Lifang Hou

List of Publications by Year
in descending order

248 papers	16,579 citations	28190 55 h-index	20307 116 g-index
256 all docs	256 docs citations	256 times ranked	22231 citing authors

#	Article	IF	Citations
1	Comparison of Beta-value and M-value methods for quantifying methylation levels by microarray analysis. BMC Bioinformatics, 2010, 11, 587.	1.2	1,597
2	An epigenetic biomarker of aging for lifespan and healthspan. Aging, 2018, 10, 573-591.	1.4	1,552
3	DNA methylation GrimAge strongly predicts lifespan and healthspan. Aging, 2019, 11, 303-327.	1.4	1,128
4	DNA methylation-based measures of biological age: meta-analysis predicting time to death. Aging, 2016, 8, 1844-1865.	1.4	786
5	Changes in DNA Methylation Patterns in Subjects Exposed to Low-Dose Benzene. Cancer Research, 2007, 67, 876-880.	0.4	575
6	Epigenetic clock analysis of diet, exercise, education, and lifestyle factors. Aging, 2017, 9, 419-446.	1.4	521
7	Epigenetic clock for skin and blood cells applied to Hutchinson Gilford Progeria Syndrome and ex vivo studies. Aging, 2018, 10, 1758-1775.	1.4	406
8	Environmental chemical exposures and human epigenetics. International Journal of Epidemiology, 2012, 41, 79-105.	0.9	377
9	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	13.7	376
10	Effects of Particulate Matter on Genomic DNA Methylation Content and *iNOS* Promoter Methylation. Environmental Health Perspectives, 2009, 117, 217-222.	2.8	310
11	Construct validation of the dietary inflammatory index among postmenopausal women. Annals of Epidemiology, 2015, 25, 398-405.	0.9	301
12	Maternal Prepregnancy Body Mass Index and Gestational Weight Gain on Pregnancy Outcomes. PLoS ONE, 2013, 8, e82310.	1.1	266
13	DNA methylation-based estimator of telomere length. Aging, 2019, 11, 5895-5923.	1.4	198
14	Predictors of global methylation levels in blood DNA of healthy subjects: a combined analysis. International Journal of Epidemiology, 2012, 41, 126-139.	0.9	187
15	Effects of airborne pollutants on mitochondrial DNA Methylation. Particle and Fibre Toxicology, 2013, 10, 18.	2.8	169
16	Blood Epigenetic Age may Predict Cancer Incidence and Mortality. EBioMedicine, 2016, 5, 68-73.	2.7	162
17	Longitudinally collected CTCs and CTC-clusters and clinical outcomes of metastatic breast cancer. Breast Cancer Research and Treatment, 2017, 161, 83-94.	1.1	156
18	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. American Journal of Human Genetics, 2017, 101, 888-902.	2.6	154

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19	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. Nature Communications, 2018, 9, 387.	5.8	151
20	Blood Leukocyte DNA Methylation Predicts Risk of Future Myocardial Infarction and Coronary Heart Disease. Circulation, 2019, 140, 645-657.	1.6	151
21	Inhalable Metal-Rich Air Particles and Histone H3K4 Dimethylation and H3K9 Acetylation in a Cross-sectional Study of Steel Workers. Environmental Health Perspectives, 2011, 119, 964-969.	2.8	138
22	Body mass index is negatively associated with telomere length: a collaborative cross-sectional meta-analysis of 87 observational studies. American Journal of Clinical Nutrition, 2018, 108, 453-475.	2.2	137
23	Environmental chemicals and microRNAs. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2011, 714, 105-112.	0.4	136
24	Airborne particulate matter and mitochondrial damage: a cross-sectional study. Environmental Health, 2010, 9, 48.	1.7	133
25	Air pollution exposure and telomere length in highly exposed subjects in Beijing, China: A repeated-measure study. Environment International, 2012, 48, 71-77.	4.8	132
26	Genetic determinants of telomere length and risk of common cancers: a Mendelian randomization study. Human Molecular Genetics, 2015, 24, 5356-5366.	1.4	128
27	Effect of cervical cancer education and provider recommendation for screening on screening rates: A systematic review and meta-analysis. PLoS ONE, 2017, 12, e0183924.	1.1	126
28	Genome-wide association study of breast cancer in Latinas identifies novel protective variants on 6q25. Nature Communications, 2014, 5, 5260.	5.8	123
