

Steve Horvath

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4363858/publications.pdf>

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	WGCNA: an R package for weighted correlation network analysis. BMC Bioinformatics, 2008, 9, 559.	2.6	17,294
2	A General Framework for Weighted Gene Co-Expression Network Analysis. Statistical Applications in Genetics and Molecular Biology, 2005, 4, Article17.	0.6	4,608
3	DNA methylation age of human tissues and cell types. Genome Biology, 2013, 14, R115.	9.6	4,566
4	An anatomically comprehensive atlas of the adult human brain transcriptome. Nature, 2012, 489, 391-399.	27.8	2,321
5	DNA methylation-based biomarkers and the epigenetic clock theory of ageing. Nature Reviews Genetics, 2018, 19, 371-384.	16.3	1,741
6	Defining clusters from a hierarchical cluster tree: the Dynamic Tree Cut package for R. Bioinformatics, 2008, 24, 719-720.	4.1	1,665
7	Transcriptomic analysis of autistic brain reveals convergent molecular pathology. Nature, 2011, 474, 380-384.	27.8	1,654
8	An epigenetic biomarker of aging for lifespan and healthspan. Aging, 2018, 10, 573-591.	3.1	1,552
9	Molecular Determinants of the Response of Glioblastomas to EGFR Kinase Inhibitors. New England Journal of Medicine, 2005, 353, 2012-2024.	27.0	1,376
10	DNA methylation GrimAge strongly predicts lifespan and healthspan. Aging, 2019, 11, 303-327.	3.1	1,128
11	Global histone modification patterns predict risk of prostate cancer recurrence. Nature, 2005, 435, 1262-1266.	27.8	991
12	Integrative Functional Genomic Analyses Implicate Specific Molecular Pathways and Circuits in Autism. Cell, 2013, 155, 1008-1021.	28.9	948
13	DNA methylation age of blood predicts all-cause mortality in later life. Genome Biology, 2015, 16, 25.	8.8	928
14	Is My Network Module Preserved and Reproducible?. PLoS Computational Biology, 2011, 7, e1001057.	3.2	885
15	Genetic programs in human and mouse early embryos revealed by single-cell RNA sequencing. Nature, 2013, 500, 593-597.	27.8	859
16	Fast R Functions for Robust Correlations and Hierarchical Clustering. Journal of Statistical Software, 2012, 46, .	3.7	856
17	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. Science, 2018, 359, 693-697.	12.6	851
18	Variations in DNA elucidate molecular networks that cause disease. Nature, 2008, 452, 429-435.	27.8	840

#	ARTICLE	IF	CITATIONS
19	DNA methylation-based measures of biological age: meta-analysis predicting time to death. <i>Aging</i> , 2016, 8, 1844-1865.	3.1	786
20	Epigenetic Predictor of Age. <i>PLoS ONE</i> , 2011, 6, e14821.	2.5	781
21	Functional organization of the transcriptome in human brain. <i>Nature Neuroscience</i> , 2008, 11, 1271-1282.	14.8	743
22	Geometric Interpretation of Gene Coexpression Network Analysis. <i>PLoS Computational Biology</i> , 2008, 4, e1000117.	3.2	719
23	The family based association test method: strategies for studying general genotype-phenotype associations. <i>European Journal of Human Genetics</i> , 2001, 9, 301-306.	2.8	696
24	Gene Expression Profiling of Gliomas Strongly Predicts Survival. <i>Cancer Research</i> , 2004, 64, 6503-6510.	0.9	659
25	Obesity accelerates epigenetic aging of human liver. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15538-15543.	7.1	620
26	Genome-wide changes in lncRNA, splicing, and regional gene expression patterns in autism. <i>Nature</i> , 2016, 540, 423-427.	27.8	603
27	Conservation and evolution of gene coexpression networks in human and chimpanzee brains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 17973-17978.	7.1	580
28	Role of the Murine Reprogramming Factors in the Induction of Pluripotency. <i>Cell</i> , 2009, 136, 364-377.	28.9	579
29	Gene network interconnectedness and the generalized topological overlap measure. <i>BMC Bioinformatics</i> , 2007, 8, 22.	2.6	567
30	DNA methylation aging clocks: challenges and recommendations. <i>Genome Biology</i> , 2019, 20, 249.	8.8	552
31	Aging effects on DNA methylation modules in human brain and blood tissue. <i>Genome Biology</i> , 2012, 13, R97.	9.6	536
32	An epigenetic clock analysis of race/ethnicity, sex, and coronary heart disease. <i>Genome Biology</i> , 2016, 17, 171.	8.8	535
33	Epigenetic clock analysis of diet, exercise, education, and lifestyle factors. <i>Aging</i> , 2017, 9, 419-446.	3.1	521
34	Global analysis of gene activity during <i>Arabidopsis</i> seed development and identification of seed-specific transcription factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 8063-8070.	7.1	509
35	Antitumor Activity of Rapamycin in a Phase I Trial for Patients with Recurrent PTEN-Deficient Glioblastoma. <i>PLoS Medicine</i> , 2008, 5, e8.	8.4	499
36	Carbonic anhydrase IX is an independent predictor of survival in advanced renal clear cell carcinoma: implications for prognosis and therapy. <i>Clinical Cancer Research</i> , 2003, 9, 802-11.	7.0	492

