

Ke Hao

List of Publications by Year in descending order

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Version: 2024-02-01

132
papers

8,921
citations

71102

41
h-index

53230

85
g-index

142
all docs

142
docs citations

142
times ranked

18912
citing authors

#	ARTICLE	IF	CITATIONS
1	Mapping the Genetic Architecture of Gene Expression in Human Liver. <i>PLoS Biology</i> , 2008, 6, e107.	5.6	872
2	Opportunities and challenges for transcriptome-wide association studies. <i>Nature Genetics</i> , 2019, 51, 592-599.	21.4	592
3	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. <i>Nature Genetics</i> , 2019, 51, 804-814.	21.4	402
4	Particulate Matter Exposure and Stress Hormone Levels. <i>Circulation</i> , 2017, 136, 618-627.	1.6	364
5	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. <i>Nature Genetics</i> , 2019, 51, 481-493.	21.4	350
6	Novel insights into the genetics of smoking behaviour, lung function, and chronic obstructive pulmonary disease (UK BiLEVE): a genetic association study in UK Biobank. <i>Lancet Respiratory Medicine</i> , 2015, 3, 769-781.	10.7	346
7	A common haplotype lowers PU.1 expression in myeloid cells and delays onset of Alzheimer's disease. <i>Nature Neuroscience</i> , 2017, 20, 1052-1061.	14.8	330
8	Impact of Type 2 Diabetes Susceptibility Variants on Quantitative Glycemic Traits Reveals Mechanistic Heterogeneity. <i>Diabetes</i> , 2014, 63, 2158-2171.	0.6	297
9	Lung eQTLs to Help Reveal the Molecular Underpinnings of Asthma. <i>PLoS Genetics</i> , 2012, 8, e1003029.	3.5	261
10	Genome-wide association analyses for lung function and chronic obstructive pulmonary disease identify new loci and potential druggable targets. <i>Nature Genetics</i> , 2017, 49, 416-425.	21.4	257
11	Cardiometabolic risk loci share downstream cis- and trans-gene regulation across tissues and diseases. <i>Science</i> , 2016, 353, 827-830.	12.6	241
12	Massive parallel sequencing uncovers actionable FGFR2-PPHLN1 fusion and ARAF mutations in intrahepatic cholangiocarcinoma. <i>Nature Communications</i> , 2015, 6, 6087.	12.8	240
13	Meta-analysis of 65,734 Individuals Identifies TSPAN15 and SLC44A2 as Two Susceptibility Loci for Venous Thromboembolism. <i>American Journal of Human Genetics</i> , 2015, 96, 532-542.	6.2	222
14	A functional genomics predictive network model identifies regulators of inflammatory bowel disease. <i>Nature Genetics</i> , 2017, 49, 1437-1449.	21.4	199
15	Genome-wide association study identifies peanut allergy-specific loci and evidence of epigenetic mediation in US children. <i>Nature Communications</i> , 2015, 6, 6304.	12.8	192
16	Identification of <i>TMPRSS2</i> as a Susceptibility Gene for Severe 2009 Pandemic A(H1N1) Influenza and A(H7N9) Influenza. <i>Journal of Infectious Diseases</i> , 2015, 212, 1214-1221.	4.0	170
17	Trunk mutational events present minimal intra- and inter-tumoral heterogeneity in hepatocellular carcinoma. <i>Journal of Hepatology</i> , 2017, 67, 1222-1231.	3.7	121
18	Mixed hepatocellular cholangiocarcinoma tumors: Cholangiolocellular carcinoma is a distinct molecular entity. <i>Journal of Hepatology</i> , 2017, 66, 952-961.	3.7	120