29	Effects of Short-Term Exposure to Inhalable Particulate Matter on Telomere Length, Telomerase Expression, and Telomerase Methylation in Steel Workers. Environmental Health Perspectives, 2011, 119, 622-627.	2.8	109
30	Surrogate tissue telomere length and cancer risk: Shorter or Longer?. Cancer Letters, 2012, 319, 130-135.	3.2	109
31	Telomere Length in Peripheral Leukocyte DNA and Gastric Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 3103-3109.	1.1	106
32	Prediction of genome-wide DNA methylation in repetitive elements. Nucleic Acids Research, 2017, 45, 8697-8711.	6.5	106
33	Blood leukocyte DNA hypomethylation and gastric cancer risk in a high‐risk Polish population. International Journal of Cancer, 2010, 127, 1866-1874.	2.3	103
34	Lung Cancer Screening, Version 1.2015. Journal of the National Comprehensive Cancer Network: JNCCN, 2015, 13, 23-34.	2.3	102
35	Inhalable particulate matter and mitochondrial DNA copy number in highly exposed individuals in Beijing, China: a repeated-measure study. Particle and Fibre Toxicology, 2013, 10, 17.	2.8	99
36	Environmental and occupational exposure to chemicals and telomere length in human studies. Occupational and Environmental Medicine, 2013, 70, 743-749.	1.3	98

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37	Association of air particulate pollution with bone loss over time and bone fracture risk: analysis of data from two independent studies. Lancet Planetary Health, The, 2017, 1, e337-e347.	5.1	96
38	Association between dietary inflammatory potential and breast cancer incidence and death: results from the Women's Health Initiative. British Journal of Cancer, 2016, 114, 1277-1285.	2.9	83
39	DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons. JAMA Psychiatry, 2018, 75, 949.	6.0	78
40	Commuting Physical Activity and Risk of Colon Cancer in Shanghai, China. American Journal of Epidemiology, 2004, 160, 860-867.	1.6	76
41	Effects of particulate air pollution on blood pressure in a highly exposed population in Beijing, China: a repeated-measure study. Environmental Health, 2011, 10, 108.	1.7	76
42	Air pollution exposure and lung function in highly exposed subjects in Beijing, China: a repeated-measure study. Particle and Fibre Toxicology, 2014, 11, 51.	2.8	76
43	Repetitive element hypomethylation in blood leukocyte DNA and cancer incidence, prevalence, and mortality in elderly individuals: the Normative Aging Study. Cancer Causes and Control, 2011, 22, 437-447.	0.8	74
44	NSAID Use and Risk of Hepatocellular Carcinoma and Intrahepatic Cholangiocarcinoma: The Liver Cancer Pooling Project. Cancer Prevention Research, 2015, 8, 1156-1162.	0.7	74
45	A-clustering: a novel method for the detection of co-regulated methylation regions, and regions associated with exposure. Bioinformatics, 2013, 29, 2884-2891.	1.8	73
46	Dietary Intake of Fiber, Fruit and Vegetables Decreases the Risk of Incident Kidney Stones in Women: A Women's Health Initiative Report. Journal of Urology, 2014, 192, 1694-1699.	0.2	73
47	Pendimethalin Exposure and Cancer Incidence Among Pesticide Applicators. Epidemiology, 2006, 17, 302-307.	1.2	70
48	DNA methylation alterations in response to pesticide exposure *in vitro*. Environmental and Molecular Mutagenesis, 2012, 53, 542-549.	0.9	68
49	Long-term ambient particle exposures and blood DNA methylation age: findings from the VA normative aging study. Environmental Epigenetics, 2016, 2, dvw006.	0.9	68
50	Nasal cell DNA methylation, inflammation, lung function and wheezing in children with asthma. Epigenomics, 2012, 4, 91-100.	1.0	66
51	Lifetime Pesticide Use and Telomere Shortening among Male Pesticide Applicators in the Agricultural Health Study. Environmental Health Perspectives, 2013, 121, 919-924.	2.8	63
52	Effects of particulate matter exposure on blood 5-hydroxymethylation: results from the Beijing truck driver air pollution study. Epigenetics, 2015, 10, 633-642.	1.3	63
53	Blood Telomere Length Attrition and Cancer Development in the Normative Aging Study Cohort. EBioMedicine, 2015, 2, 591-596.	2.7	62
54	Long-term outdoor air pollution and DNA methylation in circulating monocytes: results from the Multi-Ethnic Study of Atherosclerosis (MESA). Environmental Health, 2016, 15, 119.	1.7	62