#	ARTICLE	IF	CITATIONS
37	Divergence of human and mouse brain transcriptome highlights Alzheimer disease pathways. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 12698-12703.	7.1	487
38	The epigenetic clock is correlated with physical and cognitive fitness in the Lothian Birth Cohort 1936. International Journal of Epidemiology, 2015, 44, 1388-1396.	1.9	472
39	HIV-1 Infection Accelerates Age According to the Epigenetic Clock. Journal of Infectious Diseases, 2015, 212, 1563-1573.	4.0	467
40	Global Levels of Histone Modifications Predict Prognosis in Different Cancers. American Journal of Pathology, 2009, 174, 1619-1628.	3.8	448
41	Accelerated epigenetic aging in Down syndrome. Aging Cell, 2015, 14, 491-495.	6.7	446
42	Reprogramming to recover youthful epigenetic information and restore vision. Nature, 2020, 588, 124-129.	27.8	424
43	Integrating Genetic and Network Analysis to Characterize Genes Related to Mouse Weight. PLoS Genetics, 2006, 2, e130.	3.5	419
44	Epigenetic clock for skin and blood cells applied to Hutchinson Gilford Progeria Syndrome and ex vivo studies. Aging, 2018, 10, 1758-1775.	3.1	406
45	Family-based tests for associating haplotypes with general phenotype data: Application to asthma genetics. Genetic Epidemiology, 2004, 26, 61-69.	1.3	395
46	Unsupervised Learning With Random Forest Predictors. Journal of Computational and Graphical Statistics, 2006, 15, 118-138.	1.7	379
47	Epigenetic age of the pre-frontal cortex is associated with neuritic plaques, amyloid load, and Alzheimer's disease related cognitive functioning. Aging, 2015, 7, 1198-1211.	3.1	368
48	Menopause accelerates biological aging. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9327-9332.	7.1	363
49	Increased epigenetic age and granulocyte counts in the blood of Parkinson's disease patients. Aging, 2015, 7, 1130-1142.	3.1	344
50	Integrated genomics and proteomics define huntingtin CAG length-dependent networks in mice. Nature Neuroscience, 2016, 19, 623-633.	14.8	342
51	Analysis of the phosphatidylinositol 3'-kinase signaling pathway in glioblastoma patients in vivo. Cancer Research, 2003, 63, 2742-6.	0.9	342
52	Weighted gene coexpression network analysis strategies applied to mouse weight. Mammalian Genome, 2007, 18, 463-472.	2.2	337
53	Reversal of epigenetic aging and immunosenescent trends in humans. Aging Cell, 2019, 18, e13028.	6.7	335
54	A Systems-Level Analysis of the Peripheral Nerve Intrinsic Axonal Growth Program. Neuron, 2016, 89, 956-970.	8.1	314

#	ARTICLE	IF	CITATIONS
55	Differential Sensitivity of Glioma- versus Lung Cancer-Specific EGFR Mutations to EGFR Kinase Inhibitors. <i>Cancer Discovery</i> , 2012, 2, 458-471.	9.4	304
56	Identification of inflammatory gene modules based on variations of human endothelial cell responses to oxidized lipids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 12741-12746.	7.1	303
57	Sexually dimorphic gene expression in mouse brain precedes gonadal differentiation. <i>Molecular Brain Research</i> , 2003, 118, 82-90.	2.3	301
58	Mutations in CLCN2 encoding a voltage-gated chloride channel are associated with idiopathic generalized epilepsies. <i>Nature Genetics</i> , 2003, 33, 527-532.	21.4	297
59	Strategies for aggregating gene expression data: The collapseRows R function. <i>BMC Bioinformatics</i> , 2011, 12, 322.	2.6	290
60	EGFR Signaling Through an Akt-SREBP-1-Dependent, Rapamycin-Resistant Pathway Sensitizes Glioblastomas to Antiplogenic Therapy. <i>Science Signaling</i> , 2009, 2, ra82.	3.6	282
61	Decreased epigenetic age of PBMCs from Italian semi-supercentenarians and their offspring. <i>Aging</i> , 2015, 7, 1159-1170.	3.1	276
62	Genes and pathways underlying regional and cell type changes in Alzheimer's disease. <i>Genome Medicine</i> , 2013, 5, 48.	8.2	267
63	Gene expression profiling identifies molecular subtypes of gliomas. <i>Oncogene</i> , 2003, 22, 4918-4923.	5.9	264
64	Kidney Transplant Rejection and Tissue Injury by Gene Profiling of Biopsies and Peripheral Blood Lymphocytes. <i>American Journal of Transplantation</i> , 2004, 4, 1475-1489.	4.7	264
65	Network Organization of the Huntingtin Proteomic Interactome in Mammalian Brain. <i>Neuron</i> , 2012, 75, 41-57.	8.1	262
66	DNA methylation age of blood predicts future onset of lung cancer in the women's health initiative. <i>Aging</i> , 2015, 7, 690-700.	3.1	254
67	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. <i>Genome Biology</i> , 2016, 17, 255.	8.8	251
68	Identification of molecular subtypes of glioblastoma by gene expression profiling. <i>Oncogene</i> , 2003, 22, 2361-2373.	5.9	247
69	When Is Hub Gene Selection Better than Standard Meta-Analysis?. <i>PLoS ONE</i> , 2013, 8, e61505.	2.5	243
70	Weighted Network Analysis. , 2011, , .		241
71	Single-Cell Transcriptome Analyses Reveal Signals to Activate Dormant Neural Stem Cells. <i>Cell</i> , 2015, 161, 1175-1186.	28.9	239
72	A Discordant-Sibship Test for Disequilibrium and Linkage: No Need for Parental Data. <i>American Journal of Human Genetics</i> , 1998, 63, 1886-1897.	6.2	233