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19	Gut microbiota density influences host physiology and is shaped by host and microbial factors. <i>ELife</i> , 2019, 8, .	6.0	118
20	Integration of Alzheimer's disease genetics and myeloid genomics identifies disease risk regulatory elements and genes. <i>Nature Communications</i> , 2021, 12, 1610.	12.8	118
21	Unique Genomic Profile of Fibrolamellar Hepatocellular Carcinoma. <i>Gastroenterology</i> , 2015, 148, 806-818.e10.	1.3	109
22	Intestinal Inflammation Modulates the Expression of ACE2 and TMPRSS2 and Potentially Overlaps With the Pathogenesis of SARS-CoV-2-related Disease. <i>Gastroenterology</i> , 2021, 160, 287-301.e20.	1.3	98
23	A large lung gene expression study identifying fibulin-5 as a novel player in tissue repair in COPD. <i>Thorax</i> , 2015, 70, 21-32.	5.6	89
24	Prioritization of candidate causal genes for asthma in susceptibility loci derived from UK Biobank. <i>Communications Biology</i> , 2021, 4, 700.	4.4	77
25	Development and clinical application of an integrative genomic approach to personalized cancer therapy. <i>Genome Medicine</i> , 2016, 8, 62.	8.2	71
26	Radiogenomics Consortium Genome-Wide Association Study Meta-Analysis of Late Toxicity After Prostate Cancer Radiotherapy. <i>Journal of the National Cancer Institute</i> , 2020, 112, 179-190.	6.3	71
27	Genetic variants near MLST8 and DHX57 affect the epigenetic age of the cerebellum. <i>Nature Communications</i> , 2016, 7, 10561.	12.8	69
28	Cadmium-Associated Differential Methylation throughout the Placental Genome: Epigenome-Wide Association Study of Two U.S. Birth Cohorts. <i>Environmental Health Perspectives</i> , 2018, 126, 017010.	6.0	69
29	Molecular mechanisms underlying variations in lung function: a systems genetics analysis. <i>Lancet Respiratory Medicine</i> , 2015, 3, 782-795.	10.7	66
30	Shared genetic etiology underlying Alzheimer's disease and type 2 diabetes. <i>Molecular Aspects of Medicine</i> , 2015, 43-44, 66-76.	6.4	63
31	The gut microbiota composition affects dietary polyphenols-mediated cognitive resilience in mice by modulating the bioavailability of phenolic acids. <i>Scientific Reports</i> , 2019, 9, 3546.	3.3	61
32	Age-Stratified Risk of Unexpected Uterine Sarcoma Following Surgery for Presumed Benign Leiomyoma. <i>Oncologist</i> , 2015, 20, 433-439.	3.7	59
33	Expression quantitative trait loci (eQTLs) in human placentas suggest developmental origins of complex diseases. <i>Human Molecular Genetics</i> , 2017, 26, 3432-3441.	2.9	58
34	Integrative metabolomics-genomics approach reveals key metabolic pathways and regulators of Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2022, 18, 1260-1278.	0.8	57
35	Air pollution and chronic obstructive pulmonary disease. <i>Chronic Diseases and Translational Medicine</i> , 2020, 6, 260-269.	1.2	56
36	Prenatal exposure to benzophenones, parabens and triclosan and neurocognitive development at 2 years. <i>Environment International</i> , 2019, 126, 413-421.	10.0	55