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55	A longitudinal study of DNA methylation as a potential mediator of age-related diabetes risk. GeroScience, 2017, 39, 475-489.	2.1	62
56	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. Nature Communications, 2019, 10, 2581.	5.8	62
57	Associations between long-term exposure to PM2.5 component species and blood DNA methylation age in the elderly: The VA normative aging study. Environment International, 2017, 102, 57-65.	4.8	58
58	Methylome-wide association study provides evidence of particulate matter air pollution-associated DNA methylation. Environment International, 2019, 132, 104723.	4.8	58
59	Birth weight and subsequent risk of cancer. Cancer Epidemiology, 2014, 38, 538-543.	0.8	57
60	Genetic variation in sodium-dependent ascorbic acid transporters and risk of gastric cancer in Poland. European Journal of Cancer, 2009, 45, 1824-1830.	1.3	56
61	Epigenetic Age Acceleration Reflects Long-Term Cardiovascular Health. Circulation Research, 2021, 129, 770-781.	2.0	55
62	Ambient PM exposure and DNA methylation in tumor suppressor genes: a cross-sectional study. Particle and Fibre Toxicology, 2011, 8, 25.	2.8	53
63	Leukocyte Telomere Length and Risks of Incident Coronary Heart Disease and Mortality in a Racially Diverse Population of Postmenopausal Women. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 2225-2231.	1.1	53
64	Traffic-derived particulate matter exposure and histone H3 modification: A repeated measures study. Environmental Research, 2017, 153, 112-119.	3.7	52
65	Differential DNA methylation and $PM_{2.5}$ species in a 450K epigenome-wide association study. Epigenetics, 2017, 12, 139-148.	1.3	52
66	Impacts of air pollution, temperature, and relative humidity on leukocyte distribution: An epigenetic perspective. Environment International, 2019, 126, 395-405.	4.8	52
67	CYP1A1 Val 462 and NQO1 Ser 187 polymorphisms, cigarette use, and risk for colorectal adenoma. Carcinogenesis, 2005, 26, 1122-1128.	1.3	51
68	Status of Cardiovascular Health in US Children Up to 11 Years of Age. Circulation: Cardiovascular Quality and Outcomes, 2015, 8, 164-171.	0.9	51
69	Blood monocyte transcriptome and epigenome analyses reveal loci associated with human atherosclerosis. Nature Communications, 2017, 8, 393.	5.8	51
70	GDM Women's Pre-Pregnancy Overweight/Obesity and Gestational Weight Gain on Offspring Overweight Status. PLoS ONE, 2015, 10, e0129536.	1.1	50
71	Gestational Diabetes History and Glucose Tolerance After Pregnancy Associated With Coronary Artery Calcium in Women During Midlife. Circulation, 2021, 143, 974-987.	1.6	49
72	Epigenetic age acceleration and metabolic syndrome in the coronary artery risk development in young adults study. Clinical Epigenetics, 2019, 11, 160.	1.8	48

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73	Childhood Risk Factors and Adulthood Cardiovascular Disease: A Systematic Review. Journal of Pediatrics, 2021, 232, 118-126.e23.	0.9	48
74	Genome-wide study of DNA methylation alterations in response to diazinon exposure in vitro. Environmental Toxicology and Pharmacology, 2012, 34, 959-968.	2.0	47
75	Folate receptor alpha is associated with cervical carcinogenesis and regulates cervical cancer cells growth by activating ERK1/2/c-Fos/c-Jun. Biochemical and Biophysical Research Communications, 2017, 491, 1083-1091.	1.0	47
76	Genetic Polymorphisms in Folate Metabolism and the Risk of Stomach Cancer. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 115-121.	1.1	45
77	Cancer Incidence and Mortality during the Intervention and Postintervention Periods of the Women's Health Initiative Dietary Modification Trial. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 2924-2935.	1.1	45
78	Cardiovascular Health and Incident Cardiovascular Disease and Cancer. American Journal of Preventive Medicine, 2016, 50, 236-240.	1.6	45
79	Altered methylation in tandem repeat element and elemental component levels in inhalable air particles. Environmental and Molecular Mutagenesis, 2014, 55, 256-265.	0.9	43
80	Temporal Stability of Epigenetic Markers: Sequence Characteristics and Predictors of Short-Term DNA Methylation Variations. PLoS ONE, 2012, 7, e39220.	1.1	43
