

Steve Horvath

List of Publications by Year in descending order

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Version: 2024-02-01

321
papers

83,301
citations

1877

105
h-index

626

265
g-index

386
all docs

386
docs citations

386
times ranked

85029
citing authors

#	ARTICLE	IF	CITATIONS
1	Additive Effects of Stress and Alcohol Exposure on Accelerated Epigenetic Aging in Alcohol Use Disorder. <i>Biological Psychiatry</i> , 2023, 93, 331-341.	0.7	10
2	Accelerated epigenetic aging in adolescents living with HIV is associated with altered development of brain structures. <i>Journal of NeuroVirology</i> , 2022, 28, 208-216.	1.0	11
3	Higher diet quality relates to decelerated epigenetic aging. <i>American Journal of Clinical Nutrition</i> , 2022, 115, 163-170.	2.2	42
4	Association of Epigenetic Age Acceleration With Incident Mild Cognitive Impairment and Dementia Among Older Women. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2022, 77, 1239-1244.	1.7	13
5	Epigenetic clock and methylation studies in vervet monkeys. <i>GeroScience</i> , 2022, 44, 699-717.	2.1	18
6	Methylation studies in <i>Peromyscus</i> : aging, altitude adaptation, and monogamy. <i>GeroScience</i> , 2022, 44, 447-461.	2.1	4
7	DNA methylation as a tool to explore ageing in wild roe deer populations. <i>Molecular Ecology Resources</i> , 2022, 22, 1002-1015.	2.2	19
8	Stochastic Epigenetic Mutations Influence Parkinson's Disease Risk, Progression, and Mortality. <i>Journal of Parkinson's Disease</i> , 2022, 12, 545-556.	1.5	5
9	Epigenetic aging of the demographically non-aging naked mole-rat. <i>Nature Communications</i> , 2022, 13, 355.	5.8	26
10	DNA methylation aging and transcriptomic studies in horses. <i>Nature Communications</i> , 2022, 13, 40.	5.8	34
11	Plasma lipid profiles in early adulthood are associated with epigenetic aging in the Coronary Artery Risk Development in Young Adults (CARDIA) Study. <i>Clinical Epigenetics</i> , 2022, 14, 16.	1.8	9
12	DNA methylation signatures in Blood DNA of Hutchinson's Gilford Progeria syndrome. <i>Aging Cell</i> , 2022, 21, e13555.	3.0	18
13	Uninterrupted CAG repeat drives striatum-selective transcriptionopathy and nuclear pathogenesis in human Huntington BAC mice. <i>Neuron</i> , 2022, 110, 1173-1192.e7.	3.8	30
14	A mammalian methylation array for profiling methylation levels at conserved sequences. <i>Nature Communications</i> , 2022, 13, 783.	5.8	93
15	DNA methylation clocks tick in naked mole rats but queens age more slowly than nonbreeders. <i>Nature Aging</i> , 2022, 2, 46-59.	5.3	47
16	Abstract P2-11-06: Differential gene expression patterns in healthy breast tissue exhibiting epigenetic age acceleration. <i>Cancer Research</i> , 2022, 82, P2-11-06-P2-11-06.	0.4	0
17	Assessing the causal role of epigenetic clocks in the development of multiple cancers: a Mendelian randomization study. <i>ELife</i> , 2022, 11, .	2.8	19
18	Hibernation slows epigenetic ageing in yellow-bellied marmots. <i>Nature Ecology and Evolution</i> , 2022, 6, 418-426.	3.4	23