#	ARTICLE	IF	CITATIONS
73	Using Protein Expressions to Predict Survival in Clear Cell Renal Carcinoma. <i>Clinical Cancer Research</i> , 2004, 10, 5464-5471.	7.0	210
74	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
75	Signed weighted gene co-expression network analysis of transcriptional regulation in murine embryonic stem cells. <i>BMC Genomics</i> , 2009, 10, 327.	2.8	209
76	Neurosphere Formation Is an Independent Predictor of Clinical Outcome in Malignant Glioma. <i>Stem Cells</i> , 2009, 27, 980-987.	3.2	207
77	Prenatal and early life influences on epigenetic age in children: a study of mother-offspring pairs from two cohort studies. <i>Human Molecular Genetics</i> , 2016, 25, 191-201.	2.9	205
78	Cellular Histone Modification Patterns Predict Prognosis and Treatment Response in Resectable Pancreatic Adenocarcinoma: Results From RTOG 9704. <i>Journal of Clinical Oncology</i> , 2010, 28, 1358-1365.	1.6	202
79	Genetic analysis of DNA methylation and gene expression levels in whole blood of healthy human subjects. <i>BMC Genomics</i> , 2012, 13, 636.	2.8	200
80	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
81	DNA methylation-based estimator of telomere length. <i>Aging</i> , 2019, 11, 5895-5923.	3.1	198
82	Prostate Stem Cell Antigen Is Overexpressed in Prostate Cancer Metastases. <i>Clinical Cancer Research</i> , 2005, 11, 2591-2596.	7.0	195
83	An epigenetic clock for gestational age at birth based on blood methylation data. <i>Genome Biology</i> , 2016, 17, 206.	8.8	193
84	Huntington's disease accelerates epigenetic aging of human brain and disrupts DNA methylation levels. <i>Aging</i> , 2016, 8, 1485-1512.	3.1	192
85	Long-term maturation of human cortical organoids matches key early postnatal transitions. <i>Nature Neuroscience</i> , 2021, 24, 331-342.	14.8	188
86	Longitudinal changes of telomere length and epigenetic age related to traumatic stress and post-traumatic stress disorder. <i>Psychoneuroendocrinology</i> , 2015, 51, 506-512.	2.7	186
87	Transient non-integrative expression of nuclear reprogramming factors promotes multifaceted amelioration of aging in human cells. <i>Nature Communications</i> , 2020, 11, 1545.	12.8	183
88	Resting-State Quantitative Electroencephalography Reveals Increased Neurophysiologic Connectivity in Depression. <i>PLoS ONE</i> , 2012, 7, e32508.	2.5	179
89	MCT1 Modulates Cancer Cell Pyruvate Export and Growth of Tumors that Co-express MCT1 and MCT4. <i>Cell Reports</i> , 2016, 14, 1590-1601.	6.4	174
90	A Systems Genetics Approach Implicates USF1, FADS3, and Other Causal Candidate Genes for Familial Combined Hyperlipidemia. <i>PLoS Genetics</i> , 2009, 5, e1000642.	3.5	168

#	ARTICLE	IF	CITATIONS
91	A multi-tissue full lifespan epigenetic clock for mice. <i>Aging</i> , 2018, 10, 2832-2854.	3.1	166
92	The cerebellum ages slowly according to the epigenetic clock. <i>Aging</i> , 2015, 7, 294-306.	3.1	162
93	Tumor classification by tissue microarray profiling: random forest clustering applied to renal cell carcinoma. <i>Modern Pathology</i> , 2005, 18, 547-557.	5.5	159
94	Maintenance of age in human neurons generated by microRNA-based neuronal conversion of fibroblasts. <i>ELife</i> , 2016, 5, .	6.0	159
95	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
96	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , 2017, 101, 888-902.	6.2	154
97	Accelerated epigenetic aging in Werner syndrome. <i>Aging</i> , 2017, 9, 1143-1152.	3.1	152
98	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. <i>Nature Communications</i> , 2018, 9, 387.	12.8	151
99	Network methods for describing sample relationships in genomic datasets: application to Huntington's disease. <i>BMC Systems Biology</i> , 2012, 6, 63.	3.0	149
100	A Modular Organization of the Human Intestinal Mucosal Microbiota and Its Association with Inflammatory Bowel Disease. <i>PLoS ONE</i> , 2013, 8, e80702.	2.5	147
101	Clinicopathologic and molecular correlations of necrosis in the primary tumor of patients with renal cell carcinoma. <i>Cancer</i> , 2005, 103, 2517-2525.	4.1	145
102	Maternal embryonic leucine zipper kinase is a key regulator of the proliferation of malignant brain tumors, including brain tumor stem cells. <i>Journal of Neuroscience Research</i> , 2008, 86, 48-60.	2.9	144
103	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
104	Protein interaction network of alternatively spliced isoforms from brain links genetic risk factors for autism. <i>Nature Communications</i> , 2014, 5, 3650.	12.8	131
105	High concentrations of long interspersed nuclear element sequence distinguish monoallelically expressed genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 9940-9945.	7.1	129
106	A Gene Co-Expression Network in Whole Blood of Schizophrenia Patients Is Independent of Antipsychotic-Use and Enriched for Brain-Expressed Genes. <i>PLoS ONE</i> , 2012, 7, e39498.	2.5	125
107	Epigenetic clock analyses of cellular senescence and ageing. <i>Oncotarget</i> , 2016, 7, 8524-8531.	1.8	125
108	An epigenetic aging clock for dogs and wolves. <i>Aging</i> , 2017, 9, 1055-1068.	3.1	125