81	Whole Blood DNA Methylation Signatures of Diet Are Associated With Cardiovascular Disease Risk Factors and All-Cause Mortality. Circulation Genomic and Precision Medicine, 2020, 13, e002766.	1.6	42
82	Pesticide Use and Relative Leukocyte Telomere Length in the Agricultural Health Study. PLoS ONE, 2015, 10, e0133382.	1.1	42
83	Body mass index and colon cancer risk in Chinese people: Menopause as an effect modifier. European Journal of Cancer, 2006, 42, 84-90.	1.3	41
84	Prospective changes in global DNA methylation and cancer incidence and mortality. British Journal of Cancer, 2016, 115, 465-472.	2.9	41
85	A Peripheral Blood DNA Methylation Signature of Hepatic Fat Reveals a Potential Causal Pathway for Nonalcoholic Fatty Liver Disease. Diabetes, 2019, 68, 1073-1083.	0.3	41
86	Republished: Environmental and occupational exposure to chemicals and telomere length in human studies. Postgraduate Medical Journal, 2013, 89, 722-728.	0.9	40
87	Diabetes, metformin and incidence of and death from invasive cancer in postmenopausal women: Results from the women's health initiative. International Journal of Cancer, 2016, 138, 1915-1927.	2.3	39
88	Red Meat Intake, NAT2, and Risk of Colorectal Cancer: A Pooled Analysis of 11 Studies. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 198-205.	1.1	38
89	Impact of folic acid fortification on global DNA methylation and one-carbon biomarkers in the Women's Health Initiative Observational Study cohort. Epigenetics, 2014, 9, 396-403.	1.3	37
90	Characterization of genome-wide H3K27ac profiles reveals a distinct PM2.5-associated histone modification signature. Environmental Health, 2015, 14, 65.	1.7	37

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91	Magnesium intake and mortality due to liver diseases: Results from the Third National Health and Nutrition Examination Survey Cohort. Scientific Reports, 2017, 7, 17913.	1.6	36
92	Residential proximity to major roadways and incident hypertension in post-menopausal women. Environmental Research, 2015, 142, 522-528.	3.7	35
93	Intakes of magnesium, calcium and risk of fatty liver disease and prediabetes. Public Health Nutrition, 2018, 21, 2088-2095.	1.1	35
94	Association of clinical outcomes in metastatic breast cancer patients with circulating tumour cell and circulating cell-free DNA. European Journal of Cancer, 2019, 106, 133-143.	1.3	35
95	A Signature of Four Circulating microRNAs as Potential Biomarkers for Diagnosing Early-Stage Breast Cancer. International Journal of Molecular Sciences, 2021, 22, 6121.	1.8	35
96	Particulate Air Pollution Exposure and Expression of Viral and Human MicroRNAs in Blood: The Beijing Truck Driver Air Pollution Study. Environmental Health Perspectives, 2016, 124, 344-350.	2.8	34
97	Genetic polymorphisms in alcohol metabolism, alcohol intake and the risk of stomach cancer in Warsaw, Poland. International Journal of Cancer, 2007, 121, 2060-2064.	2.3	33
98	Short-term air pollution, cognitive performance and nonsteroidal anti-inflammatory drug use in the Veterans Affairs Normative Aging Study. Nature Aging, 2021, 1, 430-437.	5.3	33
99	Anthropometric Measurements, Physical Activity, and the Risk of Symptomatic Gallstone Disease in Chinese Women. Annals of Epidemiology, 2009, 19, 344-350.	0.9	32
100	Dietary factors, gut microbiota, and serum trimethylamine-N-oxide associated with cardiovascular disease in the Hispanic Community Health Study/Study of Latinos. American Journal of Clinical Nutrition, 2021, 113, 1503-1514.	2.2	32
101	DNA methylation of individual repetitive elements in hepatitis C virus infection-induced hepatocellular carcinoma. Clinical Epigenetics, 2019, 11, 145.	1.8	31
102	Polymorphisms in estrogen- and androgen-metabolizing genes and the risk of gastric cancer. Carcinogenesis, 2009, 30, 71-77.	1.3	30
103	Prognostic value of HER2 status on circulating tumor cells in advanced-stage breast cancer patients with HER2-negative tumors. Breast Cancer Research and Treatment, 2020, 181, 679-689.	1.1	30
104	Glioblastoma as an age-related neurological disorder in adults. Neuro-Oncology Advances, 2021, 3, vdab125.	0.4	30