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19	Erratum to "Increased Menopausal Age Reduces the Risk of Parkinson's Disease: A Mendelian Approach". <i>Movement Disorders</i> , 2022, 37, 1282-1283.	2.2	1
20	In vivo partial reprogramming alters age-associated molecular changes during physiological aging in mice. <i>Nature Aging</i> , 2022, 2, 243-253.	5.3	101
21	Genetic loci and metabolic states associated with murine epigenetic aging. <i>ELife</i> , 2022, 11, .	2.8	26
22	Association of subjective social status with epigenetic aging among Black and White women. <i>Psychoneuroendocrinology</i> , 2022, 141, 105748.	1.3	9
23	Development of Epigenetic Clocks for Key Ruminant Species. <i>Genes</i> , 2022, 13, 96.	1.0	12
24	Epigenetic Clocks. , 2022, , 261-276.		2
25	The impact of reproductive factors on DNA methylation-based telomere length in healthy breast tissue. <i>Npj Breast Cancer</i> , 2022, 8, 48.	2.3	3
26	HIV, pathology and epigenetic age acceleration in different human tissues. <i>GeroScience</i> , 2022, 44, 1609-1620.	2.1	15
27	Epigenetic clock and methylation studies in marsupials: opossums, Tasmanian devils, kangaroos, and wallabies. <i>GeroScience</i> , 2022, 44, 1825-1845.	2.1	12
28	Making sense of the ageing methylome. <i>Nature Reviews Genetics</i> , 2022, 23, 585-605.	7.7	86
29	The relationship between epigenetic age and the hallmarks of aging in human cells. <i>Nature Aging</i> , 2022, 2, 484-493.	5.3	51
30	DNA methylation clocks for dogs and humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2120887119.	3.3	26
31	Telomere length and epigenetic clocks as markers of cellular aging: a comparative study. <i>GeroScience</i> , 2022, 44, 1861-1869.	2.1	18
32	Accelerated epigenetic aging in newborns with Down syndrome. <i>Aging Cell</i> , 2022, 21, .	3.0	17
33	Alcohol use disorder is associated with DNA methylation-based shortening of telomere length and regulated by TESP1: implications for aging. <i>Molecular Psychiatry</i> , 2022, 27, 3875-3884.	4.1	7
34	DNA methylation profile in beef cattle is influenced by additive genetics and age. <i>Scientific Reports</i> , 2022, 12, .	1.6	7
35	Accelerated aging with HIV occurs at the time of initial HIV infection. <i>IScience</i> , 2022, 25, 104488.	1.9	22
36	An epigenetic predictor of death captures multi-modal measures of brain health. <i>Molecular Psychiatry</i> , 2021, 26, 3806-3816.	4.1	77

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37	GrimAge Outperforms Other Epigenetic Clocks in the Prediction of Age-Related Clinical Phenotypes and All-Cause Mortality. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2021, 76, 741-749.	1.7	200
38	Epigenome-wide association study of diet quality in the Women's Health Initiative and TwinsUK cohort. <i>International Journal of Epidemiology</i> , 2021, 50, 675-684.	0.9	19
39	Occurrence of Accelerated Epigenetic Aging and Methylation Disruptions in Human Immunodeficiency Virus Infection Before Antiretroviral Therapy. <i>Journal of Infectious Diseases</i> , 2021, 223, 1681-1689.	1.9	19
40	Early life adversity, pubertal timing, and epigenetic age acceleration in adulthood. <i>Developmental Psychobiology</i> , 2021, 63, 890-902.	0.9	42
41	Long-term maturation of human cortical organoids matches key early postnatal transitions. <i>Nature Neuroscience</i> , 2021, 24, 331-342.	7.1	188
42	An epigenetic clock to estimate the age of living beluga whales. <i>Evolutionary Applications</i> , 2021, 14, 1263-1273.	1.5	32
43	DNA methylation predicts age and provides insight into exceptional longevity of bats. <i>Nature Communications</i> , 2021, 12, 1615.	5.8	80
44	DNA methylation biomarker for cumulative lead exposure is associated with Parkinson's disease. <i>Clinical Epigenetics</i> , 2021, 13, 59.	1.8	13
45	The Effects of Lifetime Estrogen Exposure on Breast Epigenetic Age. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021, 30, 1241-1249.	1.1	7
46	Epigenome-wide association study of kidney function identifies trans-ethnic and ethnic-specific loci. <i>Genome Medicine</i> , 2021, 13, 74.	3.6	20
47	Epigenetic Aging and Hematopoietic Cell Transplantation in Patients With Severe Aplastic Anemia. <i>Transplantation and Cellular Therapy</i> , 2021, 27, 313.e1-313.e8.	0.6	8
48	Incorporation of a nucleoside analog maps genome repair sites in postmitotic human neurons. <i>Science</i> , 2021, 372, 91-94.	6.0	68
49	Epigenetic clock and methylation study of oocytes from a bovine model of reproductive aging. <i>Aging Cell</i> , 2021, 20, e13349.	3.0	25
50	Multi-species and multi-tissue methylation clocks for age estimation in toothed whales and dolphins. <i>Communications Biology</i> , 2021, 4, 642.	2.0	39
51	Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. <i>Aging Cell</i> , 2021, 20, e13366.	3.0	72
52	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021, 22, 194.	3.8	90
53	Epigenetic clock and methylation studies in elephants. <i>Aging Cell</i> , 2021, 20, e13414.	3.0	43
54	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. <i>Nature Communications</i> , 2021, 12, 3987.	5.8	18

