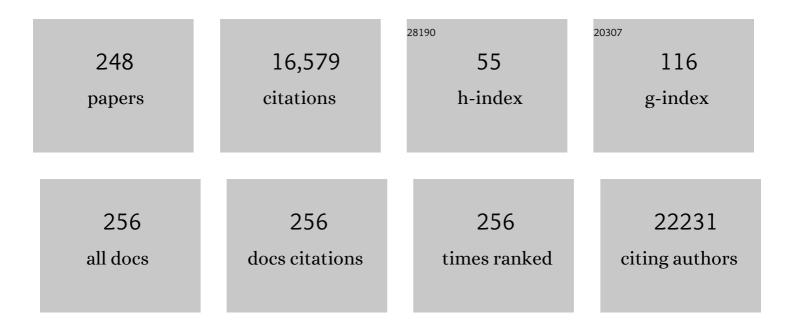
Lifang Hou

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Impact of paternal education on epigenetic ageing in adolescence and mid-adulthood: a multi-cohort study in the USA and Mexico. International Journal of Epidemiology, 2022, 51, 870-884.	0.9	6
2	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
3	Plasma lipid profiles in early adulthood are associated with epigenetic aging in the Coronary Artery Risk Development in Young Adults (CARDIA) Study. Clinical Epigenetics, 2022, 14, 16.	1.8	9
4	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	3.0	29
5	Blood DNA methylation signatures are associated with social determinants of health among survivors of childhood cancer. Epigenetics, 2022, , 1-15.	1.3	5
6	Pulmonary Function in Midlife as a Predictor of Later-Life Cognition: The Coronary Artery Risk Development in Adults (CARDIA) Study. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2022, 77, 2517-2523.	1.7	2
7	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
8	Rare coding variants in RCN3 are associated with blood pressure. BMC Genomics, 2022, 23, 148.	1.2	2
9	Analyses of Kaposi Sarcoma trends among adults establishing initial outpatient HIV care in Nigeria: 2006–2017. Infectious Agents and Cancer, 2022, 17, 10.	1.2	1
10	Accelerated Epigenetic Age Among Women with Invasive Cervical Cancer and HIV-Infection in Nigeria. Frontiers in Public Health, 2022, 10, 834800.	1.3	0
11	Integrative analysis of clinical and epigenetic biomarkers of mortality. Aging Cell, 2022, 21, e13608.	3.0	8
12	Gaseous air pollutants and DNA methylation in a methylome-wide association study of an ethnically and environmentally diverse population of U.S. adults. Environmental Research, 2022, 212, 113360.	3.7	7
13	A Review of High-Dimensional Mediation Analyses in DNA Methylation Studies. Methods in Molecular Biology, 2022, 2432, 123-135.	0.4	3
14	Abstract CT534: Magnesium treatment on the demethylation of <i>chemokine (C-X-C motif) ligand 9 (CXCL9) gene</i> , results from the personalized prevention of colorectal cancer trial. Cancer Research, 2022, 82, CT534-CT534.	0.4	0
15	Epigenetic age acceleration in U.S. testicular cancer survivors (TCS) Journal of Clinical Oncology, 2022, 40, 5033-5033.	0.8	1
16	Association of the Interleukin-10-592C/A Polymorphism and Cervical Cancer Risk: A Meta-Analysis. Genetical Research, 2022, 2022, 1-10.	0.3	0
17	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
18	Prenatal gestational diabetes mellitus exposure and accelerated offspring DNA methylation age in early childhood. Epigenetics, 2021, 16, 186-195.	1.3	25