#	ARTICLE	IF	CITATIONS
109	Parkinson's disease is associated with DNA methylation levels in human blood and saliva. <i>Genome Medicine</i> , 2017, 9, 76.	8.2	122
110	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
111	The organization of the transcriptional network in specific neuronal classes. <i>Molecular Systems Biology</i> , 2009, 5, 291.	7.2	114
112	Transcriptome analyses reveal molecular mechanisms underlying functional recovery after spinal cord injury. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13360-13365.	7.1	113
113	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
114	IL-32 is a molecular marker of a host defense network in human tuberculosis. <i>Science Translational Medicine</i> , 2014, 6, 250ra114.	12.4	110
115	Epigenetic measures of ageing predict the prevalence and incidence of leading causes of death and disease burden. <i>Clinical Epigenetics</i> , 2020, 12, 115.	4.1	109
116	Relationship between Survival and Edema in Malignant Gliomas: Role of Vascular Endothelial Growth Factor and Neuronal Pentraxin 2. <i>Clinical Cancer Research</i> , 2007, 13, 2592-2598.	7.0	108
117	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
118	Molecular Microcircuitry Underlies Functional Specification in a Basal Ganglia Circuit Dedicated to Vocal Learning. <i>Neuron</i> , 2012, 73, 537-552.	8.1	104
119	Accelerated epigenetic aging in brain is associated with pre-mortem HIV-associated neurocognitive disorders. <i>Journal of NeuroVirology</i> , 2016, 22, 366-375.	2.1	101
120	Acceleration of Age-Associated Methylation Patterns in HIV-1-Infected Adults. <i>PLoS ONE</i> , 2015, 10, e0119201.	2.5	101
121	In vivo partial reprogramming alters age-associated molecular changes during physiological aging in mice. <i>Nature Aging</i> , 2022, 2, 243-253.	11.6	101
122	Breast Cancer Molecular Signatures as Determined by SAGE: Correlation with Lymph Node Status. <i>Molecular Cancer Research</i> , 2007, 5, 881-890.	3.4	99
123	Neuropathological and transcriptomic characteristics of the aged brain. <i>ELife</i> , 2017, 6, .	6.0	97
124	Correlation of Ki-67 and gelsolin expression to clinical outcome in renal clear cell carcinoma. <i>Urology</i> , 2003, 61, 845-850.	1.0	95
125	"Good Enough Solutions" and the Genetics of Complex Diseases. <i>Circulation Research</i> , 2012, 111, 493-504.	4.5	94
126	Low CD38 Identifies Progenitor-like Inflammation-Associated Luminal Cells that Can Initiate Human Prostate Cancer and Predict Poor Outcome. <i>Cell Reports</i> , 2016, 17, 2596-2606.	6.4	94

#	ARTICLE	IF	CITATIONS
127	A mammalian methylation array for profiling methylation levels at conserved sequences. <i>Nature Communications</i> , 2022, 13, 783.	12.8	93
128	Genetic architecture of epigenetic and neuronal ageing rates in human brain regions. <i>Nature Communications</i> , 2017, 8, 15353.	12.8	92
129	Expression of colony-stimulating factor 1 receptor during prostate development and prostate cancer progression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 14404-14409.	7.1	91
130	Development of a Real-time RT-PCR Assay for Detecting EGFRvIII in Glioblastoma Samples. <i>Clinical Cancer Research</i> , 2008, 14, 488-493.	7.0	91
131	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021, 22, 194.	8.8	90
132	Gene Coexpression Network Topology of Cardiac Development, Hypertrophy, and Failure. <i>Circulation: Cardiovascular Genetics</i> , 2011, 4, 26-35.	5.1	88
133	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
134	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
135	Making sense of the ageing methylome. <i>Nature Reviews Genetics</i> , 2022, 23, 585-605.	16.3	86
136	Analysis of DNA methylation associates the cystine-glutamate antiporter SLC7A11 with risk of Parkinson's disease. <i>Nature Communications</i> , 2020, 11, 1238.	12.8	85
137	Flap endonuclease 1 is overexpressed in prostate cancer and is associated with a high Gleason score. <i>BJU International</i> , 2006, 98, 445-451.	2.5	83
138	A meta-analysis of genome-wide association studies of epigenetic age acceleration. <i>PLoS Genetics</i> , 2019, 15, e1008104.	3.5	83
139	Tissue microarray analysis of cytoskeletal actin-associated biomarkers gelsolin and E-cadherin in urothelial carcinoma. <i>Cancer</i> , 2002, 95, 1247-1257.	4.1	82
140	Perinatally acquired HIV infection accelerates epigenetic aging in South African adolescents. <i>Aids</i> , 2018, 32, 1465-1474.	2.2	81
141	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
142	Detecting network modules in fMRI time series: A weighted network analysis approach. <i>NeuroImage</i> , 2010, 52, 1465-1476.	4.2	80
143	DNA methylation predicts age and provides insight into exceptional longevity of bats. <i>Nature Communications</i> , 2021, 12, 1615.	12.8	80
144	Placental epigenetic clocks: estimating gestational age using placental DNA methylation levels. <i>Aging</i> , 2019, 11, 4238-4253.	3.1	79

