

Hong Ji

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

3,715
citations

411340

20
h-index

340414

39
g-index

45
all docs

45
docs citations

45
times ranked

7967
citing authors

#	ARTICLE	IF	CITATIONS
1	Long-term effects of wildfire smoke exposure during early life on the nasal epigenome in rhesus macaques. <i>Environment International</i> , 2022, 158, 106993.	4.8	9
2	Association Between Maternal Adverse Childhood Experiences and Neonatal SCG5 DNA Methylation—Effect Modification by Prenatal Home Visiting. <i>American Journal of Epidemiology</i> , 2022, 191, 636-645.	1.6	11
3	Single-Cell RNA-Seq Analysis Reveals Lung Epithelial Cell Type-Specific Responses to HDM and Regulation by Tet1. <i>Genes</i> , 2022, 13, 880.	1.0	6
4	Nasal DNA methylation differentiates severe from non-severe asthma in African-American children. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2021, 76, 1836-1845.	2.7	19
5	Methylation quantitative trait locus analysis of chronic postsurgical pain uncovers epigenetic mediators of genetic risk. <i>Epigenomics</i> , 2021, 13, 613-630.	1.0	5
6	Exploring the evidence for epigenetic regulation of environmental influences on child health across generations. <i>Communications Biology</i> , 2021, 4, 769.	2.0	65
7	Pregnancy and Infant Development (PRIDE)—a preliminary observational study of maternal adversity and infant development. <i>BMC Pediatrics</i> , 2021, 21, 452.	0.7	5
8	Induced sputum metabolomic profiles and oxidative stress are associated with chronic obstructive pulmonary disease (COPD) severity: potential use for predictive, preventive, and personalized medicine. <i>EPMA Journal</i> , 2020, 11, 645-659.	3.3	27
9	Associations Between Maternal Community Deprivation and Infant DNA Methylation of the SLC6A4 Gene. <i>Frontiers in Public Health</i> , 2020, 8, 557195.	1.3	10
10	Disease-associated KIF3A variants alter gene methylation and expression impacting skin barrier and atopic dermatitis risk. <i>Nature Communications</i> , 2020, 11, 4092.	5.8	24
11	Adoptive transfer of bone marrow-derived dendritic cells (BMDCs) alleviates OVA-induced allergic airway inflammation in asthmatic mice. <i>Scientific Reports</i> , 2020, 10, 13915.	1.6	5
12	The Emerging Role of Ten-Eleven Translocation 1 in Epigenetic Responses to Environmental Exposures. <i>Epigenetics Insights</i> , 2020, 13, 251686572091015.	0.6	15
13	DNA methylation Variation Associated with the Severity of Childhood Asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 145, AB344.	1.5	0
14	TET1 contributes to allergic airway inflammation and regulates interferon and aryl hydrocarbon receptor signaling pathways in bronchial epithelial cells. <i>Scientific Reports</i> , 2019, 9, 7361.	1.6	28
15	Disease-Associated KIF3A Genetic Variants Alter Gene Methylation And Expression Resulting In Skin Barrier Dysfunction And Increased Risk For Atopic Dermatitis. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, AB90.	1.5	1
16	Neonatal NR3C1 Methylation and Social-Emotional Development at 6 and 18 Months of Age. <i>Frontiers in Behavioral Neuroscience</i> , 2019, 13, 14.	1.0	19
17	Enrichment of Genomic Pathways Based on Differential DNA Methylation Associated With Chronic Postsurgical Pain and Anxiety in Children: A Prospective, Pilot Study. <i>Journal of Pain</i> , 2019, 20, 771-785.	0.7	28
18	Nasal DNA methylation is associated with childhood asthma. <i>Epigenomics</i> , 2018, 10, 629-641.	1.0	38

