Hui-Qi Qu

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/2068182/publications.pdf

Version: 2024-02-01

104 papers	3,976 citations	172386 29 h-index	133188 59 g-index
121 all docs	121 docs citations	121 times ranked	8832 citing authors

#	Article	IF	Citations
1	A genome-wide association meta-analysis identifies new eosinophilic esophagitis loci. Journal of Allergy and Clinical Immunology, 2022, 149, 988-998.	1.5	19
2	Application of deep learning algorithm on whole genome sequencing data uncovers structural variants associated with multiple mental disorders in African American patients. Molecular Psychiatry, 2022, 27, 1469-1478.	4.1	13
3	Identification of Mitochondrial DNA Variants Associated With Risk of Neuroblastoma. Journal of the National Cancer Institute, 2022, 114, 910-913.	3.0	4
4	Circulating LIGHT (TNFSF14) and Interleukin-18 Levels in Sepsis-Induced Multi-Organ Injuries. Biomedicines, 2022, 10, 264.	1.4	7
5	Mendelian randomization study of obesity and type 2 diabetes in hospitalized COVID-19 patients. Metabolism: Clinical and Experimental, 2022, 129, 155156.	1.5	17
6	Improved genetic risk scoring algorithm for type 1 diabetes prediction. Pediatric Diabetes, 2022, 23, 320-323.	1.2	11
7	Genetic analysis for type 1 diabetes genes in juvenile dermatomyositis unveils genetic disease overlap. Rheumatology, 2022, , .	0.9	2
8	Expansion of Schizophrenia Gene Network Knowledge Using Machine Learning Selected Signals From Dorsolateral Prefrontal Cortex and Amygdala RNA-seq Data. Frontiers in Psychiatry, 2022, 13, 797329.	1.3	9
9	Identification of Novel Loci Shared by Juvenile Idiopathic Arthritis Subtypes Through Integrative Genetic Analysis. Arthritis and Rheumatology, 2022, 74, 1420-1429.	2.9	4
10	Burden of rare coding variants reveals genetic heterogeneity between obese and non-obese asthma patients in the African American population. Respiratory Research, 2022, 23, 116.	1.4	1
11	Mutation burden analysis of six common mental disorders in African Americans by whole genome sequencing. Human Molecular Genetics, 2022, 31, 3769-3776.	1.4	4
12	Association of DLL1 with type 1 diabetes in patients characterized by low polygenic risk score. Metabolism: Clinical and Experimental, 2021, 114, 154418.	1.5	6
13	<i>FLNC</i> and <i>MYLK2</i> Gene Mutations in a Chinese Family with Different Phenotypes of Cardiomyopathy. International Heart Journal, 2021, 62, 127-134.	0.5	6
14	Association of novel rare coding variants with juvenile idiopathic arthritis. Annals of the Rheumatic Diseases, 2021, 80, 626-631.	0.5	6
15	Prevalence of overweight/obesity and associated factors among adults in Wolaita Sodo Town, Southern Ethiopia. Cogent Medicine, 2021, 8, 1965709.	0.7	0
16	Rare Recurrent Variants in Noncoding Regions Impact Attention-Deficit Hyperactivity Disorder (ADHD) Gene Networks in Children of both African American and European American Ancestry. Genes, 2021, 12, 310.	1.0	10
17	Machine Learning Reduced Gene/Non-Coding RNA Features That Classify Schizophrenia Patients Accurately and Highlight Insightful Gene Clusters. International Journal of Molecular Sciences, 2021, 22, 3364.	1.8	4
18	New insights into hallux valgus by whole exome sequencing study. Experimental Biology and Medicine, 2021, 246, 1607-1616.	1.1	2