#	ARTICLE	IF	CITATIONS
145	An epigenetic predictor of death captures multi-modal measures of brain health. <i>Molecular Psychiatry</i> , 2021, 26, 3806-3816.	7.9	77
146	Expression of X-Linked Inhibitor of Apoptosis Protein Is a Strong Predictor of Human Prostate Cancer Recurrence. <i>Clinical Cancer Research</i> , 2007, 13, 6056-6063.	7.0	74
147	Biomarkers for Early and Late Stage Chronic Allograft Nephropathy by Proteogenomic Profiling of Peripheral Blood. <i>PLoS ONE</i> , 2009, 4, e6212.	2.5	74
148	Loss of CD10 (neutral endopeptidase) is a frequent and early event in human prostate cancer. <i>Prostate</i> , 2003, 55, 71-80.	2.3	73
149	DNA methylation age is accelerated in alcohol dependence. <i>Translational Psychiatry</i> , 2018, 8, 182.	4.8	73
150	Alteration in basal and depolarization induced transcriptional network in iPSC derived neurons from Timothy syndrome. <i>Genome Medicine</i> , 2014, 6, 75.	8.2	72
151	Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. <i>Aging Cell</i> , 2021, 20, e13366.	6.7	72
152	An epigenetic clock for human skeletal muscle. <i>Journal of Cachexia, Sarcopenia and Muscle</i> , 2020, 11, 887-898.	7.3	70
153	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
154	Genetic variants near MLST8 and DHX57 affect the epigenetic age of the cerebellum. <i>Nature Communications</i> , 2016, 7, 10561.	12.8	69
155	Extreme skewing of X chromosome inactivation in mothers of homosexual men. <i>Human Genetics</i> , 2006, 118, 691-694.	3.8	68
156	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
157	Incorporation of a nucleoside analog maps genome repair sites in postmitotic human neurons. <i>Science</i> , 2021, 372, 91-94.	12.6	68
158	Systems biology analysis of sjögren's syndrome and mucosa-associated lymphoid tissue lymphoma in parotid glands. <i>Arthritis and Rheumatism</i> , 2009, 60, 81-92.	6.7	66
159	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
160	An Epigenetic Signature in Peripheral Blood Associated with the Haplotype on 17q21.31, a Risk Factor for Neurodegenerative Tauopathy. <i>PLoS Genetics</i> , 2014, 10, e1004211.	3.5	65
161	Gene expression signatures affected by alcohol-induced DNA methylomic deregulation in human embryonic stem cells. <i>Stem Cell Research</i> , 2014, 12, 791-806.	0.7	65
162	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

#	ARTICLE	IF	CITATIONS
163	Antibody-Based Profiling of the Phosphoinositide 3-Kinase Pathway in Clinical Prostate Cancer. <i>Clinical Cancer Research</i> , 2004, 10, 8351-8356.	7.0	60
164	Methylome-wide association study provides evidence of particulate matter air pollution-associated DNA methylation. <i>Environment International</i> , 2019, 132, 104723.	10.0	58
165	Statistical Methods for Analyzing Tissue Microarray Data. <i>Journal of Biopharmaceutical Statistics</i> , 2004, 14, 671-685.	0.8	57
166	Organophosphate pesticide exposure and differential genome-wide DNA methylation. <i>Science of the Total Environment</i> , 2018, 645, 1135-1143.	8.0	56
167	Epigenetic Age Acceleration Reflects Long-Term Cardiovascular Health. <i>Circulation Research</i> , 2021, 129, 770-781.	4.5	55
168	The Transmission/Disequilibrium Test and Parental-Genotype Reconstruction for X-Chromosomal Markers. <i>American Journal of Human Genetics</i> , 2000, 66, 1161-1167.	6.2	54
169	Trefoil factor 3 is overexpressed in human prostate cancer. <i>Prostate</i> , 2004, 61, 209-214.	2.3	53
170	Glycerol kinase deficiency alters expression of genes involved in lipid metabolism, carbohydrate metabolism, and insulin signaling. <i>European Journal of Human Genetics</i> , 2007, 15, 646-657.	2.8	53
171	Presence of a Putative Tumor-Initiating Progenitor Cell Population Predicts Poor Prognosis in Smokers with Non-Small Cell Lung Cancer. <i>Cancer Research</i> , 2010, 70, 6639-6648.	0.9	53
172	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
173	Psychosocial stress and epigenetic aging. <i>International Review of Neurobiology</i> , 2020, 150, 107-128.	2.0	53
174	An Integrative Genetics Approach to Identify Candidate Genes Regulating BMD: Combining Linkage, Gene Expression, and Association. <i>Journal of Bone and Mineral Research</i> , 2009, 24, 105-116.	2.8	52
175	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
176	Breast cancer treatment and its effects on aging. <i>Journal of Geriatric Oncology</i> , 2019, 10, 346-355.	1.0	51
177	The relationship between epigenetic age and the hallmarks of aging in human cells. <i>Nature Aging</i> , 2022, 2, 484-493.	11.6	51
178	CLCN2 variants in idiopathic generalized epilepsy. <i>Nature Genetics</i> , 2009, 41, 954-955.	21.4	50
179	Mapping of Gene Expression Reveals CYP27A1 as a Susceptibility Gene for Sporadic ALS. <i>PLoS ONE</i> , 2012, 7, e35333.	2.5	50
180	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

