

# Steve Horvath

## List of Publications by Year in descending order

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Version: 2024-02-01

321  
papers

83,301  
citations

1606

105  
h-index

538

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.	1.2	17,294
2	A General Framework for Weighted Gene Co-Expression Network Analysis. Statistical Applications in Genetics and Molecular Biology, 2005, 4, Article17.	0.2	4,608
3	DNA methylation age of human tissues and cell types. Genome Biology, 2013, 14, R115.	13.9	4,566
4	An anatomically comprehensive atlas of the adult human brain transcriptome. Nature, 2012, 489, 391-399.	13.7	2,321
5	DNA methylation-based biomarkers and the epigenetic clock theory of ageing. Nature Reviews Genetics, 2018, 19, 371-384.	7.7	1,741
6	Defining clusters from a hierarchical cluster tree: the Dynamic Tree Cut package for R. Bioinformatics, 2008, 24, 719-720.	1.8	1,665
7	Transcriptomic analysis of autistic brain reveals convergent molecular pathology. Nature, 2011, 474, 380-384.	13.7	1,654
8	An epigenetic biomarker of aging for lifespan and healthspan. Aging, 2018, 10, 573-591.	1.4	1,552
9	Molecular Determinants of the Response of Glioblastomas to EGFR Kinase Inhibitors. New England Journal of Medicine, 2005, 353, 2012-2024.	13.9	1,376
10	DNA methylation GrimAge strongly predicts lifespan and healthspan. Aging, 2019, 11, 303-327.	1.4	1,128
11	Global histone modification patterns predict risk of prostate cancer recurrence. Nature, 2005, 435, 1262-1266.	13.7	991
12	Integrative Functional Genomic Analyses Implicate Specific Molecular Pathways and Circuits in Autism. Cell, 2013, 155, 1008-1021.	13.5	948
13	DNA methylation age of blood predicts all-cause mortality in later life. Genome Biology, 2015, 16, 25.	3.8	928
14	Is My Network Module Preserved and Reproducible?. PLoS Computational Biology, 2011, 7, e1001057.	1.5	885
15	Genetic programs in human and mouse early embryos revealed by single-cell RNA sequencing. Nature, 2013, 500, 593-597.	13.7	859
16	Fast R Functions for Robust Correlations and Hierarchical Clustering. Journal of Statistical Software, 2012, 46, .	1.8	856
17	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. Science, 2018, 359, 693-697.	6.0	851
18	Variations in DNA elucidate molecular networks that cause disease. Nature, 2008, 452, 429-435.	13.7	840

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19	DNA methylation-based measures of biological age: meta-analysis predicting time to death. <i>Aging</i> , 2016, 8, 1844-1865.	1.4	786
20	Epigenetic Predictor of Age. <i>PLoS ONE</i> , 2011, 6, e14821.	1.1	781
21	Functional organization of the transcriptome in human brain. <i>Nature Neuroscience</i> , 2008, 11, 1271-1282.	7.1	743
22	Geometric Interpretation of Gene Coexpression Network Analysis. <i>PLoS Computational Biology</i> , 2008, 4, e1000117.	1.5	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.	1.4	696
24	Gene Expression Profiling of Gliomas Strongly Predicts Survival. <i>Cancer Research</i> , 2004, 64, 6503-6510.	0.4	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.	3.3	620
26	Genome-wide changes in lncRNA, splicing, and regional gene expression patterns in autism. <i>Nature</i> , 2016, 540, 423-427.	13.7	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.	3.3	580
28	Role of the Murine Reprogramming Factors in the Induction of Pluripotency. <i>Cell</i> , 2009, 136, 364-377.	13.5	579
29	Gene network interconnectedness and the generalized topological overlap measure. <i>BMC Bioinformatics</i> , 2007, 8, 22.	1.2	567
30	DNA methylation aging clocks: challenges and recommendations. <i>Genome Biology</i> , 2019, 20, 249.	3.8	552
31	Aging effects on DNA methylation modules in human brain and blood tissue. <i>Genome Biology</i> , 2012, 13, R97.	13.9	536
32	An epigenetic clock analysis of race/ethnicity, sex, and coronary heart disease. <i>Genome Biology</i> , 2016, 17, 171.	3.8	535
33	Epigenetic clock analysis of diet, exercise, education, and lifestyle factors. <i>Aging</i> , 2017, 9, 419-446.	1.4	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.	3.3	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.	3.9	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.	3.2	492

