

Steve Horvath

List of Publications by Year in descending order

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Version: 2024-02-01

321
papers

83,301
citations

1614
105
h-index

540
265
g-index

386
all docs

386
docs citations

386
times ranked

77066
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.	1.3	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.	2.1	11
3	Higher diet quality relates to decelerated epigenetic aging. <i>American Journal of Clinical Nutrition</i> , 2022, 115, 163-170.	4.7	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.	3.6	13
5	Epigenetic clock and methylation studies in vervet monkeys. <i>GeroScience</i> , 2022, 44, 699-717.	4.6	18
6	Methylation studies in <i>Peromyscus</i> : aging, altitude adaptation, and monogamy. <i>GeroScience</i> , 2022, 44, 447-461.	4.6	4
7	DNA methylation as a tool to explore ageing in wild roe deer populations. <i>Molecular Ecology Resources</i> , 2022, 22, 1002-1015.	4.8	19
8	Stochastic Epigenetic Mutations Influence Parkinson's Disease Risk, Progression, and Mortality. <i>Journal of Parkinson's Disease</i> , 2022, 12, 545-556.	2.8	5
9	Epigenetic aging of the demographically non-aging naked mole-rat. <i>Nature Communications</i> , 2022, 13, 355.	12.8	26
10	DNA methylation aging and transcriptomic studies in horses. <i>Nature Communications</i> , 2022, 13, 40.	12.8	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.	4.1	9
12	DNA methylation signatures in Blood DNA of Hutchinson's Gilford Progeria syndrome. <i>Aging Cell</i> , 2022, 21, e13555.	6.7	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.	8.1	30
14	A mammalian methylation array for profiling methylation levels at conserved sequences. <i>Nature Communications</i> , 2022, 13, 783.	12.8	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.	11.6	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.	0.9	0
17	Assessing the causal role of epigenetic clocks in the development of multiple cancers: a Mendelian randomization study. <i>ELife</i> , 2022, 11, .	6.0	19
18	Hibernation slows epigenetic ageing in yellow-bellied marmots. <i>Nature Ecology and Evolution</i> , 2022, 6, 418-426.	7.8	23

