Ake T Lu

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

52	3,977 citations	22	59
papers		h-index	g-index
59	6,104 ext. citations	9.9	5.25
ext. papers		avg, IF	L-index

#	Paper Paper	IF	Citations
52	An epigenetic biomarker of aging for lifespan and healthspan. <i>Aging</i> , 2018 , 10, 573-591	5.6	658
51	DNA methylation-based measures of biological age: meta-analysis predicting time to death. <i>Aging</i> , 2016 , 8, 1844-1865	5.6	531
50	DNA methylation GrimAge strongly predicts lifespan and healthspan. <i>Aging</i> , 2019 , 11, 303-327	5.6	424
49	An epigenetic clock analysis of race/ethnicity, sex, and coronary heart disease. <i>Genome Biology</i> , 2016 , 17, 171	18.3	357
48	Epigenetic clock analysis of diet, exercise, education, and lifestyle factors. <i>Aging</i> , 2017 , 9, 419-446	5.6	317
47	Epigenetic age of the pre-frontal cortex is associated with neuritic plaques, amyloid load, and Alzheimer disease related cognitive functioning. <i>Aging</i> , 2015 , 7, 1198-211	5.6	251
46	Menopause accelerates biological aging. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 9327-32	11.5	248
45	Epigenetic clock for skin and blood cells applied to Hutchinson Gilford Progeria Syndrome and studies. <i>Aging</i> , 2018 , 10, 1758-1775	5.6	187
44	The cerebellum ages slowly according to the epigenetic clock. <i>Aging</i> , 2015 , 7, 294-306	5.6	117
43	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. <i>Nature Communications</i> , 2018 , 9, 387	17.4	106
42	Association of the cannabinoid receptor gene (CNR1) with ADHD and post-traumatic stress disorder. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2008 , 147B, 1488-94	3.5	78
41	EPIGENETIC CLOCKS OF COMPUTED TOMOGRAPHY MEASURES OF FATTY ORGANS. <i>Innovation in Aging</i> , 2019 , 3, S735-S736	0.1	78
40	DNA methylation-based estimator of telomere length. <i>Aging</i> , 2019 , 11, 5895-5923	5.6	69
39	Genetic architecture of epigenetic and neuronal ageing rates in human brain regions. <i>Nature Communications</i> , 2017 , 8, 15353	17.4	57
38	Genetic variants near MLST8 and DHX57 affect the epigenetic age of the cerebellum. <i>Nature Communications</i> , 2016 , 7, 10561	17.4	55
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	6.4	45
36	A meta-analysis of genome-wide association studies of epigenetic age acceleration. <i>PLoS Genetics</i> , 2019 , 15, e1008104	6	38

(2021-2019)