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19	Epigenome-wide association study of diet quality in the Women's Health Initiative and TwinsUK cohort. International Journal of Epidemiology, 2021, 50, 675-684.	0.9	19
20	Association of cardiovascular health and epigenetic age acceleration. Clinical Epigenetics, 2021, 13, 42.	1.8	20
21	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
22	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
23	Epigenome-wide association study of kidney function identifies trans-ethnic and ethnic-specific loci. Genome Medicine, 2021, 13, 74.	3.6	20
24	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
25	DNA Methylation GrimAge and Incident Diabetes: The Coronary Artery Risk Development in Young Adults (CARDIA) Study. Diabetes, 2021, 70, 1404-1413.	0.3	19
26	Global line-1 hypomethylation as novel biomarker for cervical cancer in Nigerian women living with HIV Journal of Clinical Oncology, 2021, 39, e17513-e17513.	0.8	0
27	Acceleration of blood-based circulating cell-free DNA epigenetic age among HIV-infected patients with hepatocellular carcinoma in Nigeria Journal of Clinical Oncology, 2021, 39, e16137-e16137.	0.8	0
28	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
29	Hearing loss after cisplatin-based chemotherapy: Patient-reported outcomes versus audiometric assessments Journal of Clinical Oncology, 2021, 39, 5016-5016.	0.8	1
30	Childhood Risk Factors and Adulthood Cardiovascular Disease: A Systematic Review. Journal of Pediatrics, 2021, 232, 118-126.e23.	0.9	48
31	Accelerated epigenetic age among HIV-infected Nigerian women with invasive cervical cancer Journal of Clinical Oncology, 2021, 39, e17504-e17504.	0.8	1
32	Factors associated with use of medications for anxiety and depression in testicular cancer survivors after cisplatin-based chemotherapy Journal of Clinical Oncology, 2021, 39, 5025-5025.	0.8	2
33	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. Nature Communications, 2021, 12, 3987.	5.8	18
34	Association of the V122I Transthyretin Amyloidosis Genetic Variant With Cardiac Structure and Function in Middle-aged Black Adults. JAMA Cardiology, 2021, 6, 718.	3.0	7
35	DNAm-based signatures of accelerated aging and mortality in blood are associated with low renal function. Clinical Epigenetics, 2021, 13, 121.	1.8	13
36	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

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37	Risks of Macrosomia Associated with Catechol-O-Methyltransferase Genotypes and Genetic–Epigenetic Interactions among Children with and without Gestational Diabetes Exposure. Childhood Obesity, 2021, 17, 365-370.	0.8	0
38	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
39	Epigenetically mediated electrocardiographic manifestations of sub-chronic exposures to ambient particulate matter air pollution in the Women's Health Initiative and Atherosclerosis Risk in Communities Study. Environmental Research, 2021, 198, 111211.	3.7	4
40	Mediation analysis for survival data with high-dimensional mediators. Bioinformatics, 2021, 37, 3815-3821.	1.8	17
41	Epigenome-wide association study of mitochondrial genome copy number. Human Molecular Genetics, 2021, 31, 309-319.	1.4	6
42	Novel epigenetic link between gestational diabetes mellitus and macrosomia. Epigenomics, 2021, 13, 1221-1230.	1.0	4
43	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
44	Magnesium treatment on methylation changes of transmembrane serine protease 2 (TMPRSS2). Nutrition, 2021, 89, 111340.	1.1	6
45	Glioblastoma as an age-related neurological disorder in adults. Neuro-Oncology Advances, 2021, 3, vdab125.	0.4	30
46	Epigenetic Age Acceleration Reflects Long-Term Cardiovascular Health. Circulation Research, 2021, 129, 770-781.	2.0	55
47	The presence of emphysema on chest imaging and mid-life cognition. ERJ Open Research, 2021, 7, 00048-2021.	1.1	0
48	Cisplatin, environmental metals, and cardiovascular disease: an urgent need to understand underlying mechanisms. Cardio-Oncology, 2021, 7, 34.	0.8	4
49	Gene expression of oxidative stress markers and lung function: A CARDIA lung study. Molecular Genetics & Genomic Medicine, 2021, 9, e1832.	0.6	5
50	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. Nature Communications, 2021, 12, 7173.	5.8	8
51	Meta-analyses identify DNA methylation associated with kidney function and damage. Nature Communications, 2021, 12, 7174.	5.8	30
52	Physical activity, dietary calcium to magnesium intake and mortality in the National Health and Examination Survey 1999–2006 cohort. International Journal of Cancer, 2020, 146, 2979-2986.	2.3	19
53	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
54	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	13.7	376