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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.	3.3	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.	0.9	472
39	HIV-1 Infection Accelerates Age According to the Epigenetic Clock. Journal of Infectious Diseases, 2015, 212, 1563-1573.	1.9	467
40	Global Levels of Histone Modifications Predict Prognosis in Different Cancers. American Journal of Pathology, 2009, 174, 1619-1628.	1.9	448
41	Accelerated epigenetic aging in Down syndrome. Aging Cell, 2015, 14, 491-495.	3.0	446
42	Reprogramming to recover youthful epigenetic information and restore vision. Nature, 2020, 588, 124-129.	13.7	424
43	Integrating Genetic and Network Analysis to Characterize Genes Related to Mouse Weight. PLoS Genetics, 2006, 2, e130.	1.5	419
44	Epigenetic clock for skin and blood cells applied to Hutchinson Gilford Progeria Syndrome and ex vivo studies. Aging, 2018, 10, 1758-1775.	1.4	406
45	Family-based tests for associating haplotypes with general phenotype data: Application to asthma genetics. Genetic Epidemiology, 2004, 26, 61-69.	0.6	395
46	Unsupervised Learning With Random Forest Predictors. Journal of Computational and Graphical Statistics, 2006, 15, 118-138.	0.9	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.	1.4	368
48	Menopause accelerates biological aging. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9327-9332.	3.3	363
49	Increased epigenetic age and granulocyte counts in the blood of Parkinson's disease patients. Aging, 2015, 7, 1130-1142.	1.4	344
50	Integrated genomics and proteomics define huntingtin CAG length-dependent networks in mice. Nature Neuroscience, 2016, 19, 623-633.	7.1	342
51	Analysis of the phosphatidylinositol 3'-kinase signaling pathway in glioblastoma patients in vivo. Cancer Research, 2003, 63, 2742-6.	0.4	342
52	Weighted gene coexpression network analysis strategies applied to mouse weight. Mammalian Genome, 2007, 18, 463-472.	1.0	337
53	Reversal of epigenetic aging and immunosenescent trends in humans. Aging Cell, 2019, 18, e13028.	3.0	335
54	A Systems-Level Analysis of the Peripheral Nerve Intrinsic Axonal Growth Program. Neuron, 2016, 89, 956-970.	3.8	314

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55	Differential Sensitivity of Glioma- versus Lung Cancer-Specific EGFR Mutations to EGFR Kinase Inhibitors. <i>Cancer Discovery</i> , 2012, 2, 458-471.	7.7	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.	3.3	303
57	Sexually dimorphic gene expression in mouse brain precedes gonadal differentiation. <i>Molecular Brain Research</i> , 2003, 118, 82-90.	2.5	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.	9.4	297
59	Strategies for aggregating gene expression data: The collapseRows R function. <i>BMC Bioinformatics</i> , 2011, 12, 322.	1.2	290
60	EGFR Signaling Through an Akt-SREBP-1-Dependent, Rapamycin-Resistant Pathway Sensitizes Glioblastomas to Antitipogenic Therapy. <i>Science Signaling</i> , 2009, 2, ra82.	1.6	282
61	Decreased epigenetic age of PBMCs from Italian semi-supercentenarians and their offspring. <i>Aging</i> , 2015, 7, 1159-1170.	1.4	276
62	Genes and pathways underlying regional and cell type changes in Alzheimer's disease. <i>Genome Medicine</i> , 2013, 5, 48.	3.6	267
63	Gene expression profiling identifies molecular subtypes of gliomas. <i>Oncogene</i> , 2003, 22, 4918-4923.	2.6	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.	2.6	264
65	Network Organization of the Huntingtin Proteomic Interactome in Mammalian Brain. <i>Neuron</i> , 2012, 75, 41-57.	3.8	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.	1.4	254
67	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. <i>Genome Biology</i> , 2016, 17, 255.	3.8	251
68	Identification of molecular subtypes of glioblastoma by gene expression profiling. <i>Oncogene</i> , 2003, 22, 2361-2373.	2.6	247
69	When Is Hub Gene Selection Better than Standard Meta-Analysis?. <i>PLoS ONE</i> , 2013, 8, e61505.	1.1	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.	13.5	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.	2.6	233