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55	Meta-analysis of genome-wide DNA methylation and integrative omics of age in human skeletal muscle. <i>Journal of Cachexia, Sarcopenia and Muscle</i> , 2021, 12, 1064-1078.	2.9	37
56	Postpartum sleep loss and accelerated epigenetic aging. <i>Sleep Health</i> , 2021, 7, 362-367.	1.3	20
57	DNAm-based signatures of accelerated aging and mortality in blood are associated with low renal function. <i>Clinical Epigenetics</i> , 2021, 13, 121.	1.8	13
58	DNA-methylation-based telomere length estimator: comparisons with measurements from flow FISH and qPCR. <i>Aging</i> , 2021, 13, 14675-14686.	1.4	11
59	An Analysis of Methylome Evolution in Primates. <i>Molecular Biology and Evolution</i> , 2021, 38, 4700-4714.	3.5	2
60	Castration delays epigenetic aging and feminizes DNA methylation at androgen-regulated loci. <i>ELife</i> , 2021, 10, .	2.8	45
61	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. <i>Environmental Research</i> , 2021, 198, 111211.	3.7	4
62	Accurate Epigenetic Aging in Bottlenose Dolphins (<i>Tursiops truncatus</i>), an Essential Step in the Conservation of at-Risk Dolphins. <i>Journal of Zoological and Botanical Gardens</i> , 2021, 2, 416-420.	1.0	8
63	Epigenetic clock and methylation studies in cats. <i>GeroScience</i> , 2021, 43, 2363-2378.	2.1	26
64	Towards epigenomic and metabolomic profiles of chronic organophosphate exposure in residents of California's Central Valley. <i>ISEE Conference Abstracts</i> , 2021, 2021, .	0.0	0
65	Pesticide Exposure, Systems Biology, and Parkinson's disease. <i>ISEE Conference Abstracts</i> , 2021, 2021, .	0.0	0
66	Increased Menopausal Age Reduces the Risk of Parkinson's Disease: A Mendelian Randomization Approach. <i>Movement Disorders</i> , 2021, 36, 2264-2272.	2.2	28
67	Age-dependent instability of mature neuronal fate in induced neurons from Alzheimer's patients. <i>Cell Stem Cell</i> , 2021, 28, 1533-1548.e6.	5.2	119
68	Epigenetic clock and DNA methylation analysis of porcine models of aging and obesity. <i>GeroScience</i> , 2021, 43, 2467-2483.	2.1	27
69	Transposon-triggered innate immune response confers cancer resistance to the blind mole rat. <i>Nature Immunology</i> , 2021, 22, 1219-1230.	7.0	45
70	Epigenetic clock and methylation studies in the rhesus macaque. <i>GeroScience</i> , 2021, 43, 2441-2453.	2.1	28
71	Multi-Tissue Methylation Clocks for Age and Sex Estimation in the Common Bottlenose Dolphin. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	8
72	Accelerated hematopoietic mitotic aging measured by DNA methylation, blood cell lineage, and Parkinson's disease. <i>BMC Genomics</i> , 2021, 22, 696.	1.2	14