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19	Erratum to “Increased Menopausal Age Reduces the Risk of Parkinson's Disease: A Mendelian Approach” Movement Disorders, 2022, 37, 1282-1283.	3.9	1
20	In vivo partial reprogramming alters age-associated molecular changes during physiological aging in mice. Nature Aging, 2022, 2, 243-253.	11.6	101
21	Genetic loci and metabolic states associated with murine epigenetic aging. ELife, 2022, 11, .	6.0	26
22	Association of subjective social status with epigenetic aging among Black and White women. Psychoneuroendocrinology, 2022, 141, 105748.	2.7	9
23	Development of Epigenetic Clocks for Key Ruminant Species. Genes, 2022, 13, 96.	2.4	12
24	Epigenetic Clocks. , 2022, , 261-276.		2
25	The impact of reproductive factors on DNA methylation-based telomere length in healthy breast tissue. Npj Breast Cancer, 2022, 8, 48.	5.2	3
26	HIV, pathology and epigenetic age acceleration in different human tissues. GeroScience, 2022, 44, 1609-1620.	4.6	15
27	Epigenetic clock and methylation studies in marsupials: opossums, Tasmanian devils, kangaroos, and wallabies. GeroScience, 2022, 44, 1825-1845.	4.6	12
28	Making sense of the ageing methylome. Nature Reviews Genetics, 2022, 23, 585-605.	16.3	86
29	The relationship between epigenetic age and the hallmarks of aging in human cells. Nature Aging, 2022, 2, 484-493.	11.6	51
30	DNA methylation clocks for dogs and humans. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2120887119.	7.1	26
31	Telomere length and epigenetic clocks as markers of cellular aging: a comparative study. GeroScience, 2022, 44, 1861-1869.	4.6	18
32	Accelerated epigenetic aging in newborns with Down syndrome. Aging Cell, 2022, 21, .	6.7	17
33	Alcohol use disorder is associated with DNA methylation-based shortening of telomere length and regulated by TESPA1: implications for aging. Molecular Psychiatry, 2022, 27, 3875-3884.	7.9	7
34	DNA methylation profile in beef cattle is influenced by additive genetics and age. Scientific Reports, 2022, 12, .	3.3	7
35	Accelerated aging with HIV occurs at the time of initial HIV infection. IScience, 2022, 25, 104488.	4.1	22
36	An epigenetic predictor of death captures multi-modal measures of brain health. Molecular Psychiatry, 2021, 26, 3806-3816.	7.9	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.	3.6	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.	1.9	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.	4.0	19
40	Early life adversity, pubertal timing, and epigenetic age acceleration in adulthood. <i>Developmental Psychobiology</i> , 2021, 63, 890-902.	1.6	42
41	Long-term maturation of human cortical organoids matches key early postnatal transitions. <i>Nature Neuroscience</i> , 2021, 24, 331-342.	14.8	188
42	An epigenetic clock to estimate the age of living beluga whales. <i>Evolutionary Applications</i> , 2021, 14, 1263-1273.	3.1	32
43	DNA methylation predicts age and provides insight into exceptional longevity of bats. <i>Nature Communications</i> , 2021, 12, 1615.	12.8	80
44	DNA methylation biomarker for cumulative lead exposure is associated with Parkinson's disease. <i>Clinical Epigenetics</i> , 2021, 13, 59.	4.1	13
45	The Effects of Lifetime Estrogen Exposure on Breast Epigenetic Age. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021, 30, 1241-1249.	2.5	7
46	Epigenome-wide association study of kidney function identifies trans-ethnic and ethnic-specific loci. <i>Genome Medicine</i> , 2021, 13, 74.	8.2	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.	1.2	8
48	Incorporation of a nucleoside analog maps genome repair sites in postmitotic human neurons. <i>Science</i> , 2021, 372, 91-94.	12.6	68
49	Epigenetic clock and methylation study of oocytes from a bovine model of reproductive aging. <i>Aging Cell</i> , 2021, 20, e13349.	6.7	25
50	Multi-species and multi-tissue methylation clocks for age estimation in toothed whales and dolphins. <i>Communications Biology</i> , 2021, 4, 642.	4.4	39
51	Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. <i>Aging Cell</i> , 2021, 20, e13366.	6.7	72
52	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021, 22, 194.	8.8	90
53	Epigenetic clock and methylation studies in elephants. <i>Aging Cell</i> , 2021, 20, e13414.	6.7	43
54	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. <i>Nature Communications</i> , 2021, 12, 3987.	12.8	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.	7.3	37
56	Postpartum sleep loss and accelerated epigenetic aging. <i>Sleep Health</i> , 2021, 7, 362-367.	2.5	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.	4.1	13
58	DNA-methylation-based telomere length estimator: comparisons with measurements from flow FISH and qPCR. <i>Aging</i> , 2021, 13, 14675-14686.	3.1	11
59	An Analysis of Methylome Evolution in Primates. <i>Molecular Biology and Evolution</i> , 2021, 38, 4700-4714.	8.9	2
60	Castration delays epigenetic aging and feminizes DNA methylation at androgen-regulated loci. <i>ELife</i> , 2021, 10, .	6.0	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.	7.5	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.	1.8	8
63	Epigenetic clock and methylation studies in cats. <i>GeroScience</i> , 2021, 43, 2363-2378.	4.6	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.	3.9	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.	11.1	119
68	Epigenetic clock and DNA methylation analysis of porcine models of aging and obesity. <i>GeroScience</i> , 2021, 43, 2467-2483.	4.6	27
69	Transposon-triggered innate immune response confers cancer resistance to the blind mole rat. <i>Nature Immunology</i> , 2021, 22, 1219-1230.	14.5	45
70	Epigenetic clock and methylation studies in the rhesus macaque. <i>GeroScience</i> , 2021, 43, 2441-2453.	4.6	28
71	Multi-Tissue Methylation Clocks for Age and Sex Estimation in the Common Bottlenose Dolphin. <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	8
72	Accelerated hematopoietic mitotic aging measured by DNA methylation, blood cell lineage, and Parkinson's disease. <i>BMC Genomics</i> , 2021, 22, 696.	2.8	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.	4.6	26
75	Epigenetic Age Acceleration Reflects Long-Term Cardiovascular Health. <i>Circulation Research</i> , 2021, 129, 770-781.	4.5	55
76	Sex hormones and Alzheimer's disease: A Mendelian randomization approach. <i>Journal of the Neurological Sciences</i> , 2021, 429, 118981.	0.6	0
77	Host methylation predicts SARS-CoV-2 infection and clinical outcome. <i>Communications Medicine</i> , 2021, 1, 42.	4.2	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.	0.6	3
79	Epigenetic models developed for plains zebras predict age in domestic horses and endangered equids. <i>Communications Biology</i> , 2021, 4, 1412.	4.4	23
80	Increased Rate of Epigenetic Aging in Men Living With HIV Prior to Treatment. <i>Frontiers in Genetics</i> , 2021, 12, 796547.	2.3	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.	4.1	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.	12.8	8
83	Meta-analyses identify DNA methylation associated with kidney function and damage. <i>Nature Communications</i> , 2021, 12, 7174.	12.8	30
84	Epigenetic aging is accelerated in alcohol use disorder and regulated by genetic variation in APOL2. <i>Neuropsychopharmacology</i> , 2020, 45, 327-336.	5.4	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.	7.1	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.	6.0	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.	4.5	53
88	Psychosocial stress and epigenetic aging. <i>International Review of Neurobiology</i> , 2020, 150, 107-128.	2.0	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.	3.8	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.	2.9	17