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55	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
56	Mediation by differential DNA methylation of known associations between single nucleotide polymorphisms and bladder cancer risk. BMC Medical Genetics, 2020, 21, 228.	2.1	4
57	Host Genetic Factors Associated with Vaginal Microbiome Composition in Kenyan Women. MSystems, 2020, 5, .	1.7	29
58	HIV and development of epithelial cell abnormalities in women with prior normal cervical cytology in Nigeria. Infectious Agents and Cancer, 2020, 15, 50.	1.2	1
59	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
60	p.Arg72Pro polymorphism of P53 and breast cancer risk: a meta-analysis of case-control studies. BMC Medical Genetics, 2020, 21, 206.	2.1	8
61	Methylome-wide association study of central adiposity implicates genes involved in immune and endocrine systems. Epigenomics, 2020, 12, 1483-1499.	1.0	6
62	Metabolic Signatures of Gestational Weight Gain and Postpartum Weight Loss in a Lifestyle Intervention Study of Overweight and Obese Women. Metabolites, 2020, 10, 498.	1.3	5
63	Impact of the COVID-19 pandemic on global health research training and education. Journal of Global Health, 2020, 10, 020366.	1.2	11
64	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
65	Race-specific associations of 25-hydroxyvitamin D and parathyroid hormone with cardiometabolic biomarkers among US white and black postmenopausal women. American Journal of Clinical Nutrition, 2020, 112, 257-267.	2.2	4
66	Glucose metabolism among obese and non-obese children of mothers with gestational diabetes. BMJ Open Diabetes Research and Care, 2020, 8, e000822.	1.2	4
67	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
68	Lung Function and Gene Expression of Pathogen Recognition Pathway Receptors: the Cardia Lung Study. Scientific Reports, 2020, 10, 9360.	1.6	2
69	Predictors of Mortality From a Population-Based Cancer Registry Data in Jos, Nigeria: A Resource-Limited Setting. Frontiers in Medicine, 2020, 7, 227.	1.2	1
70	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
71	Estimating breast tissue-specific DNA methylation age using next-generation sequencing data. Clinical Epigenetics, 2020, 12, 45.	1.8	15
72	Association of PIN3 16-bp duplication polymorphism of TP53 with breast cancer risk in Mali and a meta-analysis. BMC Medical Genetics, 2020, 21, 142.	2.1	4

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73	Epigenomic analysis of 5-hydroxymethylcytosine (5hmC) reveals novel DNA methylation markers for lung cancers. Neoplasia, 2020, 22, 154-161.	2.3	15
74	Effect of bisphenols on telomerase expression and activity in breast cancer cell lines. Molecular Biology Reports, 2020, 47, 3541-3549.	1.0	8
75	Biomarkers of aging and lung function in the normative aging study. Aging, 2020, 12, 11942-11966.	1.4	15
76	Blood DNA methylation sites predict death risk in a longitudinal study of 12, 300 individuals. Aging, 2020, 12, 14092-14124.	1.4	15
77	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
78	Lactation intensity and duration to postpartum diabetes and prediabetes risk in women with gestational diabetes. Diabetes/Metabolism Research and Reviews, 2019, 35, e3115.	1.7	6
79	Blood Leukocyte DNA Methylation Predicts Risk of Future Myocardial Infarction and Coronary Heart Disease. Circulation, 2019, 140, 645-657.	1.6	151
80	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
81	DASH diet and prevalent metabolic syndrome in the Hispanic Community Health Study/Study of Latinos. Preventive Medicine Reports, 2019, 15, 100950.	0.8	22
82	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
83	Joint Associations of Maternal Gestational Diabetes and Hypertensive Disorders of Pregnancy With Overweight in Offspring. Frontiers in Endocrinology, 2019, 10, 645.	1.5	15
84	DNA methylation of individual repetitive elements in hepatitis C virus infection-induced hepatocellular carcinoma. Clinical Epigenetics, 2019, 11, 145.	1.8	31
85	Racial differences of incident diabetes postpartum in women with a history of gestational diabetes. Journal of Diabetes and Its Complications, 2019, 33, 107472.	1.2	6
86	Epigenetic age acceleration and metabolic syndrome in the coronary artery risk development in young adults study. Clinical Epigenetics, 2019, 11, 160.	1.8	48
87	Optimism is not associated with two indicators of DNA methylation aging. Aging, 2019, 11, 4970-4989.	1.4	6
88	Methylome-wide association study provides evidence of particulate matter air pollution-associated DNA methylation. Environment International, 2019, 132, 104723.	4.8	58
89	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. Nature Communications, 2019, 10, 2581.	5.8	62
90	DNA methylation GrimAge strongly predicts lifespan and healthspan. Aging, 2019, 11, 303-327.	1.4	1,128