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73	Epigenetic Age and the Risk of Incident Atrial Fibrillation. <i>Circulation</i> , 2021, 144, 1899-1911.	1.6	35
74	DNA methylation age analysis of rapamycin in common marmosets. <i>GeroScience</i> , 2021, 43, 2413-2425.	2.1	26
75	Epigenetic Age Acceleration Reflects Long-Term Cardiovascular Health. <i>Circulation Research</i> , 2021, 129, 770-781.	2.0	55
76	Sex hormones and Alzheimer's disease: A Mendelian randomization approach. <i>Journal of the Neurological Sciences</i> , 2021, 429, 118981.	0.3	0
77	Host methylation predicts SARS-CoV-2 infection and clinical outcome. <i>Communications Medicine</i> , 2021, 1, 42.	1.9	35
78	DNA methylation-based surrogates of plasma proteins are associated with Parkinson's disease risk. <i>Journal of the Neurological Sciences</i> , 2021, 431, 120046.	0.3	3
79	Epigenetic models developed for plains zebras predict age in domestic horses and endangered equids. <i>Communications Biology</i> , 2021, 4, 1412.	2.0	23
80	Increased Rate of Epigenetic Aging in Men Living With HIV Prior to Treatment. <i>Frontiers in Genetics</i> , 2021, 12, 796547.	1.1	9
81	Associations between DNA methylation and BMI vary by metabolic health status: a potential link to disparate cardiovascular outcomes. <i>Clinical Epigenetics</i> , 2021, 13, 230.	1.8	11
82	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. <i>Nature Communications</i> , 2021, 12, 7173.	5.8	8
83	Meta-analyses identify DNA methylation associated with kidney function and damage. <i>Nature Communications</i> , 2021, 12, 7174.	5.8	30
84	Epigenetic aging is accelerated in alcohol use disorder and regulated by genetic variation in APOL2. <i>Neuropsychopharmacology</i> , 2020, 45, 327-336.	2.8	62
85	The PedBE clock accurately estimates DNA methylation age in pediatric buccal cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 23329-23335.	3.3	140
86	Leukocyte Traits and Exposure to Ambient Particulate Matter Air Pollution in the Women's Health Initiative and Atherosclerosis Risk in Communities Study. <i>Environmental Health Perspectives</i> , 2020, 128, 17004.	2.8	17
87	DNA Methylation Analysis Validates Organoids as a Viable Model for Studying Human Intestinal Aging. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2020, 9, 527-541.	2.3	53
88	Psychosocial stress and epigenetic aging. <i>International Review of Neurobiology</i> , 2020, 150, 107-128.	0.9	53
89	Coagulation factor VIII: Relationship to cardiovascular disease risk and whole genome sequence and epigenome-wide analysis in African Americans. <i>Journal of Thrombosis and Haemostasis</i> , 2020, 18, 1335-1347.	1.9	17
90	Accelerated epigenetic aging in adolescents from low-income households is associated with altered development of brain structures. <i>Metabolic Brain Disease</i> , 2020, 35, 1287-1298.	1.4	17

