

# 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	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
2	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
3	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
4	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
5	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
6	A mechanistic framework for cardiometabolic and coronary artery diseases. , 2022, 1, 85-100.		51
7	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
8	Transcriptome-wide association study of coronary artery disease identifies novel susceptibility genes. <i>Basic Research in Cardiology</i> , 2022, 117, 6.	5.9	22
9	Integrative Prioritization of Causal Genes for Coronary Artery Disease. <i>Circulation Genomic and Precision Medicine</i> , 2022, 15, CIRCGEN121003365.	3.6	11
10	Ambient Air Pollutants and Traffic Factors Were Associated with Blood and Urine Biomarkers and Asthma Risk. <i>Environmental Science &amp; Technology</i> , 2022, 56, 7298-7307.	10.0	6
11	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
12	Placental multi-omics integration identifies candidate functional genes for birthweight. <i>Nature Communications</i> , 2022, 13, 2384.	12.8	13
13	Maternal Pre-pregnancy BMI Associates With Sex-Specific Placental microRNA Patterns. <i>Current Developments in Nutrition</i> , 2022, 6, 671.	0.3	0
14	The HDAC9-associated risk locus promotes coronary artery disease by governing TWIST1. <i>PLoS Genetics</i> , 2022, 18, e1010261.	3.5	2
15	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
16	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
17	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
18	Meta-analysis of sample-level dbGaP data reveals novel shared genetic link between body height and Crohn&TM's disease. <i>Human Genetics</i> , 2021, 140, 865-877.	3.8	3

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19	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
20	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
21	Intestinal Dysbiosis in Young Cystic Fibrosis Rabbits. <i>Journal of Personalized Medicine</i> , 2021, 11, 132.	2.5	6
22	Chronic Exposure to PM <sub>2.5</sub> Nitrate, Sulfate, and Ammonium Causes Respiratory System Impairments in Mice. <i>Environmental Science &amp; Technology</i> , 2021, 55, 3081-3090.	10.0	28
23	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
24	Precision Medicine Approaches to Vascular Disease. <i>Journal of the American College of Cardiology</i> , 2021, 77, 2531-2550.	2.8	10
25	Prioritization of candidate causal genes for asthma in susceptibility loci derived from UK Biobank. <i>Communications Biology</i> , 2021, 4, 700.	4.4	77
26	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
27	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
28	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
29	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
30	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
31	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
32	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
33	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
34	A plasma proteogenomic signature for fibromuscular dysplasia. <i>Cardiovascular Research</i> , 2020, 116, 63-77.	3.8	27
35	Copper associates with differential methylation in placentae from two US birth cohorts. <i>Epigenetics</i> , 2020, 15, 215-230.	2.7	11
36	Association of adverse birth outcomes with prenatal uranium exposure: A population-based cohort study. <i>Environment International</i> , 2020, 135, 105391.	10.0	20

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37	Air pollution and chronic obstructive pulmonary disease. <i>Chronic Diseases and Translational Medicine</i> , 2020, 6, 260-269.	1.2	56
38	Seasonally variant gene expression in full-term human placenta. <i>FASEB Journal</i> , 2020, 34, 10431-10442.	0.5	9
39	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
40	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
41	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
42	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
43	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
44	Genetic architecture of cardiometabolic risks in people living with HIV. <i>BMC Medicine</i> , 2020, 18, 288.	5.5	11
45	Placental lncRNA expression associated with placental cadmium concentrations and birth weight. <i>Environmental Epigenetics</i> , 2020, 6, dvaa003.	1.8	17
46	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
47	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
48	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
49	Variants associated with HHIP expression have sex-differential effects on lung function. <i>Wellcome Open Research</i> , 2020, 5, 111.	1.8	3
50	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
51	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
52	Gene expression network analysis provides potential targets against SARS-CoV-2. <i>Scientific Reports</i> , 2020, 10, 21863.	3.3	9
53	ACE inhibition and cardiometabolic risk factors, lung ACE2 and TMPRSS2 gene expression, and plasma ACE2 levels: a Mendelian randomization study. <i>Royal Society Open Science</i> , 2020, 7, 200958.	2.4	12
54	GIGSEA: genotype imputed gene set enrichment analysis using GWAS summary level data. <i>Bioinformatics</i> , 2019, 35, 160-163.	4.1	11