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37	Whole-transcriptome analysis delineates the human placenta gene network and its associations with fetal growth. <i>BMC Genomics</i> , 2017, 18, 520.	2.8	53
38	Heterogeneity in gut microbiota drive polyphenol metabolism that influences α -synuclein misfolding and toxicity. <i>Journal of Nutritional Biochemistry</i> , 2019, 64, 170-181.	4.2	52
39	Epigenome-wide association study links site-specific DNA methylation changes with cow's milk allergy. <i>Journal of Allergy and Clinical Immunology</i> , 2016, 138, 908-911.e9.	2.9	51
40	A mechanistic framework for cardiometabolic and coronary artery diseases. , 2022, 1, 85-100.		51
41	Common genes underlying asthma and COPD? Genome-wide analysis on the Dutch hypothesis. <i>European Respiratory Journal</i> , 2014, 44, 860-872.	6.7	49
42	Variants in the fetal genome near pro-inflammatory cytokine genes on 2q13 associate with gestational duration. <i>Nature Communications</i> , 2019, 10, 3927.	12.8	49
43	Airway microbiome is associated with respiratory functions and responses to ambient particulate matter exposure. <i>Ecotoxicology and Environmental Safety</i> , 2019, 167, 269-277.	6.0	48
44	Molecularly defined unfolded protein response subclasses have distinct correlations with fatty liver disease in zebrafish. <i>DMM Disease Models and Mechanisms</i> , 2014, 7, 823-835.	2.4	47
45	Intrauterine multi-metal exposure is associated with reduced fetal growth through modulation of the placental gene network. <i>Environment International</i> , 2018, 120, 373-381.	10.0	46
46	Surfactant protein D is a causal risk factor for COPD: results of Mendelian randomisation. <i>European Respiratory Journal</i> , 2017, 50, 1700657.	6.7	45
47	Functional variants regulating LGALS1 (Galectin 1) expression affect human susceptibility to influenza A(H7N9). <i>Scientific Reports</i> , 2015, 5, 8517.	3.3	43
48	Role of the Lung Microbiome in the Pathogenesis of Chronic Obstructive Pulmonary Disease. <i>Chinese Medical Journal</i> , 2017, 130, 2107-2111.	2.3	43
49	Maternal exposure to selenium and cadmium, fetal growth, and placental expression of steroidogenic and apoptotic genes. <i>Environmental Research</i> , 2017, 158, 233-244.	7.5	41
50	Placental DNA methylation signatures of maternal smoking during pregnancy and potential impacts on fetal growth. <i>Nature Communications</i> , 2021, 12, 5095.	12.8	41
51	High-Throughput Characterization of Blood Serum Proteomics of IBD Patients with Respect to Aging and Genetic Factors. <i>PLoS Genetics</i> , 2017, 13, e1006565.	3.5	41
52	Blood and Intestine eQTLs from an Anti-TNF-Resistant Crohn's Disease Cohort Inform IBD Genetic Association Loci. <i>Clinical and Translational Gastroenterology</i> , 2016, 7, e177.	2.5	40
53	SAAS-CNV: A Joint Segmentation Approach on Aggregated and Allele Specific Signals for the Identification of Somatic Copy Number Alterations with Next-Generation Sequencing Data. <i>PLoS Computational Biology</i> , 2015, 11, e1004618.	3.2	40
54	Genome-wide DNA methylation associations with spontaneous preterm birth in US blacks: findings in maternal and cord blood samples. <i>Epigenetics</i> , 2018, 13, 163-172.	2.7	38

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55	Genetic regulation of the placental transcriptome underlies birth weight and risk of childhood obesity. <i>PLoS Genetics</i> , 2018, 14, e1007799.	3.5	38
56	Leveraging lung tissue transcriptome to uncover candidate causal genes in COPD genetic associations. <i>Human Molecular Genetics</i> , 2018, 27, 1819-1829.	2.9	37
57	A Systems Approach Identifies Networks and Genes Linking Sleep and Stress: Implications for Neuropsychiatric Disorders. <i>Cell Reports</i> , 2015, 11, 835-848.	6.4	36
58	Multi-omics highlights ABO plasma protein as a causal risk factor for COVID-19. <i>Human Genetics</i> , 2021, 140, 969-979.	3.8	36
59	An integrative multiomic network model links lipid metabolism to glucose regulation in coronary artery disease. <i>Nature Communications</i> , 2021, 12, 547.	12.8	35
60	Genome-wide interaction study of gene-by-occupational exposure and effects on FEV1 levels. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 136, 1664-1672.e14.	2.9	34
61	Recipient APOL1 risk alleles associate with death-censored renal allograft survival and rejection episodes. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	33
62	Genome-wide approach identifies a novel gene-maternal pre-pregnancy BMI interaction on preterm birth. <i>Nature Communications</i> , 2017, 8, 15608.	12.8	31
63	Collagenous Colitis Is Associated With HLA Signature and Shares Genetic Risks With Other Immune-Mediated Diseases. <i>Gastroenterology</i> , 2020, 159, 549-561.e8.	1.3	31
64	Genetic regulation of gene expression in the lung identifies <i>CST3</i> and <i>CD22</i> as potential causal genes for airflow obstruction. <i>Thorax</i> , 2014, 69, 997-1004.	5.6	30
65	Airway Epithelial Expression Quantitative Trait Loci Reveal Genes Underlying Asthma and Other Airway Diseases. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2016, 54, 177-187.	2.9	28
66	Integrative Genomics of Emphysema-Associated Genes Reveals Potential Disease Biomarkers. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2017, 57, 411-418.	2.9	28
67	Chronic Exposure to PM _{2.5} Nitrate, Sulfate, and Ammonium Causes Respiratory System Impairments in Mice. <i>Environmental Science & Technology</i> , 2021, 55, 3081-3090.	10.0	28
68	Responsiveness to Ipratropium Bromide in Male and Female Patients with Mild to Moderate Chronic Obstructive Pulmonary Disease. <i>EBioMedicine</i> , 2017, 19, 139-145.	6.1	27
69	A plasma proteogenomic signature for fibromuscular dysplasia. <i>Cardiovascular Research</i> , 2020, 116, 63-77.	3.8	27
70	A loss of function variant in <i>CASP7</i> protects against Alzheimer's disease in homozygous APOE ϵ 4 allele carriers. <i>BMC Genomics</i> , 2016, 17, 445.	2.8	26
71	Integrative Analysis of the Inflammatory Bowel Disease Serum Metabolome Improves Our Understanding of Genetic Etiology and Points to Novel Putative Therapeutic Targets. <i>Gastroenterology</i> , 2022, 162, 828-843.e11.	1.3	26
72	Genome-wide non-HLA donor-recipient genetic differences influence renal allograft survival via early allograft fibrosis. <i>Kidney International</i> , 2020, 98, 758-768.	5.2	25