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91	An epigenome-wide association study of ambient pyrethroid pesticide exposures in California's central valley. <i>International Journal of Hygiene and Environmental Health</i> , 2020, 229, 113569.	2.1	17
92	Reprogramming to recover youthful epigenetic information and restore vision. <i>Nature</i> , 2020, 588, 124-129.	13.7	424
93	Analysis of epigenetic aging <i>in vivo</i> and <i>in vitro</i> : Factors controlling the speed and direction. <i>Experimental Biology and Medicine</i> , 2020, 245, 1543-1551.	1.1	7
94	Epigenetic age and pregnancy outcomes: GrimAge acceleration is associated with shorter gestational length and lower birthweight. <i>Clinical Epigenetics</i> , 2020, 12, 120.	1.8	32
95	Epigenetic measures of ageing predict the prevalence and incidence of leading causes of death and disease burden. <i>Clinical Epigenetics</i> , 2020, 12, 115.	1.8	109
96	DNA methylation study of Huntington's disease and motor progression in patients and in animal models. <i>Nature Communications</i> , 2020, 11, 4529.	5.8	45
97	A candidate gene study of intermediate histopathological phenotypes in HIV-associated neurocognitive disorders. <i>Journal of NeuroVirology</i> , 2020, 26, 496-508.	1.0	1
98	The acute effects of adjuvant radiation and chemotherapy on peripheral blood epigenetic age in early stage breast cancer patients. <i>Npj Breast Cancer</i> , 2020, 6, 23.	2.3	37
99	Analysis of DNA methylation associates the cystine-glutamate antiporter SLC7A11 with risk of Parkinson's disease. <i>Nature Communications</i> , 2020, 11, 1238.	5.8	85
100	Transient non-integrative expression of nuclear reprogramming factors promotes multifaceted amelioration of aging in human cells. <i>Nature Communications</i> , 2020, 11, 1545.	5.8	183
101	Estimating breast tissue-specific DNA methylation age using next-generation sequencing data. <i>Clinical Epigenetics</i> , 2020, 12, 45.	1.8	15
102	Current perspectives on the cellular and molecular features of epigenetic ageing. <i>Experimental Biology and Medicine</i> , 2020, 245, 1532-1542.	1.1	44
103	An epigenetic clock for human skeletal muscle. <i>Journal of Cachexia, Sarcopenia and Muscle</i> , 2020, 11, 887-898.	2.9	70
104	DNA Methylation Age Is More Closely Associated With Infection Risk Than Chronological Age in Kidney Transplant Recipients. <i>Transplantation Direct</i> , 2020, 6, e576.	0.8	9
105	Blood DNA methylation sites predict death risk in a longitudinal study of 12, 300 individuals. <i>Aging</i> , 2020, 12, 14092-14124.	1.4	15
106	Epigenetic mutation load is weakly correlated with epigenetic age acceleration. <i>Aging</i> , 2020, 12, 17863-17894.	1.4	12
107	ARDD 2020: from aging mechanisms to interventions. <i>Aging</i> , 2020, 12, 24484-24503.	1.4	32
108	The Effects of Anti-retroviral Therapy on Epigenetic Age Acceleration Observed in HIV-1-infected Adults. <i>Pathogens and Immunity</i> , 2020, 5, 291.	1.4	22

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109	Breast cancer treatment and its effects on aging. <i>Journal of Geriatric Oncology</i> , 2019, 10, 346-355.	0.5	51
110	Reversal of epigenetic aging and immunosenescent trends in humans. <i>Aging Cell</i> , 2019, 18, e13028.	3.0	335
111	Epigenetic age acceleration and metabolic syndrome in the coronary artery risk development in young adults study. <i>Clinical Epigenetics</i> , 2019, 11, 160.	1.8	48
112	Rapamycin retards epigenetic ageing of keratinocytes independently of its effects on replicative senescence, proliferation and differentiation. <i>Aging</i> , 2019, 11, 3238-3249.	1.4	39
113	Optimism is not associated with two indicators of DNA methylation aging. <i>Aging</i> , 2019, 11, 4970-4989.	1.4	6
114	DNA methylation patterns of adult survivors of adolescent/young adult Hodgkin lymphoma compared to their unaffected monozygotic twin. <i>Leukemia and Lymphoma</i> , 2019, 60, 1429-1437.	0.6	11
115	Methylome-wide association study provides evidence of particulate matter air pollution-associated DNA methylation. <i>Environment International</i> , 2019, 132, 104723.	4.8	58
116	Human aging DNA methylation signatures are conserved but accelerated in cultured fibroblasts. <i>Epigenetics</i> , 2019, 14, 961-976.	1.3	36
117	DNA methylation GrimAge strongly predicts lifespan and healthspan. <i>Aging</i> , 2019, 11, 303-327.	1.4	1,128
118	Synchrony and asynchrony between an epigenetic clock and developmental timing. <i>Scientific Reports</i> , 2019, 9, 3770.	1.6	37
119	Longitudinal Epigenome-Wide Methylation Study of Cognitive Decline and Motor Progression in Parkinson's Disease. <i>Journal of Parkinson's Disease</i> , 2019, 9, 389-400.	1.5	37
120	The role of epigenetic aging in education and racial/ethnic mortality disparities among older U.S. Women. <i>Psychoneuroendocrinology</i> , 2019, 104, 18-24.	1.3	47
121	EPIGENETIC PREDICTORS OF LIFESPAN AND HEALTHSPAN. <i>Innovation in Aging</i> , 2019, 3, S33-S33.	0.0	0
122	A meta-analysis of genome-wide association studies of epigenetic age acceleration. <i>PLoS Genetics</i> , 2019, 15, e1008104.	1.5	83
123	DNA methylation aging clocks: challenges and recommendations. <i>Genome Biology</i> , 2019, 20, 249.	3.8	552
124	Tracking the Epigenetic Clock Across the Human Life Course: A Meta-analysis of Longitudinal Cohort Data. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2019, 74, 57-61.	1.7	81
125	Epigenetic age is a cell-intrinsic property in transplanted human hematopoietic cells. <i>Aging Cell</i> , 2019, 18, e12897.	3.0	39
126	Epigenetic clock analysis of human fibroblasts in vitro: effects of hypoxia, donor age, and expression of hTERT and SV40 largeT. <i>Aging</i> , 2019, 11, 3012-3022.	1.4	20