#	ARTICLE	IF	CITATIONS
181	Seasonal changes in gene expression represent cell-type composition in whole blood. <i>Human Molecular Genetics</i> , 2014, 23, 2721-2728.	2.9	49
182	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
183	Repetitive sequence environment distinguishes housekeeping genes. <i>Gene</i> , 2007, 390, 153-165.	2.2	47
184	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
185	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
186	Association analysis between the human interleukin 1 β (\sim 511) gene polymorphism and susceptibility to febrile convulsions. <i>Neuroscience Letters</i> , 2002, 334, 68-70.	2.1	45
187	High expression of AGR2 in lung cancer is predictive of poor survival. <i>BMC Cancer</i> , 2015, 15, 655.	2.6	45
188	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
189	Castration delays epigenetic aging and feminizes DNA methylation at androgen-regulated loci. <i>ELife</i> , 2021, 10, .	6.0	45
190	Transposon-triggered innate immune response confers cancer resistance to the blind mole rat. <i>Nature Immunology</i> , 2021, 22, 1219-1230.	14.5	45
191	Identification of schizophrenia-associated loci by combining DNA methylation and gene expression data from whole blood. <i>European Journal of Human Genetics</i> , 2015, 23, 1106-1110.	2.8	44
192	Current perspectives on the cellular and molecular features of epigenetic ageing. <i>Experimental Biology and Medicine</i> , 2020, 245, 1532-1542.	2.4	44
193	Epigenetic clock and methylation studies in elephants. <i>Aging Cell</i> , 2021, 20, e13414.	6.7	43
194	Early life adversity, pubertal timing, and epigenetic age acceleration in adulthood. <i>Developmental Psychobiology</i> , 2021, 63, 890-902.	1.6	42
195	Higher diet quality relates to decelerated epigenetic aging. <i>American Journal of Clinical Nutrition</i> , 2022, 115, 163-170.	4.7	42
196	Leukocyte telomere length, T cell composition and DNA methylation age. <i>Aging</i> , 2017, 9, 1983-1995.	3.1	42
197	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
198	Distinct gene expression profiles in adult mouse heart following targeted MAP kinase activation. <i>Physiological Genomics</i> , 2006, 25, 50-59.	2.3	41

#	ARTICLE	IF	CITATIONS
199	Increased epigenetic age in normal breast tissue from luminal breast cancer patients. <i>Clinical Epigenetics</i> , 2018, 10, 112.	4.1	40
200	Nitric Oxide Improves Cisplatin Cytotoxicity in Head and Neck Squamous Cell Carcinoma. <i>Laryngoscope</i> , 2001, 111, 1896-1900.	2.0	39
201	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
202	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
203	Epigenetic age is a cellâ€™s intrinsic property in transplanted human hematopoietic cells. <i>Aging Cell</i> , 2019, 18, e12897.	6.7	39
204	MicroRNA signatures of endogenous Huntingtin CAG repeat expansion in mice. <i>PLoS ONE</i> , 2018, 13, e0190550.	2.5	39
205	Epigenetic age analysis of children who seem to evade aging. <i>Aging</i> , 2015, 7, 334-339.	3.1	38
206	Specific premature epigenetic aging of cartilage in osteoarthritis. <i>Aging</i> , 2016, 8, 2222-2231.	3.1	38
207	Synchrony and asynchrony between an epigenetic clock and developmental timing. <i>Scientific Reports</i> , 2019, 9, 3770.	3.3	37
208	Longitudinal Epigenome-Wide Methylation Study of Cognitive Decline and Motor Progression in Parkinsonâ€™s Disease. <i>Journal of Parkinson's Disease</i> , 2019, 9, 389-400.	2.8	37
209	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.	5.2	37
210	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
211	Human aging DNA methylation signatures are conserved but accelerated in cultured fibroblasts. <i>Epigenetics</i> , 2019, 14, 961-976.	2.7	36
212	Epigenetic Age and the Risk of Incident Atrial Fibrillation. <i>Circulation</i> , 2021, 144, 1899-1911.	1.6	35
213	Host methylation predicts SARS-CoV-2 infection and clinical outcome. <i>Communications Medicine</i> , 2021, 1, 42.	4.2	35
214	Dynamics of epigenetic age following hematopoietic stem cell transplantation. <i>Haematologica</i> , 2017, 102, e321-e323.	3.5	34
215	DNA methylation aging and transcriptomic studies in horses. <i>Nature Communications</i> , 2022, 13, 40.	12.8	34
216	Epigenetic age and pregnancy outcomes: GrimAge acceleration is associated with shorter gestational length and lower birthweight. <i>Clinical Epigenetics</i> , 2020, 12, 120.	4.1	32

#	ARTICLE	IF	CITATIONS
217	An epigenetic clock to estimate the age of living beluga whales. <i>Evolutionary Applications</i> , 2021, 14, 1263-1273.	3.1	32
218	ARDD 2020: from aging mechanisms to interventions. <i>Aging</i> , 2020, 12, 24484-24503.	3.1	32
219	Targeted disruption of glycerol kinase gene in mice: expression analysis in liver shows alterations in network partners related to glycerol kinase activity. <i>Human Molecular Genetics</i> , 2006, 15, 405-415.	2.9	31
220	Microgeographic Proteomic Networks of the Human Colonic Mucosa and Their Association With Inflammatory Bowel Disease. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2016, 2, 567-583.	4.5	31
221	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
222	Longitudinal study of surrogate aging measures during human immunodeficiency virus seroconversion. <i>Aging</i> , 2017, 9, 687-705.	3.1	31
223	Uninterrupted CAG repeat drives striatum-selective transcriptionopathy and nuclear pathogenesis in human Huntingtin BAC mice. <i>Neuron</i> , 2022, 110, 1173-1192.e7.	8.1	30
224	Meta-analyses identify DNA methylation associated with kidney function and damage. <i>Nature Communications</i> , 2021, 12, 7174.	12.8	30
225	Weighted gene co-expression network analysis identifies biomarkers in glycerol kinase deficient mice. <i>Molecular Genetics and Metabolism</i> , 2009, 98, 203-214.	1.1	29
226	Prostate cancer cell phenotypes based on AGR2 and CD10 expression. <i>Modern Pathology</i> , 2013, 26, 849-859.	5.5	29
227	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
228	Epigenetic clock and methylation studies in the rhesus macaque. <i>GeroScience</i> , 2021, 43, 2441-2453.	4.6	28
229	Epithelial membrane protein expression is an early predictor of endometrial cancer development. <i>Cancer</i> , 2010, 116, 4718-4726.	4.1	27
230	Epigenetic clock and DNA methylation analysis of porcine models of aging and obesity. <i>GeroScience</i> , 2021, 43, 2467-2483.	4.6	27
231	Ribonucleotide Reductase Subunit M2 Predicts Survival in Subgroups of Patients with Non-Small Cell Lung Carcinoma: Effects of Gender and Smoking Status. <i>PLoS ONE</i> , 2015, 10, e0127600.	2.5	27
232	Epigenetic clock and methylation studies in cats. <i>GeroScience</i> , 2021, 43, 2363-2378.	4.6	26
233	DNA methylation age analysis of rapamycin in common marmosets. <i>GeroScience</i> , 2021, 43, 2413-2425.	4.6	26
234	Epigenetic aging of the demographically non-aging naked mole-rat. <i>Nature Communications</i> , 2022, 13, 355.	12.8	26

