Qiongshi Lu

List of Publications by Year in descending order

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

Version: 2024-02-01

68 papers	3,459 citations	236925 25 h-index	182427 51 g-index
116 all docs	116 docs citations	116 times ranked	7170 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.	2.7	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.	2.7	5
3	Detecting genetic heterogeneities in response to trauma: The case of 9/11. SSM Mental Health, 2022, 2, 100044.	1.8	0
4	Computational Genomics in the Era of Precision Medicine: Applications to Variant Analysis and Gene Therapy. Journal of Personalized Medicine, 2022, 12, 175.	2.5	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.	7.1	9
6	Principal components from untargeted cerebrospinal fluid metabolomics associated with Alzheimer's disease biomarkers. Neurobiology of Aging, 2022, 117, 12-23.	3.1	7
7	Sex differences in the genetic architecture of cognitive resilience to Alzheimerâ€™s disease. Brain, 2022, 145, 2541-2554.	7.6	26
8	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
9	Cerebrospinal fluid metabolomics identifies 19 brain-related phenotype associations. Communications Biology, 2021, 4, 63.	4.4	28
10	Comparison of methods for estimating genetic correlation between complex traits using GWAS summary statistics. Briefings in Bioinformatics, 2021, 22, .	6.5	24
11	Transcriptome-wide transmission disequilibrium analysis identifies novel risk genes for autism spectrum disorder. PLoS Genetics, 2021, 17, e1009309.	3.5	14
12	Metabolites Associated with Early Cognitive Changes Implicated in Alzheimerâ€™s Disease. Journal of Alzheimer's Disease, 2021, 79, 1041-1054.	2.6	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.	3.3	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.	1.3	1
15	Detecting local genetic correlations with scan statistics. Nature Communications, 2021, 12, 2033.	12.8	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, .	7.1	31
17	The effects of education on cognition in older age: Evidence from genotyped Siblings. Social Science and Medicine, 2021, 280, 114044.	3.8	23
18	DIAPH1 Variants in Nonâ€“East Asian Patients With Sporadic Moyamoya Disease. JAMA Neurology, 2021, 78, 993.	9.0	33

#	Article	IF	Citations
19	PUMAS: fine-tuning polygenic risk scores with GWAS summary statistics. Genome Biology, 2021, 22, 257.	8.8	22
20	SUPERGNOVA: local genetic correlation analysis reveals heterogeneous etiologic sharing of complex traits. Genome Biology, 2021, 22, 262.	8.8	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.	2.4	2
22	Integrative modeling of transmitted and de novo variants identifies novel risk genes for congenital heart disease. Quantitative Biology, 2021, 9, 216-227.	0.5	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.	1.7	8
24	Whatâ€™s the use?. ELife, 2021, 10, .	6.0	1
25	CSF metabolites associated with CSF NeuroToolKit biomarkers. Alzheimer's and Dementia, 2021, 17, .	0.8	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.	1.7	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.	1.3	1
28	Exome sequencing implicates genetic disruption of prenatal neuro-gliogenesis in sporadic congenital hydrocephalus. Nature Medicine, 2020, 26, 1754-1765.	30.7	84
29	Mutations disrupting neuritogenesis genes confer risk for cerebral palsy. Nature Genetics, 2020, 52, 1046-1056.	21.4	96
30	Exome Sequencing Implicates Impaired GABA Signaling and Neuronal Ion Transport in Trigeminal Neuralgia. IScience, 2020, 23, 101552.	4.1	32
31	Genetic variants and functional pathways associated with resilience to Alzheimerâ€™s disease. Brain, 2020, 143, 2561-2575.	7.6	93
32	Sex differences in genetic predictors of resilience to Alzheimerâ€™s disease. Alzheimer's and Dementia, 2020, 16, e043259.	0.8	0
33	Principal components from untargeted CSF metabolomics associated with tau. Alzheimer's and Dementia, 2020, 16, e046065.	0.8	1
34	Leveraging functional annotation to identify genes associated with complex diseases. PLoS Computational Biology, 2020, 16, e1008315.	3.2	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

#	Article	IF	Citations
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.	3.8	6
42	Genome-wide association study of post-traumatic stress disorder reexperiencing symptoms in >165,000 US veterans. Nature Neuroscience, 2019, 22, 1394-1401.	14.8	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.	6.5	3
44	Integrated analysis of genomics, longitudinal metabolomics, and Alzheimer's risk factors among 1,111 cohort participants. Genetic Epidemiology, 2019, 43, 657-674.	1.3	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.	1.3	82
46	Genome-wide association study reveals sex-specific genetic architecture of facial attractiveness. PLoS Genetics, 2019, 15, e1007973.	3.5	5
47	A statistical framework for cross-tissue transcriptome-wide association analysis. Nature Genetics, 2019, 51, 568-576.	21.4	262
48	Mutations in Chromatin Modifier and Ephrin Signaling Genes in Vein of Galen Malformation. Neuron, 2019, 101, 429-443.e4.	8.1	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.	1.9	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.	0.8	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.	0.8	0
52	125 De Novo Mutations in Genes Regulating Neural Stem Cell Fate in Human Congenital Hydrocephalus. Neurosurgery, 2018, 65, 88-89.	1.1	0
53	De Novo Mutation in Genes Regulating Neural Stem Cell Fate in Human Congenital Hydrocephalus. Neuron, 2018, 99, 302-314.e4.	8.1	112
54	Post-GWAS Prioritization Through Data Integration Provides Novel Insights on Chronic Obstructive Pulmonary Disease. Statistics in Biosciences, 2017, 9, 605-621.	1.2	2

#	Article	IF	Citations
55	Contribution of rare inherited and de novo variants in 2,871 congenital heart disease probands. Nature Genetics, 2017, 49, 1593-1601.	21.4	624
56	A Powerful Approach to Estimating Annotation-Stratified Genetic Covariance via GWAS Summary Statistics. American Journal of Human Genetics, 2017, 101, 939-964.	6.2	141
57	High frequency of mitochondrial DNA mutations in HIVâ€infected treatmentâ€experienced individuals. HIV Medicine, 2017, 18, 45-55.	2.2	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.	5.6	31
59	Leveraging functional annotations in genetic risk prediction for human complex diseases. PLoS Computational Biology, 2017, 13, e1005589.	3.2	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.	3.5	96
61	Joint modeling of genetically correlated diseases and functional annotations increases accuracy of polygenic risk prediction. PLoS Genetics, 2017, 13, e1006836.	3.5	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.	3.5	94
63	GenoWAP: GWAS signal prioritization through integrated analysis of genomic functional annotation. Bioinformatics, 2016, 32, 542-548.	4.1	47
64	Two locus inheritance of non-syndromic midline craniosynostosis via rare SMAD6 and common BMP2 alleles. ELife, 2016, 5, .	6.0	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.	3.3	144
66	A review of study designs and statistical methods for genomic epidemiology studies using next generation sequencing. Frontiers in Genetics, 2015, 6, 149.	2.3	48
67	Computational prediction of associations between long non-coding RNAs and proteins. BMC Genomics, 2013, 14, 651.	2.8	208
68	Quantifying concordant genetic effects of de novo mutations on multiple disorders. ELife, 0, 11, .	6.0	3