Rapamycin retards epigenetic ageing of keratinocytes independently of its effects on replicative senescence, proliferation and differentiation. <i>Aging</i> , 2019 , 11, 3238-3249	5.6	32	
A mammalian methylation array for profiling methylation levels at conserved sequences		31	
Universal DNA methylation age across mammalian tissues		31	
Placental epigenetic clocks: estimating gestational age using placental DNA methylation levels. <i>Aging</i> , 2019 , 11, 4238-4253	5.6	29	
DNA methylation predicts age and provides insight into exceptional longevity of bats. <i>Nature Communications</i> , 2021 , 12, 1615	17.4	23	
Online self-report data for duchenne muscular dystrophy confirms natural history and can be used to assess for therapeutic benefits. <i>PLOS Currents</i> , 2014 , 6,		22	
Castration delays epigenetic aging and feminizes DNA methylation at androgen-regulated loci. <i>ELife</i> , 2021 , 10,	8.9	16	
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	5.3	15	
A mammalian methylation array for profiling methylation levels at conserved sequences <i>Nature Communications</i> , 2022 , 13, 783	17.4	15	
DNA methylation study of Huntington disease and motor progression in patients and in animal models. <i>Nature Communications</i> , 2020 , 11, 4529	17.4	15	
Incorporation of a nucleoside analog maps genome repair sites in postmitotic human neurons. <i>Science</i> , 2021 , 372, 91-94	33.3	14	
Multi-species and multi-tissue methylation clocks for age estimation in toothed whales and dolphins. <i>Communications Biology</i> , 2021 , 4, 642	6.7	14	
Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021 , 22, 194	18.3	14	
DNA methylation age analysis of rapamycin in common marmosets. <i>GeroScience</i> , 2021 , 43, 2413-2425	8.9	10	
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	15.4	9	
Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. <i>Aging Cell</i> , 2021 , 20, e133	3669	9	
Genome-wide association studies identify 137 loci for DNA methylation biomarkers of ageing		8	
Epigenetic Age Acceleration Reflects Long-Term Cardiovascular Health. <i>Circulation Research</i> , 2021 , 129, 770-781	15.7	7	
	A mammalian methylation array for profiling methylation levels at conserved sequences Universal DNA methylation age across mammalian tissues Placental epigenetic clocks: estimating gestational age using placental DNA methylation levels. Aging, 2019, 11, 4238-4253 DNA methylation predicts age and provides insight into exceptional longevity of bats. Nature Communications, 2021, 12, 1615 Online self-report data for duchenne muscular dystrophy confirms natural history and can be used to assess for therapeutic benefits. PLOS Currents, 2014, 6, Castration delays epigenetic aging and feminizes DNA methylation at androgen-regulated loci. ELUfe, 2021, 10. Longitudinal Epigenome-Wide Methylation Study of Cognitive Decline and Motor Progression in Parkinson's Disease. Journal of Parkinsons Disease, 2019, 9, 389-400 A mammalian methylation array for profiling methylation levels at conserved sequences Nature Communications, 2022, 13, 783 DNA methylation study of Huntington's disease and motor progression in patients and in animal models. Nature Communications, 2020, 11, 4529 Incorporation of a nucleoside analog maps genome repair sites in postmitotic human neurons. Science, 2021, 372, 91-94 Multi-species and multi-tissue methylation clocks for age estimation in toothed whales and dolphins. Communications Biology, 2021, 4, 642 Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194 DNA methylation age analysis of rapamycin in common marmosets. GeroScience, 2021, 43, 2413-2425 Coagulation factor VIII: Relationship to cardiovascular disease risk and whole genome sequence and epigenome-wide analysis in African Americans. Journal of Thrombosis and Haemostasis, 2020, 18, 1335-1347 Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. Aging Cell, 2021, 20, e13 Genome-wide association studies identify 137 loci for DNA methylation biomarkers of ageing Epigenetic Age Acceleration Reflects Long-Term Cardiovascular Health.	A mammalian methylation array for profiling methylation levels at conserved sequences Universal DNA methylation age across mammalian tissues Placental epigenetic clocks: estimating gestational age using placental DNA methylation levels. Aging, 2019, 11, 4238-4253 DNA methylation predicts age and provides insight into exceptional longevity of bats. Nature communications, 2021, 12, 1615 174 Online self-report data for duchenne muscular dystrophy confirms natural history and can be used to assess for therapeutic benefits. PLOS Currents, 2014, 6, Castration delays epigenetic aging and feminizes DNA methylation at androgen-regulated loci. ELife, 2021, 10. Longitudinal Epigenome-Wide Methylation Study of Cognitive Decline and Motor Progression in Parkinson's Disease. Journal of Parkinsons Disease, 2019, 9, 389-400 A mammalian methylation array for profiling methylation levels at conserved sequences. Nature Communications, 2022, 13, 783 DNA methylation study of Huntington's disease and motor progression in patients and in animal models. Nature Communications, 2020, 11, 4529 Incorporation of a nucleoside analog maps genome repair sites in postmitotic human neurons. Science, 2021, 372, 91-94 Multi-species and multi-tissue methylation clocks for age estimation in toothed whales and dolphins. Communications Biology, 2021, 4, 642 Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194 DNA methylation age analysis of rapamycin in common marmosets. GeroScience, 2021, 43, 2413-2425 Rog Genome-wide analysis in African Americans. Journal of Thrombosis and Haemostasis, 2020, 113, 1335-1347 Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. Aging Cell, 2021, 20, e133669 Genome-wide association studies identify 137 loci for DNA methylation biomarkers of ageing Epigenetic Age Acceleration Reflects Long-Term Cardiovascular Health. Circulation Research, 2021,	A mammalian methylation array for profiling methylation levels at conserved sequences Ji Universal DNA methylation age across mammalian tissues Ji Placental epigenetic clocks: estimating gestational age using placental DNA methylation levels. Aging, 2019, 11, 4238-4253 DNA methylation predicts age and provides insight into exceptional longevity of bats. Nature Communications, 2021, 12, 1615 Online self-report data for duchenne muscular dystrophy confirms natural history and can be used to assess for therapeutic benefits. PLOS Currents, 2014, 6, Castration delays epigenetic aging and feminizes DNA methylation at androgen-regulated loci. ELIfe, 2021, 10, Longitudinal Epigenome-Wide Methylation Study of Cognitive Decline and Motor Progression in Parkinson's Disease, Journal of Parkinsons Disease, 2019, 9, 389-400 A mammalian methylation array for profiling methylation levels at conserved sequences Nature Communications, 2022, 13, 783 DNA methylation study of Huntington's disease and motor progression in patients and in animal models. Nature Communications, 2020, 11, 4529 Incorporation of a nucleoside analog maps genome repair sites in postmitotic human neurons. Science, 2021, 372, 91-94 Multi-species and multi-tissue methylation clocks for age estimation in toothed whales and dolphins. Communications Biology, 2021, 4, 642 Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 4, 642 Genome-wide association studies identify 137 loci for DNA methylation biomarkers of aging. Genome Sequence and epigenome-wide analysis in African Americans. Journal of Thrombosis and Haemostasis, 2020, 18, 1335-1347 Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. Aging Cell, 2021, 20, e133669 Genome-wide association studies identify 137 loci for DNA methylation biomarkers of ageing Epigenetic Age Acceleration Reflects Long-Term Cardiovascular Health. Circulation Research, 2021,