#	Article	IF	Citations
19	Serum levels of the IgA isotype switch factor TGFâ€Î²1 are elevated in patients with COVIDâ€19. FEBS Letters, 2021, 595, 1819-1824.	1.3	16
20	Metabolomic profiling of anaerobic and aerobic energy metabolic pathways in chronic obstructive pulmonary disease. Experimental Biology and Medicine, 2021, 246, 1586-1596.	1.1	5
21	Genetic correlations between COVID-19 and a variety of traits and diseases. Innovation(China), 2021, 2, 100112.	5.2	7
22	Combined application of genetic and polygenic risk scores for type 1 diabetes risk prediction. Diabetes, Obesity and Metabolism, 2021, 23, 2001-2003.	2.2	2
23	Deep learning prediction of attention-deficit hyperactivity disorder in African Americans by copy number variation. Experimental Biology and Medicine, 2021, 246, 2317-2323.	1.1	8
24	Abstract 2310: Identification of novel essential genes for prostate cancer metastasis by genome scale CRISPR approaches. , 2021, , .		0
25	Genetic architecture of type 1 diabetes with low genetic risk score informed by 41 unreported loci. Communications Biology, 2021, 4, 908.	2.0	9
26	Insights into non-autoimmune type 1 diabetes with 13 novel loci in low polygenic risk score patients. Scientific Reports, 2021, 11, 16013.	1.6	7
27	Heparin-binding protein levels correlate with aggravation and multiorgan damage in severe COVID-19. ERJ Open Research, 2021, 7, 00741-2020.	1.1	11
28	The Multi-Omics Architecture of Juvenile Idiopathic Arthritis. Cells, 2020, 9, 2301.	1.8	18
29	Expression Pattern of the SARS-CoV-2 Entry Genes ACE2 and TMPRSS2 in the Respiratory Tract. Viruses, 2020, 12, 1174.	1.5	27
30	High prevalence of elevated serum liver enzymes in Chinese children suggests metabolic syndrome as a common risk factor. Journal of Paediatrics and Child Health, 2020, 56, 1590-1596.	0.4	1
31	Non-coding structural variation differentially impacts attention-deficit hyperactivity disorder (ADHD) gene networks in African American vs Caucasian children. Scientific Reports, 2020, 10, 15252.	1.6	5
32	Mitochondrial DNA haplogroups and risk of attention deficit and hyperactivity disorder in European Americans. Translational Psychiatry, 2020, 10, 370.	2.4	11
33	COVID-19: Look to the Future, Learn from the Past. Viruses, 2020, 12, 1226.	1.5	8
34	Distinct features of SARS-CoV-2-specific IgA response in COVID-19 patients. European Respiratory Journal, 2020, 56, 2001526.	3.1	292
35	Liraglutide Ameliorates Lipotoxicity-Induced Oxidative Stress by Activating the NRF2 Pathway in HepG2 Cells. Hormone and Metabolic Research, 2020, 52, 532-539.	0.7	14
36	Mitochondrial DNA Haplogroups and Susceptibility to Neuroblastoma. Journal of the National Cancer Institute, 2020, 112, 1259-1266.	3.0	10

#	Article	IF	Citations
37	Role of the ADCY9 gene in cardiac abnormalities of the Rubinstein-Taybi syndrome. Orphanet Journal of Rare Diseases, 2020, 15, 101.	1.2	2
38	Rare Genetic Variants of Large Effect Influence Risk of Type 1 Diabetes. Diabetes, 2020, 69, 784-795.	0.3	69
39	The Infection Rate of COVID-19 in Wuhan, China: Combined Analysis of Population Samples. Journal of Medical Internet Research, 2020, 22, e20914.	2.1	2
40	Interpretation of Maturity-Onset Diabetes of the Young Genetic Variants Based on American College of Medical Genetics and Genomics Criteria: Machine-Learning Model Development. JMIR Biomedical Engineering, 2020, 5, e20506.	0.7	2
41	Application of ACMG criteria to classify variants in the human gene mutation database. Journal of Human Genetics, 2019, 64, 1091-1095.	1.1	10
42	Association of Rare Recurrent Copy Number Variants With Congenital Heart Defects Based on Next-Generation Sequencing Data From Family Trios. Frontiers in Genetics, 2019, 10, 819.	1.1	15
43	Microduplications at the 15q11.2 BP1â€"BP2 locus are enriched in patients with anorexia nervosa. Journal of Psychiatric Research, 2019, 113, 34-38.	1.5	7
44	Effect of hypercortisolism on bone mineral density and bone metabolism: A potential protective effect of adrenocorticotropic hormone in patients with Cushingâ€™s disease. Journal of International Medical Research, 2018, 46, 492-503.	0.4	21
45	Nonfunctional pancreatic endocrine tumor in the peripancreatic region in a Chinese patient with multiple endocrine neoplasia type 1. Journal of International Medical Research, 2018, 46, 908-915.	0.4	2
46	Active form of vitamin D ameliorates non-alcoholic fatty liver disease by alleviating oxidative stress in a high-fat diet rat model. Endocrine Journal, 2017, 64, 663-673.	0.7	43
47	A novel AVPR2 gene mutation of X-linked congenital nephrogenic diabetes insipidus in an Asian pedigree. Journal of International Medical Research, 2016, 44, 1131-1137.	0.4	3
48	1,25(OH)2D3 downregulates the Toll-like receptor 4-mediated inflammatory pathway and ameliorates liver injury in diabetic rats. Journal of Endocrinological Investigation, 2015, 38, 1083-1091.	1.8	32
49	Clostridium difficile infection in diabetes. Diabetes Research and Clinical Practice, 2014, 105, 285-294.	1.1	24
50	Gene-Specific Function Prediction for Non-Synonymous Mutations in Monogenic Diabetes Genes. PLoS ONE, 2014, 9, e104452.	1.1	23
51	Genome-wide search for exonic variants affecting translational efficiency. Nature Communications, 2013, 4, 2260.	5.8	17
52	A case report of syndrome of inappropriate antidiuretic hormone secretion with Castlemanâ€™s disease and lymphoma. BMC Endocrine Disorders, 2013, 13, 19.	0.9	4
53	Human Coding Synonymous Single Nucleotide Polymorphisms at Ramp Regions of mRNA Translation. PLoS ONE, 2013, 8, e59706.	1.1	8
54	Translational genomic medicine: common metabolic traits and ancestral components of Mexican Americans. Journal of Medical Genetics, 2012, 49, 545-546.	1.5	4

