOCIATION METAâ€ANALYSIS IDENTIFIES NOVEL RISK GENES FOR LATEâ€ONSET ALZHEIMER'S DISEASE. Alzheimer's and Dementia, 2018, 14, P1017. | 0.4 | 0 |
| 52 | 125 De Novo Mutations in Genes Regulating Neural Stem Cell Fate in Human Congenital Hydrocephalus. Neurosurgery, 2018, 65, 88-89. | 0.6 | 0 |
| 53 | De Novo Mutation in Genes Regulating Neural Stem Cell Fate in Human Congenital Hydrocephalus. Neuron, 2018, 99, 302-314.e4. | 3.8 | 112 |
| 54 | Post-GWAS Prioritization Through Data Integration Provides Novel Insights on Chronic Obstructive Pulmonary Disease. Statistics in Biosciences, 2017, 9, 605-621. | 0.6 | 2 |

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|---|---|---|---|
| 55 | Contribution of rare inherited and de novo variants in 2,871 congenital heart disease probands. Nature Genetics, 2017, 49, 1593-1601. | 9.4 | 624 |
| 56 | A Powerful Approach to Estimating Annotation-Stratified Genetic Covariance via GWAS Summary Statistics. American Journal of Human Genetics, 2017, 101, 939-964. | 2.6 | 141 |
| 57 | High frequency of mitochondrial DNA mutations in HIVâ€infected treatmentâ€experienced individuals. HIV Medicine, 2017, 18, 45-55. | 1.0 | 19 |
| 58 | A Genome-Wide Association Study to Identify Single-Nucleotide Polymorphisms for Acute Kidney Injury. American Journal of Respiratory and Critical Care Medicine, 2017, 195, 482-490. | 2.5 | 31 |
| 59 | Leveraging functional annotations in genetic risk prediction for human complex diseases. PLoS Computational Biology, 2017, 13, e1005589. | 1.5 | 134 |
| 60 | Systematic tissue-specific functional annotation of the human genome highlights immune-related DNA elements for late-onset Alzheimerâ€™s disease. PLoS Genetics, 2017, 13, e1006933. | 1.5 | 96 |
| 61 | Joint modeling of genetically correlated diseases and functional annotations increases accuracy of polygenic risk prediction. PLoS Genetics, 2017, 13, e1006836. | 1.5 | 70 |
| 62 | Integrative Tissue-Specific Functional Annotations in the Human Genome Provide Novel Insights on Many Complex Traits and Improve Signal Prioritization in Genome Wide Association Studies. PLoS Genetics, 2016, 12, e1005947. | 1.5 | 94 |
| 63 | GenoWAP: GWAS signal prioritization through integrated analysis of genomic functional annotation. Bioinformatics, 2016, 32, 542-548. | 1.8 | 47 |
| 64 | Two locus inheritance of non-syndromic midline craniosynostosis via rare SMAD6 and common BMP2 alleles. ELife, 2016, 5, . | 2.8 | 168 |
| 65 | A Statistical Framework to Predict Functional Non-Coding Regions in the Human Genome Through Integrated Analysis of Annotation Data. Scientific Reports, 2015, 5, 10576. | 1.6 | 144 |
| 66 | A review of study designs and statistical methods for genomic epidemiology studies using next generation sequencing. Frontiers in Genetics, 2015, 6, 149. | 1.1 | 48 |
| 67 | Computational prediction of associations between long non-coding RNAs and proteins. BMC Genomics, 2013, 14, 651. | 1.2 | 208 |
| 68 | Quantifying concordant genetic effects of de novo mutations on multiple disorders. ELife, 0, 11, . | 2.8 | 3 |