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127	Placental epigenetic clocks: estimating gestational age using placental DNA methylation levels. <i>Aging</i> , 2019, 11, 4238-4253.	1.4	79
128	DNA methylation-based estimator of telomere length. <i>Aging</i> , 2019, 11, 5895-5923.	1.4	198
129	Epigenome-wide association study of leukocyte telomere length. <i>Aging</i> , 2019, 11, 5876-5894.	1.4	19
130	DNA methylation-based biomarkers and the epigenetic clock theory of ageing. <i>Nature Reviews Genetics</i> , 2018, 19, 371-384.	7.7	1,741
131	CWAS of epigenetic aging rates in blood reveals a critical role for TERT. <i>Nature Communications</i> , 2018, 9, 387.	5.8	151
132	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. <i>Science</i> , 2018, 359, 693-697.	6.0	851
133	Faster ticking rate of the epigenetic clock is associated with faster pubertal development in girls. <i>Epigenetics</i> , 2018, 13, 85-94.	1.3	86
134	An epigenetic biomarker of aging for lifespan and healthspan. <i>Aging</i> , 2018, 10, 573-591.	1.4	1,552
135	A new aging measure captures morbidity and mortality risk across diverse subpopulations from NHANES IV: A cohort study. <i>PLoS Medicine</i> , 2018, 15, e1002718.	3.9	210
136	Systematic evaluation of DNA methylation age estimation with common preprocessing methods and the Infinium MethylationEPIC BeadChip array. <i>Clinical Epigenetics</i> , 2018, 10, 123.	1.8	111
137	DNA methylation age is accelerated in alcohol dependence. <i>Translational Psychiatry</i> , 2018, 8, 182.	2.4	73
138	Increased epigenetic age in normal breast tissue from luminal breast cancer patients. <i>Clinical Epigenetics</i> , 2018, 10, 112.	1.8	40
139	Inflammation-Related Genes are Associated with Accelerated Aging in HIV. <i>American Journal of Geriatric Psychiatry</i> , 2018, 26, S118-S119.	0.6	3
140	Genetic and epigenetic changes in clonal descendants of irradiated human fibroblasts. <i>Experimental Cell Research</i> , 2018, 370, 322-332.	1.2	19
141	Organophosphate pesticide exposure and differential genome-wide DNA methylation. <i>Science of the Total Environment</i> , 2018, 645, 1135-1143.	3.9	56
142	Metabolic and inflammatory biomarkers are associated with epigenetic aging acceleration estimates in the GOLDN study. <i>Clinical Epigenetics</i> , 2018, 10, 56.	1.8	68
143	No reliable gene expression biomarkers of current or impending neurocognitive impairment in peripheral blood monocytes of persons living with HIV. <i>Journal of NeuroVirology</i> , 2018, 24, 350-361.	1.0	7
144	Perinatally acquired HIV infection accelerates epigenetic aging in South African adolescents. <i>Aids</i> , 2018, 32, 1465-1474.	1.0	81