#	Article	IF	Citations
55	Ancestry Informative Marker Set for Han Chinese Population. G3: Genes, Genomes, Genetics, 2012, 2, 339-341.	0.8	8
56	Association Between CASP8 and CASP10 Polymorphisms and Toxicity Outcomes With Platinumâ€Based Chemotherapy in Chinese Patients With Nonâ€Small Cell Lung Cancer. Oncologist, 2012, 17, 1551-1561.	1.9	20
57	Ancestral Effect on HOMA-IR Levels Quantitated in an American Population of Mexican Origin. Diabetes Care, 2012, 35, 2591-2593.	4.3	16
58	Host susceptibility to tuberculosis: insights from a longitudinal study of gene expression in diabetes [Short communication]. International Journal of Tuberculosis and Lung Disease, 2012, 16, 370-372.	0.6	18
59	Population-based Risk Factors for Elevated Alanine Aminotransferase in a South Texas Mexicanâ€"American Population. Archives of Medical Research, 2012, 43, 482-488.	1.5	13
60	Screening for novel lead compounds increasing insulin expression in medullary thymic epithelial cells. European Journal of Pharmacology, 2012, 688, 84-89.	1.7	10
61	PNPLA3 Polymorphisms and Liver Aminotransferase Levels in a Mexican American Population. Clinical and Investigative Medicine, 2012, 35, 237.	0.3	33
62	Decreased expression of ATP6V1H in type 2 diabetes: A pilot report on the diabetes risk study in Mexican Americans. Biochemical and Biophysical Research Communications, 2011, 412, 728-731.	1.0	20
63	What did we learn from the genome-wide association study for tuberculosis susceptibility?. Journal of Medical Genetics, 2011, 48, 217-218.	1.5	6
64	Molecular immunity to mycobacteria: knowledge from the mutation and phenotype spectrum analysis of Mendelian susceptibility to mycobacterial diseases. International Journal of Infectious Diseases, 2011, 15, e305-e313.	1.5	33
65	The Definition of Insulin Resistance Using HOMA-IR for Americans of Mexican Descent Using Machine Learning. PLoS ONE, 2011, 6, e21041.	1.1	149
66	Prevalence of Metabolic Syndrome and Risks of Abnormal Serum Alanine Aminotransferase in Hispanics: A Population-Based Study. PLoS ONE, 2011, 6, e21515.	1.1	42
67	Association Study of Candidate Gene Polymorphisms and Obesity in a Young Mexican-American Population from South Texas. Archives of Medical Research, 2011, 42, 523-531.	1.5	24
68	Knowledge gaining by human genetic studies on tuberculosis susceptibility. Journal of Human Genetics, 2011, 56, 177-182.	1.1	33
69	A Genome-Wide Meta-Analysis of Six Type 1 Diabetes Cohorts Identifies Multiple Associated Loci. PLoS Genetics, 2011, 7, e1002293.	1.5	297
70	Adiponectin/leptin ratio and Metabolic Syndrome in a Mexican American population. Clinical and Investigative Medicine, 2011, 34, 290.	0.3	49
71	Rfx6 directs islet formation and insulin production in mice and humans. Nature, 2010, 463, 775-780.	13.7	300
72	In silico replication of the genome-wide association results of the Type 1 Diabetes Genetics Consortium. Human Molecular Genetics, 2010, 19, 2534-2538.	1.4	16