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73	Using Protein Expressions to Predict Survival in Clear Cell Renal Carcinoma. <i>Clinical Cancer Research</i> , 2004, 10, 5464-5471.	3.2	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.	3.9	210
75	Signed weighted gene co-expression network analysis of transcriptional regulation in murine embryonic stem cells. <i>BMC Genomics</i> , 2009, 10, 327.	1.2	209
76	Neurosphere Formation Is an Independent Predictor of Clinical Outcome in Malignant Glioma. <i>Stem Cells</i> , 2009, 27, 980-987.	1.4	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.	1.4	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.	0.8	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.	1.2	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.	1.7	200
81	DNA methylation-based estimator of telomere length. <i>Aging</i> , 2019, 11, 5895-5923.	1.4	198
82	Prostate Stem Cell Antigen Is Overexpressed in Prostate Cancer Metastases. <i>Clinical Cancer Research</i> , 2005, 11, 2591-2596.	3.2	195
83	An epigenetic clock for gestational age at birth based on blood methylation data. <i>Genome Biology</i> , 2016, 17, 206.	3.8	193
84	Huntington's disease accelerates epigenetic aging of human brain and disrupts DNA methylation levels. <i>Aging</i> , 2016, 8, 1485-1512.	1.4	192
85	Long-term maturation of human cortical organoids matches key early postnatal transitions. <i>Nature Neuroscience</i> , 2021, 24, 331-342.	7.1	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.	1.3	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.	5.8	183
88	Resting-State Quantitative Electroencephalography Reveals Increased Neurophysiologic Connectivity in Depression. <i>PLoS ONE</i> , 2012, 7, e32508.	1.1	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.	2.9	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.	1.5	168

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91	A multi-tissue full lifespan epigenetic clock for mice. <i>Aging</i> , 2018, 10, 2832-2854.	1.4	166
92	The cerebellum ages slowly according to the epigenetic clock. <i>Aging</i> , 2015, 7, 294-306.	1.4	162
93	Tumor classification by tissue microarray profiling: random forest clustering applied to renal cell carcinoma. <i>Modern Pathology</i> , 2005, 18, 547-557.	2.9	159
94	Maintenance of age in human neurons generated by microRNA-based neuronal conversion of fibroblasts. <i>ELife</i> , 2016, 5, .	2.8	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.	1.3	154
96	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , 2017, 101, 888-902.	2.6	154
97	Accelerated epigenetic aging in Werner syndrome. <i>Aging</i> , 2017, 9, 1143-1152.	1.4	152
98	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. <i>Nature Communications</i> , 2018, 9, 387.	5.8	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.	1.1	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.	2.0	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.	1.3	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.	3.3	140
104	Protein interaction network of alternatively spliced isoforms from brain links genetic risk factors for autism. <i>Nature Communications</i> , 2014, 5, 3650.	5.8	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.	3.3	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.	1.1	125
107	Epigenetic clock analyses of cellular senescence and ageing. <i>Oncotarget</i> , 2016, 7, 8524-8531.	0.8	125
108	An epigenetic aging clock for dogs and wolves. <i>Aging</i> , 2017, 9, 1055-1068.	1.4	125

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109	Parkinson's disease is associated with DNA methylation levels in human blood and saliva. <i>Genome Medicine</i> , 2017, 9, 76.	3.6	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.	5.2	119
111	The organization of the transcriptional network in specific neuronal classes. <i>Molecular Systems Biology</i> , 2009, 5, 291.	3.2	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.	3.3	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.	1.8	111
114	IL-32 is a molecular marker of a host defense network in human tuberculosis. <i>Science Translational Medicine</i> , 2014, 6, 250ra114.	5.8	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.	1.8	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.	3.2	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.	0.7	108
118	Molecular Microcircuitry Underlies Functional Specification in a Basal Ganglia Circuit Dedicated to Vocal Learning. <i>Neuron</i> , 2012, 73, 537-552.	3.8	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.	1.0	101
120	Acceleration of Age-Associated Methylation Patterns in HIV-1-Infected Adults. <i>PLoS ONE</i> , 2015, 10, e0119201.	1.1	101
121	In vivo partial reprogramming alters age-associated molecular changes during physiological aging in mice. <i>Nature Aging</i> , 2022, 2, 243-253.	5.3	101
122	Breast Cancer Molecular Signatures as Determined by SAGE: Correlation with Lymph Node Status. <i>Molecular Cancer Research</i> , 2007, 5, 881-890.	1.5	99
123	Neuropathological and transcriptomic characteristics of the aged brain. <i>ELife</i> , 2017, 6, .	2.8	97
124	Correlation of Ki-67 and gelsolin expression to clinical outcome in renal clear cell carcinoma. <i>Urology</i> , 2003, 61, 845-850.	0.5	95
125	"Good Enough Solutions" and the Genetics of Complex Diseases. <i>Circulation Research</i> , 2012, 111, 493-504.	2.0	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.	2.9	94