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145	Intraindividual variability in neurocognitive performance: No influence due to HIV status or self-reported effort. <i>Journal of Clinical and Experimental Neuropsychology</i> , 2018, 40, 1044-1049.	0.8	3
146	MicroRNA signatures of endogenous Huntingtin CAG repeat expansion in mice. <i>PLoS ONE</i> , 2018, 13, e0190550.	1.1	39
147	Epigenetic clock for skin and blood cells applied to Hutchinson Gilford Progeria Syndrome and ex vivo studies. <i>Aging</i> , 2018, 10, 1758-1775.	1.4	406
148	Epigenetic ageing is distinct from senescence-mediated ageing and is not prevented by telomerase expression. <i>Aging</i> , 2018, 10, 2800-2815.	1.4	70
149	A multi-tissue full lifespan epigenetic clock for mice. <i>Aging</i> , 2018, 10, 2832-2854.	1.4	166
150	Cell and tissue type independent age-associated DNA methylation changes are not rare but common. <i>Aging</i> , 2018, 10, 3541-3557.	1.4	42
151	A High-throughput Targeted Bisulfite Sequencing-based Analysis for Epigenetic Age Quantification and Monitoring. <i>FASEB Journal</i> , 2018, 32, 674.8.	0.2	3
152	The epigenetic clock and physical development during childhood and adolescence: longitudinal analysis from a UK birth cohort. <i>International Journal of Epidemiology</i> , 2017, 46, dyw307.	0.9	86
153	DNA methylome analysis identifies accelerated epigenetic ageing associated with postmenopausal breast cancer susceptibility. <i>European Journal of Cancer</i> , 2017, 75, 299-307.	1.3	154
154	Coffee consumption is associated with DNA methylation levels of human blood. <i>European Journal of Human Genetics</i> , 2017, 25, 608-616.	1.4	31
155	Genetic architecture of epigenetic and neuronal ageing rates in human brain regions. <i>Nature Communications</i> , 2017, 8, 15353.	5.8	92
156	Dynamics of epigenetic age following hematopoietic stem cell transplantation. <i>Haematologica</i> , 2017, 102, e321-e323.	1.7	34
157	DNA methylation age is elevated in breast tissue of healthy women. <i>Breast Cancer Research and Treatment</i> , 2017, 164, 209-219.	1.1	52
158	A Weighted SNP Correlation Network Method for Estimating Polygenic Risk Scores. <i>Methods in Molecular Biology</i> , 2017, 1613, 277-290.	0.4	18
159	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , 2017, 101, 888-902.	2.6	154
160	Epigenetic Aging and Immune Senescence in Women With Insomnia Symptoms: Findings From the Women's Health Initiative Study. <i>Biological Psychiatry</i> , 2017, 81, 136-144.	0.7	108
161	DNA Methylation Profiling of Human Prefrontal Cortex Neurons in Heroin Users Shows Significant Difference between Genomic Contexts of Hyper- and Hypomethylation and a Younger Epigenetic Age. <i>Genes</i> , 2017, 8, 152.	1.0	66
162	Exosomes and Homeostatic Synaptic Plasticity Are Linked to Each other and to Huntington's, Parkinson's, and Other Neurodegenerative Diseases by Database-Enabled Analyses of Comprehensively Curated Datasets. <i>Frontiers in Neuroscience</i> , 2017, 11, 149.	1.4	50

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163	Neuropathological and transcriptomic characteristics of the aged brain. <i>ELife</i> , 2017, 6, .	2.8	97
164	Parkinson's disease is associated with DNA methylation levels in human blood and saliva. <i>Genome Medicine</i> , 2017, 9, 76.	3.6	122
165	Epigenetic clock analysis of diet, exercise, education, and lifestyle factors. <i>Aging</i> , 2017, 9, 419-446.	1.4	521
166	Accelerated epigenetic aging in Werner syndrome. <i>Aging</i> , 2017, 9, 1143-1152.	1.4	152
167	Longitudinal study of surrogate aging measures during human immunodeficiency virus seroconversion. <i>Aging</i> , 2017, 9, 687-705.	1.4	31
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