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91	An epigenome-wide association study of ambient pyrethroid pesticide exposures in California's central valley. International Journal of Hygiene and Environmental Health, 2020, 229, 113569.	4.3	17
92	Reprogramming to recover youthful epigenetic information and restore vision. Nature, 2020, 588, 124-129.	27.8	424
93	Analysis of epigenetic aging <i>in vivo</i> and <i>in vitro</i> : Factors controlling the speed and direction. Experimental Biology and Medicine, 2020, 245, 1543-1551.	2.4	7
94	Epigenetic age and pregnancy outcomes: GrimAge acceleration is associated with shorter gestational length and lower birthweight. Clinical Epigenetics, 2020, 12, 120.	4.1	32
95	Epigenetic measures of ageing predict the prevalence and incidence of leading causes of death and disease burden. Clinical Epigenetics, 2020, 12, 115.	4.1	109
96	DNA methylation study of Huntington's disease and motor progression in patients and in animal models. Nature Communications, 2020, 11, 4529.	12.8	45
97	A candidate gene study of intermediate histopathological phenotypes in HIV-associated neurocognitive disorders. Journal of NeuroVirology, 2020, 26, 496-508.	2.1	1
98	The acute effects of adjuvant radiation and chemotherapy on peripheral blood epigenetic age in early stage breast cancer patients. Npj Breast Cancer, 2020, 6, 23.	5.2	37
99	Analysis of DNA methylation associates the cystine-glutamate antiporter SLC7A11 with risk of Parkinson's disease. Nature Communications, 2020, 11, 1238.	12.8	85
100	Transient non-integrative expression of nuclear reprogramming factors promotes multifaceted amelioration of aging in human cells. Nature Communications, 2020, 11, 1545.	12.8	183
101	Estimating breast tissue-specific DNA methylation age using next-generation sequencing data. Clinical Epigenetics, 2020, 12, 45.	4.1	15
102	Current perspectives on the cellular and molecular features of epigenetic ageing. Experimental Biology and Medicine, 2020, 245, 1532-1542.	2.4	44
103	An epigenetic clock for human skeletal muscle. Journal of Cachexia, Sarcopenia and Muscle, 2020, 11, 887-898.	7.3	70
104	DNA Methylation Age Is More Closely Associated With Infection Risk Than Chronological Age in Kidney Transplant Recipients. Transplantation Direct, 2020, 6, e576.	1.6	9
105	Blood DNA methylation sites predict death risk in a longitudinal study of 12, 300 individuals. Aging, 2020, 12, 14092-14124.	3.1	15
106	Epigenetic mutation load is weakly correlated with epigenetic age acceleration. Aging, 2020, 12, 17863-17894.	3.1	12
107	ARDD 2020: from aging mechanisms to interventions. Aging, 2020, 12, 24484-24503.	3.1	32
108	The Effects of Anti-retroviral Therapy on Epigenetic Age Acceleration Observed in HIV-1-infected Adults. Pathogens and Immunity, 2020, 5, 291.	3.1	22