105	Association between Sleep Quality and C-Reactive Protein: Results from National Health and Nutrition Examination Survey, 2005-2008. PLoS ONE, 2014, 9, e92607.	1.1	30
106	Maternal gestational diabetes and different indicators of childhood obesity: a large study. Endocrine Connections, 2018, 7, 1464-1471.	0.8	30
107	Meta-analyses identify DNA methylation associated with kidney function and damage. Nature Communications, 2021, 12, 7174.	5.8	30
108	Host Genetic Factors Associated with Vaginal Microbiome Composition in Kenyan Women. MSystems, 2020, 5, .	1.7	29

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109	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	3.0	29
110	Blood methylomics in response to arsenic exposure in a low-exposed US population. Journal of Exposure Science and Environmental Epidemiology, 2014, 24, 145-149.	1.8	28
111	A genome-wide association study for colorectal cancer identifies a risk locus in 14q23.1. Human Genetics, 2015, 134, 1249-1262.	1.8	28
112	Leisure-time physical activity and leukocyte telomere length among older women. Experimental Gerontology, 2017, 95, 141-147.	1.2	28
113	CpGFilter: model-based CpG probe filtering with replicates for epigenome-wide association studies. Bioinformatics, 2016, 32, 469-471.	1.8	27
114	Longitudinal Study of DNA Methylation of Inflammatory Genes and Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1531-1538.	1.1	26
115	Relationship of prediagnostic body mass index with survival after colorectal cancer: Stage-specific associations. International Journal of Cancer, 2016, 139, 1065-1072.	2.3	26
116	COX1 and COX2 polymorphisms and gastric cancer risk in a Polish population. Anticancer Research, 2007, 27, 4243-7.	0.5	26
117	Association of Transforming Growth Factor-beta 1 Polymorphisms with Genetic Susceptibility to TNM Stage I or II Gastric Cancer. Japanese Journal of Clinical Oncology, 2008, 38, 861-866.	0.6	25
118	The modifying effect of kidney function on the association of cadmium exposure with blood pressure and cardiovascular mortality: NHANES 1999–2010. Toxicology and Applied Pharmacology, 2018, 353, 15-22.	1.3	25
119	Comparative validation of an epigenetic mortality risk score with three aging biomarkers for predicting mortality risks among older adult males. International Journal of Epidemiology, 2019, 48, 1958-1971.	0.9	25
120	Associations of smoking and air pollution with peripheral blood RNA N6-methyladenosine in the Beijing truck driver air pollution study. Environment International, 2020, 144, 106021.	4.8	25
121	Prenatal gestational diabetes mellitus exposure and accelerated offspring DNA methylation age in early childhood. Epigenetics, 2021, 16, 186-195.	1.3	25
122	DNA methylation in blood as a mediator of the association of mid-childhood body mass index with cardio-metabolic risk score in early adolescence. Epigenetics, 2018, 13, 1072-1087.	1.3	24
123	Association of Cancer Susceptibility Variants with Risk of Multiple Primary Cancers: The Population Architecture using Genomics and Epidemiology Study. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 2568-2578.	1.1	23
124	CYP17 MspA1 polymorphism and risk of biliary tract cancers and gallstones: A population-based study in Shanghai, China. International Journal of Cancer, 2006, 118, 2847-2853.	2.3	22
125	White blood cell count in young adulthood and coronary artery calcification in early middle age: coronary artery risk development in young adults (CARDIA) study. European Journal of Epidemiology, 2013, 28, 735-742.	2.5	22
126	microRNA Expression in Ethnic Specific Early Stage Breast Cancer: an Integration and Comparative Analysis. Scientific Reports, 2017, 7, 16829.	1.6	22

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127	DASH diet and prevalent metabolic syndrome in the Hispanic Community Health Study/Study of Latinos. Preventive Medicine Reports, 2019, 15, 100950.	0.8	22
128	Smoking-Related DNA Methylation is Associated with DNA Methylation Phenotypic Age Acceleration: The Veterans Affairs Normative Aging Study. International Journal of Environmental Research and Public Health, 2019, 16, 2356.	1.2	22
129	Accelerated DNA methylation age and the use of antihypertensive medication among older adults. Aging, 2018, 10, 3210-3228.	1.4	21