17	Identifying rare-variant associations in parent-child trios using a Gaussian support vector machine. BMC Proceedings, 2014 , 8, S98	2.3	6
16	Blood DNA methylation sites predict death risk in a longitudinal study of 12, 300 individuals. <i>Aging</i> , 2020 , 12, 14092-14124	5.6	6
15	Epigenetic mutation load is weakly correlated with epigenetic age acceleration. <i>Aging</i> , 2020 , 12, 17863	8-1 <u>5</u> 7. 6 94	1 5
14	Epigenome-wide association study of leukocyte telomere length. <i>Aging</i> , 2019 , 11, 5876-5894	5.6	4
13	Epigenetic clock and methylation studies in dogs		3
12	Epigenetic aging of the demographically non-aging naked mole-rat <i>Nature Communications</i> , 2022 , 13, 355	17.4	2
11	Divergent age-related methylation patterns in long and short-lived mammals		2
10	A meta-analysis of genome-wide association studies of epigenetic age acceleration		2
9	Genetic Analyses of Epigenetic Predictors that Estimate Aging, Metabolic Traits, and Lifespan		2
8	Epigenetic Age and the Risk of Incident Atrial Fibrillation. Circulation, 2021,	16.7	2
7	GWAS of epigenetic ageing rates in blood reveals a critical role forTERT		1
6	DNAm-based signatures of accelerated aging and mortality in blood are associated with low renal function. <i>Clinical Epigenetics</i> , 2021 , 13, 121	7.7	1
5	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. <i>Nature Communications</i> , 2021 , 12, 7173	17.4	1
4	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	11.5	1
3	DNA methylation-based surrogates of plasma proteins are associated with Parkinson's disease risk. <i>Journal of the Neurological Sciences</i> , 2021 , 431, 120046	3.2	0
2	Association of subjective social status with epigenetic aging among Black and White women <i>Psychoneuroendocrinology</i> , 2022 , 141, 105748	5	Ο
1	Meta-analyses identify DNA methylation associated with kidney function and damage. <i>Nature Communications</i> , 2021 , 12, 7174	17.4	O