

Ake T Lu

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3768138/publications.pdf>

Version: 2024-02-01

46
papers

7,943
citations

201674

27
h-index

223800

46
g-index

59
all docs

59
docs citations

59
times ranked

6284
citing authors

#	ARTICLE	IF	CITATIONS
1	Epigenetic aging of the demographically non-aging naked mole-rat. <i>Nature Communications</i> , 2022, 13, 355.	12.8	26
2	A mammalian methylation array for profiling methylation levels at conserved sequences. <i>Nature Communications</i> , 2022, 13, 783.	12.8	93
3	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
4	Genetic loci and metabolic states associated with murine epigenetic aging. <i>ELife</i> , 2022, 11, .	6.0	26
5	Association of subjective social status with epigenetic aging among Black and White women. <i>Psychoneuroendocrinology</i> , 2022, 141, 105748.	2.7	9
6	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.	7.1	26
7	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
8	DNA methylation predicts age and provides insight into exceptional longevity of bats. <i>Nature Communications</i> , 2021, 12, 1615.	12.8	80
9	Incorporation of a nucleoside analog maps genome repair sites in postmitotic human neurons. <i>Science</i> , 2021, 372, 91-94.	12.6	68
10	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
11	Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. <i>Aging Cell</i> , 2021, 20, e13366.	6.7	72
12	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021, 22, 194.	8.8	90
13	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
14	Castration delays epigenetic aging and feminizes DNA methylation at androgen-regulated loci. <i>ELife</i> , 2021, 10, .	6.0	45
15	Epigenetic Age and the Risk of Incident Atrial Fibrillation. <i>Circulation</i> , 2021, 144, 1899-1911.	1.6	35
16	DNA methylation age analysis of rapamycin in common marmosets. <i>GeroScience</i> , 2021, 43, 2413-2425.	4.6	26
17	Epigenetic Age Acceleration Reflects Long-Term Cardiovascular Health. <i>Circulation Research</i> , 2021, 129, 770-781.	4.5	55
18	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

#	ARTICLE	IF	CITATIONS
19	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
20	Meta-analyses identify DNA methylation associated with kidney function and damage. <i>Nature Communications</i> , 2021, 12, 7174.	12.8	30
21	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
22	DNA methylation study of Huntington's disease and motor progression in patients and in animal models. <i>Nature Communications</i> , 2020, 11, 4529.	12.8	45
23	Blood DNA methylation sites predict death risk in a longitudinal study of 12, 300 individuals. <i>Aging</i> , 2020, 12, 14092-14124.	3.1	15
24	Epigenetic mutation load is weakly correlated with epigenetic age acceleration. <i>Aging</i> , 2020, 12, 17863-17894.	3.1	12
25	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
26	DNA methylation GrimAge strongly predicts lifespan and healthspan. <i>Aging</i> , 2019, 11, 303-327.	3.1	1,128
27	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
28	EPIGENETIC CLOCKS OF COMPUTED TOMOGRAPHY MEASURES OF FATTY ORGANS. <i>Innovation in Aging</i> , 2019, 3, S735-S736.	0.1	0
29	A meta-analysis of genome-wide association studies of epigenetic age acceleration. <i>PLoS Genetics</i> , 2019, 15, e1008104.	3.5	83
30	Placental epigenetic clocks: estimating gestational age using placental DNA methylation levels. <i>Aging</i> , 2019, 11, 4238-4253.	3.1	79
31	DNA methylation-based estimator of telomere length. <i>Aging</i> , 2019, 11, 5895-5923.	3.1	198
32	Epigenome-wide association study of leukocyte telomere length. <i>Aging</i> , 2019, 11, 5876-5894.	3.1	19
33	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. <i>Nature Communications</i> , 2018, 9, 387.	12.8	151
34	An epigenetic biomarker of aging for lifespan and healthspan. <i>Aging</i> , 2018, 10, 573-591.	3.1	1,552
35	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
36	Genetic architecture of epigenetic and neuronal ageing rates in human brain regions. <i>Nature Communications</i> , 2017, 8, 15353.	12.8	92

#	ARTICLE	IF	CITATIONS
37	Epigenetic clock analysis of diet, exercise, education, and lifestyle factors. <i>Aging</i> , 2017, 9, 419-446.	3.1	521
38	Genetic variants near MLST8 and DHX57 affect the epigenetic age of the cerebellum. <i>Nature Communications</i> , 2016, 7, 10561.	12.8	69
39	An epigenetic clock analysis of race/ethnicity, sex, and coronary heart disease. <i>Genome Biology</i> , 2016, 17, 171.	8.8	535
40	Menopause accelerates biological aging. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9327-9332.	7.1	363
41	DNA methylation-based measures of biological age: meta-analysis predicting time to death. <i>Aging</i> , 2016, 8, 1844-1865.	3.1	786
42	Epigenetic age of the pre-frontal cortex is associated with neuritic plaques, amyloid load, and Alzheimer's disease related cognitive functioning. <i>Aging</i> , 2015, 7, 1198-1211.	3.1	368
43	The cerebellum ages slowly according to the epigenetic clock. <i>Aging</i> , 2015, 7, 294-306.	3.1	162
44	Identifying rare-variant associations in parent-child trios using a Gaussian support vector machine. <i>BMC Proceedings</i> , 2014, 8, S98.	1.6	6
45	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, .	1.4	25
46	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, 1488-1494.	1.7	99