130	Predictors of urinary phthalate biomarker concentrations in postmenopausal women. Environmental Research, 2019, 169, 122-130.	3.7	21
131	Analysis of repeated leukocyte DNA methylation assessments reveals persistent epigenetic alterations after an incident myocardial infarction. Clinical Epigenetics, 2018, 10, 161.	1.8	20
132	Association of cardiovascular health and epigenetic age acceleration. Clinical Epigenetics, 2021, 13, 42.	1.8	20
133	Epigenome-wide association study of kidney function identifies trans-ethnic and ethnic-specific loci. Genome Medicine, 2021, 13, 74.	3.6	20
134	Association of Accelerometer-Measured Physical Activity With Leukocyte Telomere Length Among Older Women. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2017, 72, 1532-1537.	1.7	19
135	miRNA-Processing Gene Methylation and Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 550-557.	1.1	19
136	The Inflammatory Potential of Dietary Manganese in a Cohort of Elderly Men. Biological Trace Element Research, 2018, 183, 49-57.	1.9	19
137	Metastable DNA methylation sites associated with longitudinal lung function decline and aging in humans: an epigenome-wide study in the NAS and KORA cohorts. Epigenetics, 2018, 13, 1039-1055.	1.3	19
138	Physical activity, dietary calcium to magnesium intake and mortality in the National Health and Examination Survey 1999â€"2006 cohort. International Journal of Cancer, 2020, 146, 2979-2986.	2.3	19
139	Epigenome-wide association study of diet quality in the Womenâ€™s Health Initiative and TwinsUK cohort. International Journal of Epidemiology, 2021, 50, 675-684.	0.9	19
140	DNA Methylation GrimAge and Incident Diabetes: The Coronary Artery Risk Development in Young Adults (CARDIA) Study. Diabetes, 2021, 70, 1404-1413.	0.3	19
141	Cord blood DNA methylation and adiposity measures in early and mid-childhood. Clinical Epigenetics, 2017, 9, 86.	1.8	18
142	Association of Neutrophil to Lymphocyte Ratio With Pulmonary Function in a 30-Year Longitudinal Study of US Veterans. JAMA Network Open, 2020, 3, e2010350.	2.8	18
143	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. Nature Communications, 2021, 12, 3987.	5.8	18
144	Maternal Glucose during Pregnancy and after Delivery in Women with Gestational Diabetes Mellitus on Overweight Status of Their Children. BioMed Research International, 2015, 2015, 1-9.	0.9	17

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145	Leukocyte Traits and Exposure to Ambient Particulate Matter Air Pollution in the Women's Health Initiative and Atherosclerosis Risk in Communities Study. Environmental Health Perspectives, 2020, 128, 17004.	2.8	17
146	Mediation analysis for survival data with high-dimensional mediators. Bioinformatics, 2021, 37, 3815-3821.	1.8	17
147	Association of Cardiovascular Health Through Young Adulthood With Genome-Wide DNA Methylation Patterns in Midlife: The CARDIA Study. Circulation, 2022, 146, 94-109.	1.6	17
148	Impacts of the Mitochondrial Genome on the Relationship of Long-Term Ambient Fine Particle Exposure with Blood DNA Methylation Age. Environmental Science & Technology, 2017, 51, 8185-8195.	4.6	16
149	Histone 3 modifications and blood pressure in the Beijing Truck Driver Air Pollution Study. Biomarkers, 2017, 22, 584-593.	0.9	16
150	Persistent variations of blood DNA methylation associated with treatment exposures and risk for cardiometabolic outcomes in long-term survivors of childhood cancer in the St. Jude Lifetime Cohort. Genome Medicine, 2021, 13, 53.	3.6	16
151	Mid-life epigenetic age, neuroimaging brain age, and cognitive function: coronary artery risk development in young adults (CARDIA) study. Aging, 2022, 14, 1691-1712.	1.4	16
152	Public Health Impact and Economic Costs of Volkswagen's Lack of Compliance with the United States' Emission Standards. International Journal of Environmental Research and Public Health, 2016, 13, 891.	1.2	15
153	miRNA processing gene polymorphisms, blood DNA methylation age and long-term ambient $PM_{2.5}$ exposure in elderly men. Epigenomics, 2017, 9, 1529-1542.	1.0	15