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73	Placental gene networks at the interface between maternal PM2.5 exposure early in gestation and reduced infant birthweight. <i>Environmental Research</i> , 2021, 199, 111342.	7.5	24
74	Polymorphisms Associated with Expression of BPIFA1/BPIFB1 and Lung Disease Severity in Cystic Fibrosis. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2015, 53, 607-614.	2.9	23
75	Role of BAFF in pulmonary autoantibody responses induced by chronic cigarette smoke exposure in mice. <i>Physiological Reports</i> , 2016, 4, e13057.	1.7	23
76	Maternal circadian disruption is associated with variation in placental DNA methylation. <i>PLoS ONE</i> , 2019, 14, e0215745.	2.5	22
77	Transcriptome-wide association study of coronary artery disease identifies novel susceptibility genes. <i>Basic Research in Cardiology</i> , 2022, 117, 6.	5.9	22
78	Identification and Bioinformatic Analysis of Circular RNA Expression in Peripheral Blood Mononuclear Cells from Patients with Chronic Obstructive Pulmonary Disease. <i>International Journal of COPD</i> , 2020, Volume 15, 1391-1401.	2.3	21
79	Global analysis of A-to-I RNA editing reveals association with common disease variants. <i>PeerJ</i> , 2018, 6, e4466.	2.0	21
80	Association of adverse birth outcomes with prenatal uranium exposure: A population-based cohort study. <i>Environment International</i> , 2020, 135, 105391.	10.0	20
81	Prenatal exposure to ambient air multi-pollutants significantly impairs intrauterine fetal development trajectory. <i>Ecotoxicology and Environmental Safety</i> , 2020, 201, 110726.	6.0	20
82	Selenium-associated DNA methylation modifications in placenta and neurobehavioral development of newborns: An epigenome-wide study of two U.S. birth cohorts. <i>Environment International</i> , 2020, 137, 105508.	10.0	19
83	Meta-analysis of exome array data identifies six novel genetic loci for lung function. <i>Wellcome Open Research</i> , 2018, 3, 4.	1.8	19
84	High-Throughput Identification of the Plasma Proteomic Signature of Inflammatory Bowel Disease. <i>Journal of Crohn's and Colitis</i> , 2019, 13, 462-471.	1.3	18
85	Evolution of regulatory signatures in primate cortical neurons at cell-type resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 28422-28432.	7.1	18
86	Placental lncRNA expression associated with placental cadmium concentrations and birth weight. <i>Environmental Epigenetics</i> , 2020, 6, dvaa003.	1.8	17
87	EnsembleCNV: an ensemble machine learning algorithm to identify and genotype copy number variation using SNP array data. <i>Nucleic Acids Research</i> , 2019, 47, e39-e39.	14.5	15
88	In-hospital use of ACE inhibitors/angiotensin receptor blockers associates with COVID-19 outcomes in African American patients. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	15
89	The pharmacogenomics of inhaled corticosteroids and lung function decline in COPD. <i>European Respiratory Journal</i> , 2019, 54, 1900521.	6.7	14
90	Nonsyndromic craniosynostosis: novel coding variants. <i>Pediatric Research</i> , 2019, 85, 463-468.	2.3	14