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109	Breast cancer treatment and its effects on aging. <i>Journal of Geriatric Oncology</i> , 2019, 10, 346-355.	1.0	51
110	Reversal of epigenetic aging and immunosenescent trends in humans. <i>Aging Cell</i> , 2019, 18, e13028.	6.7	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.	4.1	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.	3.1	39
113	Optimism is not associated with two indicators of DNA methylation aging. <i>Aging</i> , 2019, 11, 4970-4989.	3.1	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.	1.3	11
115	Methylome-wide association study provides evidence of particulate matter air pollution-associated DNA methylation. <i>Environment International</i> , 2019, 132, 104723.	10.0	58
116	Human aging DNA methylation signatures are conserved but accelerated in cultured fibroblasts. <i>Epigenetics</i> , 2019, 14, 961-976.	2.7	36
117	DNA methylation GrimAge strongly predicts lifespan and healthspan. <i>Aging</i> , 2019, 11, 303-327.	3.1	1,128
118	Synchrony and asynchrony between an epigenetic clock and developmental timing. <i>Scientific Reports</i> , 2019, 9, 3770.	3.3	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.	2.8	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.	2.7	47
121	EPIGENETIC PREDICTORS OF LIFESPAN AND HEALTHSPAN. <i>Innovation in Aging</i> , 2019, 3, S33-S33.	0.1	0
122	A meta-analysis of genome-wide association studies of epigenetic age acceleration. <i>PLoS Genetics</i> , 2019, 15, e1008104.	3.5	83
123	DNA methylation aging clocks: challenges and recommendations. <i>Genome Biology</i> , 2019, 20, 249.	8.8	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.	3.6	81
125	Epigenetic age is a cell-intrinsic property in transplanted human hematopoietic cells. <i>Aging Cell</i> , 2019, 18, e12897.	6.7	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.	3.1	20