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91	IP3R and RyR channels are involved in traffic-related PM _{2.5} -induced disorders of calcium homeostasis. Toxicology and Industrial Health, 2019, 35, 339-348.	0.6	8
92	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
93	Impacts of air pollution, temperature, and relative humidity on leukocyte distribution: An epigenetic perspective. Environment International, 2019, 126, 395-405.	4.8	52
94	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
95	Association of cord blood methylation with neonatal leptin: An epigenome wide association study. PLoS ONE, 2019, 14, e0226555.	1.1	10
96	HIV status, age at cervical Cancer screening and cervical cytology outcomes in an opportunistic screening setting in Nigeria: a 10-year Cross sectional data analysis. Infectious Agents and Cancer, 2019, 14, 43.	1.2	10
97	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
98	Predictors of urinary phthalate biomarker concentrations in postmenopausal women. Environmental Research, 2019, 169, 122-130.	3.7	21
99	DNA methylation-based estimator of telomere length. Aging, 2019, 11, 5895-5923.	1.4	198
100	Phase I trial of endoxifen gel versus placebo gel in women undergoing breast surgery Journal of Clinical Oncology, 2019, 37, TPS1588-TPS1588.	0.8	0
101	miRNA-Processing Gene Methylation and Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 550-557.	1.1	19
102	Intakes of magnesium, calcium and risk of fatty liver disease and prediabetes. Public Health Nutrition, 2018, 21, 2088-2095.	1.1	35
103	Neurotrophins and cholinergic enzyme regulated by calpain-2: New insights into neuronal apoptosis induced by polybrominated diphenyl ether-153. Toxicology Letters, 2018, 291, 29-38.	0.4	6
104	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. Nature Communications, 2018, 9, 387.	5.8	151
105	The Inflammatory Potential of Dietary Manganese in a Cohort of Elderly Men. Biological Trace Element Research, 2018, 183, 49-57.	1.9	19
106	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
107	The effect of genetic variants on the relationship between statins and breast cancer in postmenopausal women in the Women's Health Initiative observational study. Breast Cancer Research and Treatment, 2018, 167, 741-749.	1.1	2
108	Accelerated DNA methylation age and the use of antihypertensive medication among older adults. Aging, 2018, 10, 3210-3228.	1.4	21

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109	Association between patient-reported HIV status and provider recommendation for screening in an opportunistic cervical Cancer screening setting in Jos, Nigeria. BMC Health Services Research, 2018, 18, 885.	0.9	5
110	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
111	An epigenetic biomarker of aging for lifespan and healthspan. Aging, 2018, 10, 573-591.	1.4	1,552
112	Analysis of repeated leukocyte DNA methylation assessments reveals persistent epigenetic alterations after an incident myocardial infarction. Clinical Epigenetics, 2018, 10, 161.	1.8	20
113	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
114	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
115	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
116	DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons. JAMA Psychiatry, 2018, 75, 949.	6.0	78
117	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
118	DNA Methylation of Telomere-Related Genes and Cancer Risk. Cancer Prevention Research, 2018, 11, 511-522.	0.7	12
119	Maternal gestational diabetes and different indicators of childhood obesity: a large study. Endocrine Connections, 2018, 7, 1464-1471.	0.8	30
120	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
121	Presentation and survival in patients with hematologic malignancies in Jos, Nigeria: A retrospective cohort analysis. Journal of Medicine in the Tropics, 2018, 20, 49.	0.2	10
122	A phase IIB pre-surgical trial of oral tamoxifen (TAM) versus transdermal 4-hydroxytamoxifen (4-OHT) in women with DCIS of the breast Journal of Clinical Oncology, 2018, 36, TPS1595-TPS1595.	0.8	0
123	Evaluating intermittent dosing of aspirin for colorectal cancer prevention Journal of Clinical Oncology, 2018, 36, TPS1594-TPS1594.	0.8	1
124	Ultra-high dimensional variable selection with application to normative aging study: DNA methylation and metabolic syndrome. BMC Bioinformatics, 2017, 18, 156.	1.2	5
125	Genetic variation in SLC7A2 interacts with calcium and magnesium intakes in modulating the risk of colorectal polyps. Journal of Nutritional Biochemistry, 2017, 47, 35-40.	1.9	8
126	Editor'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