154	Application of the High-Throughput TAB-Array for the Discovery of Novel 5-Hydroxymethylcytosine Biomarkers in Pancreatic Ductal Adenocarcinoma. Epigenomes, 2019, 3, 16.	0.8	15
155	Joint Associations of Maternal Gestational Diabetes and Hypertensive Disorders of Pregnancy With Overweight in Offspring. Frontiers in Endocrinology, 2019, 10, 645.	1.5	15
156	Ca:Mg Ratio, APOE Cytosine Modifications, and Cognitive Function: Results from a Randomized Trial. Journal of Alzheimer's Disease, 2020, 75, 85-98.	1.2	15
157	Estimating breast tissue-specific DNA methylation age using next-generation sequencing data. Clinical Epigenetics, 2020, 12, 45.	1.8	15
158	Epigenomic analysis of 5-hydroxymethylcytosine (5hmC) reveals novel DNA methylation markers for lung cancers. Neoplasia, 2020, 22, 154-161.	2.3	15
159	Biomarkers of aging and lung function in the normative aging study. Aging, 2020, 12, 11942-11966.	1.4	15
160	Blood DNA methylation sites predict death risk in a longitudinal study of 12, 300 individuals. Aging, 2020, 12, 14092-14124.	1.4	15
161	Calcium/magnesium intake ratio, but not magnesium intake, interacts with genetic polymorphism in relation to colorectal neoplasia in a two-phase study. Molecular Carcinogenesis, 2016, 55, 1449-1457.	1.3	14
162	Exposure to arsenic at different life-stages and DNA methylation meta-analysis in buccal cells and leukocytes. Environmental Health, 2021, 20, 79.	1.7	14

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163	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 1836-1851.	2.6	14
164	Maternal OGTT Glucose Levels at 26â€"30 Gestational Weeks with Offspring Growth and Development in Early Infancy. BioMed Research International, 2014, 2014, 1-11.	0.9	13
165	Menopausal estrogen therapy and nonâ€‹<scp>H</scp>odgkin's lymphoma: A <i>postâ€hoc</i> analysis of women's health initiative randomized clinical trial. International Journal of Cancer, 2016, 138, 604-611.	2.3	13
166	DNAm-based signatures of accelerated aging and mortality in blood are associated with low renal function. Clinical Epigenetics, 2021, 13, 121.	1.8	13
167	Accelerated epigenetic aging as a risk factor for chronic obstructive pulmonary disease and decreased lung function in two prospective cohort studies. Aging, 2020, 12, 16539-16554.	1.4	13
168	Combined conjugated esterified estrogen plus methyltestosterone supplementation and risk of breast cancer in postmenopausal women. Maturitas, 2014, 79, 70-76.	1.0	12
169	Promoter methylation of <i>PGC1A</i> and <i>PGC1B</i> predicts cancer incidence in a veteran cohort. Epigenomics, 2018, 10, 733-743.	1.0	12
170	DNA Methylation of Telomere-Related Genes and Cancer Risk. Cancer Prevention Research, 2018, 11, 511-522.	0.7	12
171	Blood pressure and expression of microRNAs in whole blood. PLoS ONE, 2017, 12, e0173550.	1.1	12
172	Cost effectiveness of human papilloma virus vaccination in low and middle income countries: a systematic review of literature. Expert Review of Vaccines, 2018, 17, 91-98.	2.0	11
173	Impact of the COVID-19 pandemic on global health research training and education. Journal of Global Health, 2020, 10, 020366.	1.2	11
174	Short- and intermediate-term exposure to ambient fine particulate elements and leukocyte epigenome-wide DNA methylation in older men: the Normative Aging Study. Environment International, 2022, 158, 106955.	4.8	11
175	APOE Îµ4 allele modifies the association of lead exposure with age-related cognitive decline in older individuals. Environmental Research, 2016, 151, 101-105.	3.7	10
176	Editorâ€™s Highlight: Modifying Role of Endothelial Function Gene Variants on the Association of Long-Term PM2.5 Exposure With Blood DNA Methylation Age: The VA Normative Aging Study. Toxicological Sciences, 2017, 158, 116-126.	1.4	10
177	Sedentary time and postmenopausal breast cancer incidence. Cancer Causes and Control, 2017, 28, 1405-1416.	0.8	10
178	Folate deficiency and aberrant DNA methylation and expression of FHIT gene were associated with cervical pathogenesis. Oncology Letters, 2017, 15, 1963-1972.	0.8	10
179	Association of cord blood methylation with neonatal leptin: An epigenome wide association study. PLoS ONE, 2019, 14, e0226555.	1.1	10
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