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55	Gut microbiota density influences host physiology and is shaped by host and microbial factors. <i>ELife</i> , 2019, 8, .	6.0	118
56	The pharmacogenomics of inhaled corticosteroids and lung function decline in COPD. <i>European Respiratory Journal</i> , 2019, 54, 1900521.	6.7	14
57	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
58	Nonsyndromic craniosynostosis: novel coding variants. <i>Pediatric Research</i> , 2019, 85, 463-468.	2.3	14
59	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
60	Maternal circadian disruption is associated with variation in placental DNA methylation. <i>PLoS ONE</i> , 2019, 14, e0215745.	2.5	22
61	Prenatal exposure to benzophenones, parabens and triclosan and neurocognitive development at 2â€¦years. <i>Environment International</i> , 2019, 126, 413-421.	10.0	55
62	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
63	Opportunities and challenges for transcriptome-wide association studies. <i>Nature Genetics</i> , 2019, 51, 592-599.	21.4	592
64	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
65	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
66	P4â€¦492: 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
67	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
68	Heterogeneity in gut microbiota drive polyphenol metabolism that influences Î±-synuclein misfolding and toxicity. <i>Journal of Nutritional Biochemistry</i> , 2019, 64, 170-181.	4.2	52
69	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
70	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
71	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
72	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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73	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
74	Genetic regulation of the placental transcriptome underlies birth weight and risk of childhood obesity. <i>PLoS Genetics</i> , 2018, 14, e1007799.	3.5	38
75	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
76	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
77	A Dynamic Pooling Approach to Extract Complete Allele Signal Information in Somatic Copy Number Alternations Detection. , 2018, , .		0
78	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
79	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
80	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
81	Global analysis of A-to-I RNA editing reveals association with common disease variants. <i>PeerJ</i> , 2018, 6, e4466.	2.0	21
82	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
83	Mixed hepatocellular cholangiocarcinoma tumors: Cholangiolocellular carcinoma is a distinct molecular entity. <i>Journal of Hepatology</i> , 2017, 66, 952-961.	3.7	120
84	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
85	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
86	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
87	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
88	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
89	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
90	A functional genomics predictive network model identifies regulators of inflammatory bowel disease. <i>Nature Genetics</i> , 2017, 49, 1437-1449.	21.4	199

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91	APOL1 G2 risk alleleâ€™ clarifying nomenclature. <i>Kidney International</i> , 2017, 92, 518-519.	5.2	4
92	Particulate Matter Exposure and Stress Hormone Levels. <i>Circulation</i> , 2017, 136, 618-627.	1.6	364
93	Genetic Pleiotropy between Nicotine Dependence and Respiratory Outcomes. <i>Scientific Reports</i> , 2017, 7, 16907.	3.3	8
94	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
95	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
96	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
97	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
98	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
99	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
100	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
101	Genetic variants near MLST8 and DHX57 affect the epigenetic age of the cerebellum. <i>Nature Communications</i> , 2016, 7, 10561.	12.8	69
102	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
103	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
104	Cardiometabolic risk loci share downstream cis- and trans-gene regulation across tissues and diseases. <i>Science</i> , 2016, 353, 827-830.	12.6	241
105	Role of <sc>BAFF</sc> in pulmonary autoantibody responses induced by chronic cigarette smoke exposure in mice. <i>Physiological Reports</i> , 2016, 4, e13057.	1.7	23
106	A loss of function variant in CASP7 protects against Alzheimerâ€™s disease in homozygous APOE Î¼4 allele carriers. <i>BMC Genomics</i> , 2016, 17, 445.	2.8	26
107	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
108	Development and clinical application of an integrative genomic approach to personalized cancer therapy. <i>Genome Medicine</i> , 2016, 8, 62.	8.2	71

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109	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
110	Age-Stratified Risk of Unexpected Uterine Sarcoma Following Surgery for Presumed Benign Leiomyoma. <i>Oncologist</i> , 2015, 20, 433-439.	3.7	59
111	Massive parallel sequencing uncovers actionable FGFR2-PPHLN1 fusion and ARAF mutations in intrahepatic cholangiocarcinoma. <i>Nature Communications</i> , 2015, 6, 6087.	12.8	240
112	Unique Genomic Profile of Fibrolamellar Hepatocellular Carcinoma. <i>Gastroenterology</i> , 2015, 148, 806-818.e10.	1.3	109
113	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
114	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
115	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
116	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
117	Functional variants regulating LGALS1 (Galectin 1) expression affect human susceptibility to influenza A(H7N9). <i>Scientific Reports</i> , 2015, 5, 8517.	3.3	43
118	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
119	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
120	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
121	Molecular mechanisms underlying variations in lung function: a systems genetics analysis. <i>Lancet Respiratory Medicine</i> , 2015, 3, 782-795.	10.7	66
122	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
123	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
124	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
125	Impact of Type 2 Diabetes Susceptibility Variants on Quantitative Glycemic Traits Reveals Mechanistic Heterogeneity. <i>Diabetes</i> , 2014, 63, 2158-2171.	0.6	297
126	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



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127	Meta-eQTL: a tool set for flexible eQTL meta-analysis. BMC Bioinformatics, 2014, 15, 392.	2.6	7
128	Genetic regulation of gene expression in the lung identifies <i>CST3</i> and <i>CD22</i> as potential causal genes for airflow obstruction. Thorax, 2014, 69, 997-1004.	5.6	30
129	Common genes underlying asthma and COPD? Genome-wide analysis on the Dutch hypothesis. European Respiratory Journal, 2014, 44, 860-872.	6.7	49
130	F1-02-03: MULTISCALE COMPUTATIONAL APPROACH ILLUMINATING NOVEL COMMON PATHWAYS BETWEEN DIABETES AND AD. , 2014, 10, P126-P126.		0
131	Lung eQTLs to Help Reveal the Molecular Underpinnings of Asthma. PLoS Genetics, 2012, 8, e1003029.	3.5	261
132	Mapping the Genetic Architecture of Gene Expression in Human Liver. PLoS Biology, 2008, 6, e107.	5.6	872