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91	Sex-specific peripheral and central responses to stress-induced depression and treatment in a mouse model. <i>Journal of Neuroscience Research</i> , 2020, 98, 2541-2553.	2.9	14
92	Molecular Characterization of Limited Ulcerative Colitis Reveals Novel Biology and Predictors of Disease Extension. <i>Gastroenterology</i> , 2021, 161, 1953-1968.e15.	1.3	14
93	Placental MAOA expression mediates prenatal stress effects on temperament in 12-month-olds. <i>Infant and Child Development</i> , 2018, 27, e2094.	1.5	13
94	Placental multi-omics integration identifies candidate functional genes for birthweight. <i>Nature Communications</i> , 2022, 13, 2384.	12.8	13
95	Susceptibility genes for lung diseases in the major histocompatibility complex revealed by lung expression quantitative trait loci analysis. <i>European Respiratory Journal</i> , 2016, 48, 573-576.	6.7	12
96	Placental microRNA expression associates with birthweight through control of adipokines: results from two independent cohorts. <i>Epigenetics</i> , 2021, 16, 770-782.	2.7	12
97	Revealing consensus gene pathways associated with respiratory functions and disrupted by PM2.5 nitrate exposure at bulk tissue and single cell resolution. <i>Environmental Pollution</i> , 2021, 280, 116951.	7.5	12
98	ACE inhibition and cardiometabolic risk factors, lung <i>ACE2</i> and <i>TMPRSS2</i> gene expression, and plasma ACE2 levels: a Mendelian randomization study. <i>Royal Society Open Science</i> , 2020, 7, 200958.	2.4	12
99	GIGSEA: genotype imputed gene set enrichment analysis using GWAS summary level data. <i>Bioinformatics</i> , 2019, 35, 160-163.	4.1	11
100	Copper associates with differential methylation in placentae from two US birth cohorts. <i>Epigenetics</i> , 2020, 15, 215-230.	2.7	11
101	Genetic architecture of cardiometabolic risks in people living with HIV. <i>BMC Medicine</i> , 2020, 18, 288.	5.5	11
102	Integrative Prioritization of Causal Genes for Coronary Artery Disease. <i>Circulation Genomic and Precision Medicine</i> , 2022, 15, CIRCGEN121003365.	3.6	11
103	Precision Medicine Approaches to Vascular Disease. <i>Journal of the American College of Cardiology</i> , 2021, 77, 2531-2550.	2.8	10
104	Seasonally variant gene expression in full-term human placenta. <i>FASEB Journal</i> , 2020, 34, 10431-10442.	0.5	9
105	Multiple independent mechanisms link gene polymorphisms in the region of ZEB2 with risk of coronary artery disease. <i>Atherosclerosis</i> , 2020, 311, 20-29.	0.8	9
106	Gene expression network analysis provides potential targets against SARS-CoV-2. <i>Scientific Reports</i> , 2020, 10, 21863.	3.3	9
107	Genetic Pleiotropy between Nicotine Dependence and Respiratory Outcomes. <i>Scientific Reports</i> , 2017, 7, 16907.	3.3	8
108	Meta-eQTL: a tool set for flexible eQTL meta-analysis. <i>BMC Bioinformatics</i> , 2014, 15, 392.	2.6	7