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127	Placental epigenetic clocks: estimating gestational age using placental DNA methylation levels. <i>Aging</i> , 2019, 11, 4238-4253.	3.1	79
128	DNA methylation-based estimator of telomere length. <i>Aging</i> , 2019, 11, 5895-5923.	3.1	198
129	Epigenome-wide association study of leukocyte telomere length. <i>Aging</i> , 2019, 11, 5876-5894.	3.1	19
130	DNA methylation-based biomarkers and the epigenetic clock theory of ageing. <i>Nature Reviews Genetics</i> , 2018, 19, 371-384.	16.3	1,741
131	CWAS of epigenetic aging rates in blood reveals a critical role for TERT. <i>Nature Communications</i> , 2018, 9, 387.	12.8	151
132	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. <i>Science</i> , 2018, 359, 693-697.	12.6	851
133	Faster ticking rate of the epigenetic clock is associated with faster pubertal development in girls. <i>Epigenetics</i> , 2018, 13, 85-94.	2.7	86
134	An epigenetic biomarker of aging for lifespan and healthspan. <i>Aging</i> , 2018, 10, 573-591.	3.1	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.	8.4	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.	4.1	111
137	DNA methylation age is accelerated in alcohol dependence. <i>Translational Psychiatry</i> , 2018, 8, 182.	4.8	73
138	Increased epigenetic age in normal breast tissue from luminal breast cancer patients. <i>Clinical Epigenetics</i> , 2018, 10, 112.	4.1	40
139	Inflammation-Related Genes are Associated with Accelerated Aging in HIV. <i>American Journal of Geriatric Psychiatry</i> , 2018, 26, S118-S119.	1.2	3
140	Genetic and epigenetic changes in clonal descendants of irradiated human fibroblasts. <i>Experimental Cell Research</i> , 2018, 370, 322-332.	2.6	19
141	Organophosphate pesticide exposure and differential genome-wide DNA methylation. <i>Science of the Total Environment</i> , 2018, 645, 1135-1143.	8.0	56
142	Metabolic and inflammatory biomarkers are associated with epigenetic aging acceleration estimates in the GOLDN study. <i>Clinical Epigenetics</i> , 2018, 10, 56.	4.1	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.	2.1	7
144	Perinatally acquired HIV infection accelerates epigenetic aging in South African adolescents. <i>Aids</i> , 2018, 32, 1465-1474.	2.2	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.	1.3	3
146	MicroRNA signatures of endogenous Huntingtin CAG repeat expansion in mice. <i>PLoS ONE</i> , 2018, 13, e0190550.	2.5	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.	3.1	406
148	Epigenetic ageing is distinct from senescence-mediated ageing and is not prevented by telomerase expression. <i>Aging</i> , 2018, 10, 2800-2815.	3.1	70
149	A multi-tissue full lifespan epigenetic clock for mice. <i>Aging</i> , 2018, 10, 2832-2854.	3.1	166
150	Cell and tissue type independent age-associated DNA methylation changes are not rare but common. <i>Aging</i> , 2018, 10, 3541-3557.	3.1	42
151	A High-throughput Targeted Bisulfite Sequencing-based Analysis for Epigenetic Age Quantification and Monitoring. <i>FASEB Journal</i> , 2018, 32, 674.8.	0.5	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.	1.9	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.	2.8	154
154	Coffee consumption is associated with DNA methylation levels of human blood. <i>European Journal of Human Genetics</i> , 2017, 25, 608-616.	2.8	31
155	Genetic architecture of epigenetic and neuronal ageing rates in human brain regions. <i>Nature Communications</i> , 2017, 8, 15353.	12.8	92
156	Dynamics of epigenetic age following hematopoietic stem cell transplantation. <i>Haematologica</i> , 2017, 102, e321-e323.	3.5	34
157	DNA methylation age is elevated in breast tissue of healthy women. <i>Breast Cancer Research and Treatment</i> , 2017, 164, 209-219.	2.5	52
158	A Weighted SNP Correlation Network Method for Estimating Polygenic Risk Scores. <i>Methods in Molecular Biology</i> , 2017, 1613, 277-290.	0.9	18
159	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , 2017, 101, 888-902.	6.2	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.	1.3	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.	2.4	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.	2.8	50

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163	Neuropathological and transcriptomic characteristics of the aged brain. <i>ELife</i> , 2017, 6, .	6.0	97
164	Parkinson's disease is associated with DNA methylation levels in human blood and saliva. <i>Genome Medicine</i> , 2017, 9, 76.	8.2	122
165	Epigenetic clock analysis of diet, exercise, education, and lifestyle factors. <i>Aging</i> , 2017, 9, 419-446.	3.1	521
166	Accelerated epigenetic aging in Werner syndrome. <i>Aging</i> , 2017, 9, 1143-1152.	3.1	152
167	Longitudinal study of surrogate aging measures during human immunodeficiency virus seroconversion. <i>Aging</i> , 2017, 9, 687-705.	3.1	31
168	An epigenetic aging clock for dogs and wolves. <i>Aging</i> , 2017, 9, 1055-1068.	3.1	125
169	Leukocyte telomere length, T cell composition and DNA methylation age. <i>Aging</i> , 2017, 9, 1983-1995.	3.1	42
170	Huntington's disease accelerates epigenetic aging of human brain and disrupts DNA methylation levels. <i>Aging</i> , 2016, 8, 1485-1512.	3.1	192
171	Maintenance of age in human neurons generated by microRNA-based neuronal conversion of fibroblasts. <i>ELife</i> , 2016, 5, .	6.0	159
172	Epigenetic clock analyses of cellular senescence and ageing. <i>Oncotarget</i> , 2016, 7, 8524-8531.	1.8	125
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