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127	Leisure-time physical activity and leukocyte telomere length among older women. Experimental Gerontology, 2017, 95, 141-147.	1.2	28
128	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
129	Interactions between calcium intake and polymorphisms in genes essential for calcium reabsorption and risk of colorectal neoplasia in a twoâ€phase study. Molecular Carcinogenesis, 2017, 56, 2258-2266.	1.3	7
130	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
131	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
132	Traffic-derived particulate matter exposure and histone H3 modification: A repeated measures study. Environmental Research, 2017, 153, 112-119.	3.7	52
133	Differential DNA methylation and PM _{2.5} species in a 450K epigenome-wide association study. Epigenetics, 2017, 12, 139-148.	1.3	52
134	Prediction of genome-wide DNA methylation in repetitive elements. Nucleic Acids Research, 2017, 45, 8697-8711.	6.5	106
135	Sedentary time and postmenopausal breast cancer incidence. Cancer Causes and Control, 2017, 28, 1405-1416.	0.8	10
136	Formaldehyde alters triglyceride synthesis and very low-density lipoprotein secretion in a time-dependent manner. Environmental Toxicology and Pharmacology, 2017, 56, 15-20.	2.0	5
137	Blood monocyte transcriptome and epigenome analyses reveal loci associated with human atherosclerosis. Nature Communications, 2017, 8, 393.	5.8	51
138	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
139	microRNA Expression in Ethnic Specific Early Stage Breast Cancer: an Integration and Comparative Analysis. Scientific Reports, 2017, 7, 16829.	1.6	22
140	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. American Journal of Human Genetics, 2017, 101, 888-902.	2.6	154
141	A longitudinal study of DNA methylation as a potential mediator of age-related diabetes risk. GeroScience, 2017, 39, 475-489.	2.1	62
142	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
143	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
144	Histone 3 modifications and blood pressure in the Beijing Truck Driver Air Pollution Study. Biomarkers, 2017, 22, 584-593.	0.9	16

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145	Interaction between Nonsteroidal Anti-inflammatory Drugs and Low-fat Dietary Intervention on Colorectal Cancer Incidence; the Women's Health Initiative (WHI) Dietary Modification Trial. Journal of the American College of Nutrition, 2017, 36, 462-469.	1.1	3
146	Outcome of HIV-associated lymphoma in a resource-limited setting of Jos, Nigeria. Infectious Agents and Cancer, 2017, 12, 34.	1.2	9
147	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
148	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
149	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
150	Gravidity is not associated with telomere length in a biracial cohort of middle-aged women: The Coronary Artery Risk Development in Young Adults (CARDIA) study. PLoS ONE, 2017, 12, e0186495.	1.1	5
151	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
152	Cord blood DNA methylation and adiposity measures in early and mid-childhood. Clinical Epigenetics, 2017, 9, 86.	1.8	18
153	Epigenetic clock analysis of diet, exercise, education, and lifestyle factors. Aging, 2017, 9, 419-446.	1.4	521
154	Blood pressure and expression of microRNAs in whole blood. PLoS ONE, 2017, 12, e0173550.	1.1	12
155	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
156	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
157	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
158	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
159	Relationship of prediagnostic body mass index with survival after colorectal cancer: Stageâ€specific associations. International Journal of Cancer, 2016, 139, 1065-1072.	2.3	26
160	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
161	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
162	Cardiovascular Health and Incident Cardiovascular Disease and Cancer. American Journal of Preventive Medicine, 2016, 50, 236-240.	1.6	45

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163	APOE ε4 allele modifies the association of lead exposure with age-related cognitive decline in older individuals. Environmental Research, 2016, 151, 101-105.	3.7	10
164	Telomere Length: The Intersection of Sociology, Molecular Biology, and Human Disease. EBioMedicine, 2016, 11, 27-28.	2.7	1
165	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
166	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
167	Linking short tandem repeat polymorphisms with cytosine modifications in human lymphoblastoid cell lines. Human Genetics, 2016, 135, 223-232.	1.8	2
168	CpGFilter: model-based CpG probe filtering with replicates for epigenome-wide association studies. Bioinformatics, 2016, 32, 469-471.	1.8	27
169	Prospective changes in global DNA methylation and cancer incidence and mortality. British Journal of Cancer, 2016, 115, 465-472.	2.9	41
170	Blood Epigenetic Age may Predict Cancer Incidence and Mortality. EBioMedicine, 2016, 5, 68-73.	2.7	162
171	DNA methylation-based measures of biological age: meta-analysis predicting time to death. Aging, 2016, 8, 1844-1865.	1.4	786
172	DNA methylation of oxidative stress genes and cancer risk in the Normative Aging Study. American Journal of Cancer Research, 2016, 6, 553-61.	1.4	9
173	Lung Cancer Screening, Version 1.2015. Journal of the National Comprehensive Cancer Network: JNCCN, 2015, 13, 23-34.	2.3	102
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175	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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