#	Article	IF	Citations
73	Comparative genetic analysis of inflammatory bowel disease and type 1 diabetes implicates multiple loci with opposite effects. Human Molecular Genetics, 2010, 19, 2059-2067.	1.4	157
74	Genome-wide profiling using single-nucleotide polymorphism arrays identifies novel chromosomal imbalances in pediatric glioblastomas. Neuro-Oncology, 2010, 12, 153-163.	0.6	72
75	Statistical significance in genetic association studies. Clinical and Investigative Medicine, 2010, 33, 266.	0.3	30
76	Follow-Up Analysis of Genome-Wide Association Data Identifies Novel Loci for Type 1 Diabetes. Diabetes, 2009, 58, 290-295.	0.3	136
77	Association of RASGRP1 with type 1 diabetes is revealed by combined follow-up of two genome-wide studies. Journal of Medical Genetics, 2009, 46, 553-554.	1.5	36
78	A cis-Acting Regulatory Variant in the IL2RA Locus. Journal of Immunology, 2009, 183, 5158-5162.	0.4	20
79	From Disease Association to Risk Assessment: An Optimistic View from Genome-Wide Association Studies on Type 1 Diabetes. PLoS Genetics, 2009, 5, e1000678.	1.5	186
80	Identification of susceptibility genes for complex diseases using pooling-based genome-wide association scans. Human Genetics, 2009, 125, 305-318.	1.8	74
81	Remapping the type I diabetes association of the CTLA4 locus. Genes and Immunity, 2009, 10, S27-S32.	2.2	40
82	The type I diabetes association of the IL2RA locus. Genes and Immunity, 2009, 10, S42-S48.	2.2	31
83	Reassessment of the type I diabetes association of the OAS1 locus. Genes and Immunity, 2009, 10, S69-S73.	2.2	19
84	The effect of the MHC locus on autoantibodies in type 1 diabetes. Journal of Medical Genetics, 2009, 46, 469-471.	1.5	23
85	The Genetic Basis of Diabetes. , 2009, , 377-413.		1
86	The association between the IFIH1 locus and type 1 diabetes. Diabetologia, 2008, 51, 473-475.	2.9	33
87	The association between type 1 diabetes and the ITPR3 gene polymorphism due to linkage disequilibrium with HLA class II. Genes and Immunity, 2008, 9, 264-266.	2.2	15
88	Association Analysis of Type 2 Diabetes Loci in Type 1 Diabetes. Diabetes, 2008, 57, 1983-1986.	0.3	42
89	A Novel Susceptibility Locus for Type 1 Diabetes on Chr12q13 Identified by a Genome-Wide Association Study. Diabetes, 2008, 57, 1143-1146.	0.3	137
90	Genetic Control of Alternative Splicing in the TAP2 Gene: Possible Implication in the Genetics of Type 1 Diabetes. Diabetes, 2007, 56, 270-275.	0.3	27

#	Article	IF	Citations
91	A Common Variant of the PAX2 Gene Is Associated with Reduced Newborn Kidney Size. Journal of the American Society of Nephrology: JASN, 2007, 18, 1915-1921.	3.0	96
92	Toward Further Mapping of the Association Between the IL2RA Locus and Type 1 Diabetes. Diabetes, 2007, 56, 1174-1176.	0.3	82
93	The IRF5 polymorphism in type 1 diabetes. Journal of Medical Genetics, 2007, 44, 670-672.	1.5	10
94	No association of type 1 diabetes with a functional polymorphism of the LRAP gene. Molecular Immunology, 2007, 44, 2135-2138.	1.0	3
95	The TCF7L2locus and type 1 diabetes. BMC Medical Genetics, 2007, 8, 51.	2.1	18
96	A genome-wide association study identifies KIAA0350 as a type 1 diabetes gene. Nature, 2007, 448, 591-594.	13.7	497
97	Lack of association of type 1 diabetes with the IL4R gene. Diabetologia, 2006, 49, 958-961.	2.9	4
98	Strand bias in complementary single-nucleotide polymorphisms of transcribed human sequences: evidence for functional effects of synonymous polymorphisms. BMC Genomics, 2006, 7, 213.	1.2	27
99	Assessing the validity of the association between the SUMO4 M55V variant and risk of type 1 diabetes. Nature Genetics, 2005, 37, 111-112.	9.4	47
100	Type 1 diabetes and the OAS gene cluster: association with splicing polymorphism or haplotype?. Journal of Medical Genetics, 2005, 43, 129-132.	1.5	47
101	Confirmation of the association of the R620W polymorphism in the protein tyrosine phosphatase PTPN22 with type 1 diabetes in a family based study. Journal of Medical Genetics, 2005, 42, 266-270.	1.5	58
102	Allele A in Intron 4 of ecNOS Gene Will Not Increase the Risk of Diabetic Nephropathy in Type 2 Diabetes of Chinese Population. Nephron, 2002, 91, 768-768.	0.9	19
103	Restless Legs Syndrome (RLS) in Uremic Patients Is Related to the Frequency of Hemodialysis Sessions. Nephron, 2000, 86, 540-540.	0.9	30
104	Microduplications at the 15q11.2 BP1-BP2 Locus are Enriched in Patients with Anorexia Nervosa. SSRN Electronic Journal, 0, , .	0.4	0