#	ARTICLE	IF	CITATIONS
235	Genetic loci and metabolic states associated with murine epigenetic aging. <i>ELife</i> , 2022, 11, .	6.0	26
236	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
237	Epigenetic clock and methylation study of oocytes from a bovine model of reproductive aging. <i>Aging Cell</i> , 2021, 20, e13349.	6.7	25
238	Distinct Neurogenomic States in Basal Ganglia Subregions Relate Differently to Singing Behavior in Songbirds. <i>PLoS Computational Biology</i> , 2012, 8, e1002773.	3.2	24
239	Genetic dissection of a major mouse obesity QTL (<i>Carfhg2</i>): integration of gene expression and causality modeling. <i>Physiological Genomics</i> , 2009, 37, 294-302.	2.3	23
240	Transcriptome analysis of HIV-infected peripheral blood monocytes: Gene transcripts and networks associated with neurocognitive functioning. <i>Journal of Neuroimmunology</i> , 2013, 265, 96-105.	2.3	23
241	Epigenetic models developed for plains zebras predict age in domestic horses and endangered equids. <i>Communications Biology</i> , 2021, 4, 1412.	4.4	23
242	Hibernation slows epigenetic ageing in yellow-bellied marmots. <i>Nature Ecology and Evolution</i> , 2022, 6, 418-426.	7.8	23
243	A Family-Based Test for Correlation between Gene Expression and Trait Values. <i>American Journal of Human Genetics</i> , 2003, 72, 1323-1330.	6.2	22
244	The Effects of Anti-retroviral Therapy on Epigenetic Age Acceleration Observed in HIV-1-infected Adults. <i>Pathogens and Immunity</i> , 2020, 5, 291.	3.1	22
245	Accelerated aging with HIV occurs at the time of initial HIV infection. <i>IScience</i> , 2022, 25, 104488.	4.1	22
246	Epigenome-wide association study of kidney function identifies trans-ethnic and ethnic-specific loci. <i>Genome Medicine</i> , 2021, 13, 74.	8.2	20
247	Postpartum sleep loss and accelerated epigenetic aging. <i>Sleep Health</i> , 2021, 7, 362-367.	2.5	20
248	Season of Sampling and Season of Birth Influence Serotonin Metabolite Levels in Human Cerebrospinal Fluid. <i>PLoS ONE</i> , 2012, 7, e30497.	2.5	20
249	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
250	Genetic and epigenetic changes in clonal descendants of irradiated human fibroblasts. <i>Experimental Cell Research</i> , 2018, 370, 322-332.	2.6	19
251	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
252	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

#	ARTICLE	IF	CITATIONS
253	Epigenome-wide association study of leukocyte telomere length. <i>Aging</i> , 2019, 11, 5876-5894.	3.1	19
254	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
255	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
256	A Weighted SNP Correlation Network Method for Estimating Polygenic Risk Scores. <i>Methods in Molecular Biology</i> , 2017, 1613, 277-290.	0.9	18
257	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. <i>Nature Communications</i> , 2021, 12, 3987.	12.8	18
258	Epigenetic clock and methylation studies in vervet monkeys. <i>GeroScience</i> , 2022, 44, 699-717.	4.6	18
259	DNA methylation signatures in Blood DNA of Hutchinsonâ€™s Gilford Progeria syndrome. <i>Aging Cell</i> , 2022, 21, e13555.	6.7	18
260	Telomere length and epigenetic clocks as markers of cellular aging: a comparative study. <i>GeroScience</i> , 2022, 44, 1861-1869.	4.6	18
261	Leukocyte Traits and Exposure to Ambient Particulate Matter Air Pollution in the Womenâ€™s Health Initiative and Atherosclerosis Risk in Communities Study. <i>Environmental Health Perspectives</i> , 2020, 128, 17004.	6.0	17
262	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
263	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
264	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.	4.3	17
265	Accelerated epigenetic aging in newborns with Down syndrome. <i>Aging Cell</i> , 2022, 21, .	6.7	17
266	Inhibition of Atm and/or Atr disrupts gene silencing on the inactive X chromosome. <i>Biochemical and Biophysical Research Communications</i> , 2005, 337, 875-880.	2.1	15
267	Estimating breast tissue-specific DNA methylation age using next-generation sequencing data. <i>Clinical Epigenetics</i> , 2020, 12, 45.	4.1	15
268	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
269	HIV, pathology and epigenetic age acceleration in different human tissues. <i>GeroScience</i> , 2022, 44, 1609-1620.	4.6	15
270	Accelerated hematopoietic mitotic aging measured by DNA methylation, blood cell lineage, and Parkinsonâ€™s disease. <i>BMC Genomics</i> , 2021, 22, 696.	2.8	14