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127	A mammalian methylation array for profiling methylation levels at conserved sequences. <i>Nature Communications</i> , 2022, 13, 783.	5.8	93
128	Genetic architecture of epigenetic and neuronal ageing rates in human brain regions. <i>Nature Communications</i> , 2017, 8, 15353.	5.8	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.	3.3	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.	3.2	91
131	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021, 22, 194.	3.8	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.	0.9	86
134	Faster ticking rate of the epigenetic clock is associated with faster pubertal development in girls. <i>Epigenetics</i> , 2018, 13, 85-94.	1.3	86
135	Making sense of the ageing methylome. <i>Nature Reviews Genetics</i> , 2022, 23, 585-605.	7.7	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.	5.8	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.	1.3	83
138	A meta-analysis of genome-wide association studies of epigenetic age acceleration. <i>PLoS Genetics</i> , 2019, 15, e1008104.	1.5	83
139	Tissue microarray analysis of cytoskeletal actin-associated biomarkers gelsolin and E-cadherin in urothelial carcinoma. <i>Cancer</i> , 2002, 95, 1247-1257.	2.0	82
140	Perinatally acquired HIV infection accelerates epigenetic aging in South African adolescents. <i>Aids</i> , 2018, 32, 1465-1474.	1.0	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.	1.7	81
142	Detecting network modules in fMRI time series: A weighted network analysis approach. <i>NeuroImage</i> , 2010, 52, 1465-1476.	2.1	80
143	DNA methylation predicts age and provides insight into exceptional longevity of bats. <i>Nature Communications</i> , 2021, 12, 1615.	5.8	80
144	Placental epigenetic clocks: estimating gestational age using placental DNA methylation levels. <i>Aging</i> , 2019, 11, 4238-4253.	1.4	79

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145	An epigenetic predictor of death captures multi-modal measures of brain health. <i>Molecular Psychiatry</i> , 2021, 26, 3806-3816.	4.1	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.	3.2	74
147	Biomarkers for Early and Late Stage Chronic Allograft Nephropathy by Proteogenomic Profiling of Peripheral Blood. <i>PLoS ONE</i> , 2009, 4, e6212.	1.1	74
148	Loss of CD10 (neutral endopeptidase) is a frequent and early event in human prostate cancer. <i>Prostate</i> , 2003, 55, 71-80.	1.2	73
149	DNA methylation age is accelerated in alcohol dependence. <i>Translational Psychiatry</i> , 2018, 8, 182.	2.4	73
150	Alteration in basal and depolarization induced transcriptional network in iPSC derived neurons from Timothy syndrome. <i>Genome Medicine</i> , 2014, 6, 75.	3.6	72
151	Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. <i>Aging Cell</i> , 2021, 20, e13366.	3.0	72
152	An epigenetic clock for human skeletal muscle. <i>Journal of Cachexia, Sarcopenia and Muscle</i> , 2020, 11, 887-898.	2.9	70
153	Epigenetic ageing is distinct from senescence-mediated ageing and is not prevented by telomerase expression. <i>Aging</i> , 2018, 10, 2800-2815.	1.4	70
154	Genetic variants near MLST8 and DHX57 affect the epigenetic age of the cerebellum. <i>Nature Communications</i> , 2016, 7, 10561.	5.8	69
155	Extreme skewing of X chromosome inactivation in mothers of homosexual men. <i>Human Genetics</i> , 2006, 118, 691-694.	1.8	68
156	Metabolic and inflammatory biomarkers are associated with epigenetic aging acceleration estimates in the GOLDN study. <i>Clinical Epigenetics</i> , 2018, 10, 56.	1.8	68
157	Incorporation of a nucleoside analog maps genome repair sites in postmitotic human neurons. <i>Science</i> , 2021, 372, 91-94.	6.0	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.	1.0	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.	1.5	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.	0.3	65
162	Epigenetic aging is accelerated in alcohol use disorder and regulated by genetic variation in APOL2. <i>Neuropsychopharmacology</i> , 2020, 45, 327-336.	2.8	62

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163	Antibody-Based Profiling of the Phosphoinositide 3-Kinase Pathway in Clinical Prostate Cancer. <i>Clinical Cancer Research</i> , 2004, 10, 8351-8356.	3.2	60
164	Methylome-wide association study provides evidence of particulate matter air pollution-associated DNA methylation. <i>Environment International</i> , 2019, 132, 104723.	4.8	58
165	Statistical Methods for Analyzing Tissue Microarray Data. <i>Journal of Biopharmaceutical Statistics</i> , 2004, 14, 671-685.	0.4	57
166	Organophosphate pesticide exposure and differential genome-wide DNA methylation. <i>Science of the Total Environment</i> , 2018, 645, 1135-1143.	3.9	56
167	Epigenetic Age Acceleration Reflects Long-Term Cardiovascular Health. <i>Circulation Research</i> , 2021, 129, 770-781.	2.0	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.	2.6	54
169	Trefoil factor 3 is overexpressed in human prostate cancer. <i>Prostate</i> , 2004, 61, 209-214.	1.2	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.	1.4	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.	0.4	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.	2.3	53
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