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109	Potential roles of imprinted genes in the teratogenic effects of alcohol on the placenta, somatic growth, and the developing brain. <i>Experimental Neurology</i> , 2022, 347, 113919.	4.1	7
110	Intestinal Dysbiosis in Young Cystic Fibrosis Rabbits. <i>Journal of Personalized Medicine</i> , 2021, 11, 132.	2.5	6
111	Ambient Air Pollutants and Traffic Factors Were Associated with Blood and Urine Biomarkers and Asthma Risk. <i>Environmental Science & Technology</i> , 2022, 56, 7298-7307.	10.0	6
112	Using SAAS-CNV to Detect and Characterize Somatic Copy Number Alterations in Cancer Genomes from Next Generation Sequencing and SNP Array Data. <i>Methods in Molecular Biology</i> , 2018, 1833, 29-47.	0.9	5
113	Autonomic Nervous System Dysfunctions as a Basis for a Predictive Model of Risk of Neurological Disorders in Subjects with Prior History of Traumatic Brain Injury: Implications in Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2017, 56, 305-315.	2.6	4
114	APOL1 G2 risk allele clarifying nomenclature. <i>Kidney International</i> , 2017, 92, 518-519.	5.2	4
115	A Comprehensive Database and Analysis Framework To Incorporate Multiscale Data Types and Enable Integrated Analysis of Bioactive Polyphenols. <i>Molecular Pharmaceutics</i> , 2018, 15, 840-850.	4.6	4
116	Bio3Air, an integrative system for monitoring individual-level air pollutant exposure with high time and spatial resolution. <i>Ecotoxicology and Environmental Safety</i> , 2019, 169, 756-763.	6.0	3
117	Meta-analysis of sample-level dbGaP data reveals novel shared genetic link between body height and Crohn's disease. <i>Human Genetics</i> , 2021, 140, 865-877.	3.8	3
118	Variants associated with HHIP expression have sex-differential effects on lung function. <i>Wellcome Open Research</i> , 2020, 5, 111.	1.8	3
119	Selenium-associated differentially expressed microRNAs and their targeted mRNAs across the placental genome in two U.S. birth cohorts. <i>Epigenetics</i> , 2022, 17, 1234-1245.	2.7	3
120	Administration of High-Dose Methylprednisolone Worsens Bone Loss after Acute Spinal Cord Injury in Rats. <i>Neurotrauma Reports</i> , 2021, 2, 592-602.	1.4	3
121	Polygenic risk score for alcohol drinking behavior improves prediction of inflammatory bowel disease risk. <i>Human Molecular Genetics</i> , 2021, 30, 514-523.	2.9	2
122	The HDAC9-associated risk locus promotes coronary artery disease by governing TWIST1. <i>PLoS Genetics</i> , 2022, 18, e1010261.	3.5	2
123	Peripheral and cognitive benefits of physical exercise in a mouse model of midlife metabolic syndrome. <i>Scientific Reports</i> , 2022, 12, 3260.	3.3	1
124	F1-02-03: MULTISCALE COMPUTATIONAL APPROACH ILLUMINATING NOVEL COMMON PATHWAYS BETWEEN DIABETES AND AD. , 2014, 10, P126-P126.		0
125	A Dynamic Pooling Approach to Extract Complete Allele Signal Information in Somatic Copy Number Alternations Detection. , 2018, , .		0
126	P4492: GENOME-WIDE INTEGRATION OF ALZHEIMER'S DISEASE GENETICS AND MYELOID CELL GENOMICS IDENTIFIES NOVEL RISK GENES EXPRESSED IN MICROGLIA. <i>Alzheimer's and Dementia</i> , 2019, 15, P1502.	0.8	0

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127	Genetic studies of Alzheimer's disease risk implicate clearance of lipid rich debris in myeloid cells. <i>Alzheimer's and Dementia</i> , 2020, 16, e040601.	0.8	0
128	Integration of Alzheimer's disease genetics and myeloid genomics reveals novel disease risk mechanisms. <i>Alzheimer's and Dementia</i> , 2020, 16, e043897.	0.8	0
129	Abstract 386: Identification of Genetic Regulatory Networks for Insulin Resistance in Multiple Populations of Diverse Ethnicities. <i>Circulation Research</i> , 2017, 121, .	4.5	0
130	Integrated analysis of mRNA and long noncoding RNA profiles in peripheral blood mononuclear cells of patients with bronchial asthma. <i>BMC Pulmonary Medicine</i> , 2022, 22, 174.	2.0	0
131	Maternal Pre-pregnancy BMI Associates With Sex-Specific Placental microRNA Patterns. <i>Current Developments in Nutrition</i> , 2022, 6, 671.	0.3	0
132	Variation in placental microRNA expression associates with maternal family history of cardiovascular disease. <i>Journal of Developmental Origins of Health and Disease</i> , 2023, 14, 132-139.	1.4	0