#	ARTICLE	IF	CITATIONS
271	DNA methylation biomarker for cumulative lead exposure is associated with Parkinson's disease. <i>Clinical Epigenetics</i> , 2021, 13, 59.	4.1	13
272	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
273	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
274	Ridge regression based hybrid genetic algorithms for multi-locus quantitative trait mapping. <i>International Journal of Bioinformatics Research and Applications</i> , 2005, 1, 261.	0.2	12
275	Epigenetic mutation load is weakly correlated with epigenetic age acceleration. <i>Aging</i> , 2020, 12, 17863-17894.	3.1	12
276	Development of Epigenetic Clocks for Key Ruminant Species. <i>Genes</i> , 2022, 13, 96.	2.4	12
277	Epigenetic clock and methylation studies in marsupials: opossums, Tasmanian devils, kangaroos, and wallabies. <i>GeroScience</i> , 2022, 44, 1825-1845.	4.6	12
278	No evidence for association between the KCNQ3 gene and susceptibility to idiopathic generalized epilepsy. <i>Epilepsy Research</i> , 2000, 42, 57-62.	1.6	11
279	The genetics of gene expression and gene mapping. <i>Trends in Biotechnology</i> , 2003, 21, 377-378.	9.3	11
280	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
281	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
282	DNA-methylation-based telomere length estimator: comparisons with measurements from flow FISH and qPCR. <i>Aging</i> , 2021, 13, 14675-14686.	3.1	11
283	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
284	Ki67, gelsolin and PTEN expression in sarcomatoid renal tumors. <i>Urological Research</i> , 2003, 30, 387-389.	1.5	10
285	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
286	Higher expression levels of 14-3-3 β in ductal carcinoma in situ of the breast predict poorer outcome. <i>Cancer Biomarkers</i> , 2009, 5, 215-224.	1.7	9
287	DNA Methylation Age Is More Closely Associated With Infection Risk Than Chronological Age in Kidney Transplant Recipients. <i>Transplantation Direct</i> , 2020, 6, e576.	1.6	9
288	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

#	ARTICLE	IF	CITATIONS
289	Increased Rate of Epigenetic Aging in Men Living With HIV Prior to Treatment. <i>Frontiers in Genetics</i> , 2021, 12, 796547.	2.3	9
290	Association of subjective social status with epigenetic aging among Black and White women. <i>Psychoneuroendocrinology</i> , 2022, 141, 105748.	2.7	9
291	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
292	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
293	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
294	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
295	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
296	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.	2.4	7
297	The Effects of Lifetime Estrogen Exposure on Breast Epigenetic Age. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021, 30, 1241-1249.	2.5	7
298	Alcohol use disorder is associated with DNA methylation-based shortening of telomere length and regulated by TESPA1: implications for aging. <i>Molecular Psychiatry</i> , 2022, 27, 3875-3884.	7.9	7
299	DNA methylation profile in beef cattle is influenced by additive genetics and age. <i>Scientific Reports</i> , 2022, 12, .	3.3	7
300	Optimism is not associated with two indicators of DNA methylation aging. <i>Aging</i> , 2019, 11, 4970-4989.	3.1	6
301	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
302	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
303	Methylation studies in <i>Peromyscus</i> : aging, altitude adaptation, and monogamy. <i>GeroScience</i> , 2022, 44, 447-461.	4.6	4
304	The Disequilibrium Maximum-Likelihood Binomial Test Does Not Replace the Transmission/Disequilibrium Test. <i>American Journal of Human Genetics</i> , 2000, 67, 531-533.	6.2	3
305	Predicting COPD status with a random generalized linear model. <i>Systems Biomedicine (Austin, Tex)</i> , 2013, 1, 261-267.	0.7	3
306	Inflammation-Related Genes are Associated with Accelerated Aging in HIV. <i>American Journal of Geriatric Psychiatry</i> , 2018, 26, S118-S119.	1.2	3

#	ARTICLE	IF	CITATIONS
307	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
308	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
309	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
310	The impact of reproductive factors on DNA methylation-based telomere length in healthy breast tissue. <i>Npj Breast Cancer</i> , 2022, 8, 48.	5.2	3
311	An Analysis of Methylome Evolution in Primates. <i>Molecular Biology and Evolution</i> , 2021, 38, 4700-4714.	8.9	2
312	Epigenetic Clocks. , 2022, , 261-276.		2
313	A candidate gene study of intermediate histopathological phenotypes in HIV-associated neurocognitive disorders. <i>Journal of NeuroVirology</i> , 2020, 26, 496-508.	2.1	1
314	Integrating Genetic and Network Analysis to Characterize Genes Related to Mouse Weight. <i>PLoS Genetics</i> , 2005, preprint, e130.	3.5	1
315	DNA Methylation Differences in Twins Discordant for Adolescent/Young Adult Hodgkin Lymphoma. <i>Blood</i> , 2015, 126, 179-179.	1.4	1
316	Erratum to "Increased Menopausal Age Reduces the Risk of Parkinson's Disease: A Mendelian Approach". <i>Movement Disorders</i> , 2022, 37, 1282-1283.	3.9	1
317	EPIGENETIC PREDICTORS OF LIFESPAN AND HEALTHSPAN. <i>Innovation in Aging</i> , 2019, 3, S33-S33.	0.1	0
318	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
319	Pesticide Exposure, Systems Biology, and Parkinson's disease. <i>ISEE Conference Abstracts</i> , 2021, 2021, .	0.0	0
320	Sex hormones and Alzheimer's disease: A Mendelian randomization approach. <i>Journal of the Neurological Sciences</i> , 2021, 429, 118981.	0.6	0
321	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