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19	Intergenerational effects of maternal early life adversity on infant DNA methylation of NR3C1. <i>Annals of Epidemiology</i> , 2018, 28, 656.	0.9	1
20	Diesel exhaust and house dust mite allergen lead to common changes in the airway methylome and hydroxymethylome. <i>Environmental Epigenetics</i> , 2018, 4, dvy020.	0.9	37
21	Maternal distress and hair cortisol in pregnancy among women with elevated adverse childhood experiences. <i>Psychoneuroendocrinology</i> , 2018, 95, 145-148.	1.3	42
22	Epigenetics and Epigenomic Studies in Asthma. <i>Translational Bioinformatics</i> , 2018, , 69-101.	0.0	0
23	DNA methylation at the mu-1 opioid receptor gene (<i>OPRM1</i>) promoter predicts preoperative, acute, and chronic postsurgical pain after spine fusion. <i>Pharmacogenomics and Personalized Medicine</i> , 2017, Volume 10, 157-168.	0.4	40
24	Nasal DNA methylation differentiates corticosteroid treatment response in pediatric asthma: A pilot study. <i>PLoS ONE</i> , 2017, 12, e0186150.	1.1	35
25	Air pollution, epigenetics, and asthma. <i>Allergy, Asthma and Clinical Immunology</i> , 2016, 12, 51.	0.9	52
26	Cultivate Primary Nasal Epithelial Cells from Children and Reprogram into Induced Pluripotent Stem Cells. <i>Journal of Visualized Experiments</i> , 2016, , .	0.2	4
27	Ten-eleven translocation 1 (TET1) methylation is associated with childhood asthma and traffic-related air pollution. <i>Journal of Allergy and Clinical Immunology</i> , 2016, 137, 797-805.e5.	1.5	112
28	Evaluating the Role of Cellular Immune Responses in the Emergence of HCV NS3 Resistance Mutations During Protease Inhibitor Therapy. <i>Viral Immunology</i> , 2016, 29, 252-258.	0.6	9
29	HIV-Induced Epigenetic Alterations in Host Cells. <i>Advances in Experimental Medicine and Biology</i> , 2016, 879, 27-38.	0.8	35
30	Pediatric asthma and autism—genomic perspectives. <i>Clinical and Translational Medicine</i> , 2015, 4, 37.	1.7	6
31	Vanin-1 expression and methylation discriminate pediatric asthma corticosteroid treatment response. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 136, 923-931.e3.	1.5	43
32	Dynamic transcriptional and epigenomic reprogramming from pediatric nasal epithelial cells to induced pluripotent stem cells. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 135, 236-244.	1.5	15
33	Tu1046 Evaluation of the Role of the Immune Responses in Determining the Emergence of HCV Ns3 Resistance Mutations During Protease Inhibitor (PI) Therapy. <i>Gastroenterology</i> , 2015, 148, S-1095.	0.6	0
34	DNA methylation dynamics during ex vivo differentiation and maturation of human dendritic cells. <i>Epigenetics and Chromatin</i> , 2014, 7, 21.	1.8	85
35	Epigenetic Modification of FOXP3 in Patients With Chronic HIV Infection. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2014, 65, 19-26.	0.9	17
36	Forkhead box protein 3 (FOXP3) hypermethylation is associated with diesel exhaust exposure and risk for childhood asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2013, 131, 592-594.e3.	1.5	62

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37	Expressions of methyltransferase enzymes correlate with FOXP3 methylation in the colon mucosa of HIV-1 infected patients. <i>Journal of Acquired Immune Deficiency Syndromes</i> (1999), 2013, 62, 69.	0.9	0
38	Genetic and epigenetic influence on the response to environmental particulate matter. <i>Journal of Allergy and Clinical Immunology</i> , 2012, 129, 33-41.	1.5	82
39	Comprehensive methylome map of lineage commitment from haematopoietic progenitors. <i>Nature</i> , 2010, 467, 338-342.	13.7	554
40	The human colon cancer methylome shows similar hypo- and hypermethylation at conserved tissue-specific CpG island shores. <i>Nature Genetics</i> , 2009, 41, 178-186.	9.4	1,977
41	Yeast Est2p Affects Telomere Length by Influencing Association of Rap1p with Telomeric Chromatin. <i>Molecular and Cellular Biology</i> , 2008, 28, 2380-2390.	1.1	15
42	Regulation of Telomere Length by an N-Terminal Region of the Yeast Telomerase Reverse Transcriptase. <i>Molecular and Cellular Biology</i> , 2005, 25, 9103-9114.	1.1	17
43	Coordinated assembly of human translation initiation complexes by the hepatitis C virus internal ribosome entry site RNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 16990-16995.	3.3	160