

# Riccardo E Marioni

## List of Publications by Citations

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**Version:** 2024-04-23

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196  
papers

11,814  
citations

53  
h-index

107  
g-index

235  
ext. papers

16,759  
ext. citations

9.9  
avg, IF

5.86  
L-index

#	Paper	IF	Citations
196	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , <b>2016</b> , 533, 539-42	50.4	850
195	DNA methylation age of blood predicts all-cause mortality in later life. <i>Genome Biology</i> , <b>2015</b> , 16, 25	18.3	670
194	Genome-wide meta-analysis of depression identifies 102 independent variants and highlights the importance of the prefrontal brain regions. <i>Nature Neuroscience</i> , <b>2019</b> , 22, 343-352	25.5	639
193	Age-associated cognitive decline. <i>British Medical Bulletin</i> , <b>2009</b> , 92, 135-52	5.4	616
192	DNA methylation-based measures of biological age: meta-analysis predicting time to death. <i>Aging</i> , <b>2016</b> , 8, 1844-1865	5.6	531
191	Epigenetic Signatures of Cigarette Smoking. <i>Circulation: Cardiovascular Genetics</i> , <b>2016</b> , 9, 436-447		442
190	The epigenetic clock is correlated with physical and cognitive fitness in the Lothian Birth Cohort 1936. <i>International Journal of Epidemiology</i> , <b>2015</b> , 44, 1388-96	7.8	357
189	Cognitive function, dementia and type 2 diabetes mellitus in the elderly. <i>Nature Reviews Endocrinology</i> , <b>2011</b> , 7, 108-14	15.2	265
188	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. <i>Nature Communications</i> , <b>2018</b> , 9, 2098	17.4	254
187	DNA methylation aging clocks: challenges and recommendations. <i>Genome Biology</i> , <b>2019</b> , 20, 249	18.3	248
186	GWAS on family history of Alzheimer's disease. <i>Translational Psychiatry</i> , <b>2018</b> , 8, 99	8.6	238
185	Association of low-frequency and rare coding-sequence variants with blood lipids and coronary heart disease in 56,000 whites and blacks. <i>American Journal of Human Genetics</i> , <b>2014</b> , 94, 223-32	11	233
184	Genome-wide association study of depression phenotypes in UK Biobank identifies variants in excitatory synaptic pathways. <i>Nature Communications</i> , <b>2018</b> , 9, 1470	17.4	226
183	Ultra-High-Throughput Clinical Proteomics Reveals Classifiers of COVID-19 Infection. <i>Cell Systems</i> , <b>2020</b> , 11, 11-24.e4	10.6	219
182	Genomic structural equation modelling provides insights into the multivariate genetic architecture of complex traits. <i>Nature Human Behaviour</i> , <b>2019</b> , 3, 513-525	12.8	209
181	Association analysis in over 329,000 individuals identifies 116 independent variants influencing neuroticism. <i>Nature Genetics</i> , <b>2018</b> , 50, 6-11	36.3	202
180	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. <i>Nature Genetics</i> , <b>2016</b> , 48, 1151-1161	36.3	181

179	Common genetic variants associated with cognitive performance identified using the proxy-phenotype method. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 13790-4	11.5	181
178	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. <i>Genome Biology</i> , <b>2016</b> , 17, 255	18.3	171
177	Association of Body Mass Index with DNA Methylation and Gene Expression in Blood Cells and Relations to Cardiometabolic Disease: A Mendelian Randomization Approach. <i>PLoS Medicine</i> , <b>2017</b> , 14, e1002215	11.6	162
176	The epigenetic clock and telomere length are independently associated with chronological age and mortality. <i>International Journal of Epidemiology</i> , <b>2018</b> , 45, 424-432	7.8	153
175	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. <i>American Journal of Human Genetics</i> , <b>2018</b> , 103, 691-706	11	151
174	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. <i>Nature Communications</i> , <b>2018</b> , 9, 2282	17.4	147
173	Brain age and other bodily 'ages': implications for neuropsychiatry. <i>Molecular Psychiatry</i> , <b>2019</b> , 24, 266-281	11.1	146
172	Molecular genetic contributions to socioeconomic status and intelligence. <i>Intelligence</i> , <b>2014</b> , 44, 26-32	3	131
171	Molecular Genetic Contributions to Social Deprivation and Household Income in UK Biobank. <i>Current Biology</i> , <b>2016</b> , 26, 3083-3089	6.3	126
170	Genetic and environmental exposures constrain epigenetic drift over the human life course. <i>Genome Research</i> , <b>2014</b> , 24, 1725-33	9.7	123
169	Association between raised inflammatory markers and cognitive decline in elderly people with type 2 diabetes: the Edinburgh Type 2 Diabetes Study. <i>Diabetes</i> , <b>2010</b> , 59, 710-3	0.9	123
168	Social adversity and epigenetic aging: a multi-cohort study on socioeconomic differences in peripheral blood DNA methylation. <i>Scientific Reports</i> , <b>2017</b> , 7, 16266	4.9	118
167	Investigating the possible causal association of smoking with depression and anxiety using Mendelian randomisation meta-analysis: the CARTA consortium. <i>BMJ Open</i> , <b>2014</b> , 4, e006141	3	115
166	Integrative analysis of omics summary data reveals putative mechanisms underlying complex traits. <i>Nature Communications</i> , <b>2018</b> , 9, 918	17.4	110
165	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. <i>Nature Communications</i> , <b>2018</b> , 9, 387	17.4	106
164	Social activity, cognitive decline and dementia risk: a 20-year prospective cohort study. <i>BMC Public Health</i> , <b>2015</b> , 15, 1089	4.1	99
163	DNA methylation levels at individual age-associated CpG sites can be indicative for life expectancy. <i>Aging</i> , <b>2016</b> , 8, 394-401	5.6	99
162	Genetic variants linked to education predict longevity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 13366-13371	11.5	90

161	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. <i>American Journal of Human Genetics</i> , <b>2015</b> , 97, 75-85	11	85
160	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , <b>2017</b> , 101, 888-902	11	83
159	Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. <i>Genome Medicine</i> , <b>2019</b> , 11, 54	14.4	81
158	Identification of 55,000 Replicated DNA Methylation QTL. <i>Scientific Reports</i> , <b>2018</b> , 8, 17605	4.9	78
157	Epigenetic prediction of complex traits and death. <i>Genome Biology</i> , <b>2018</b> , 19, 136	18.3	77
156	Epigenetic Patterns in Blood Associated With Lipid Traits Predict Incident Coronary Heart Disease Events and Are Enriched for Results From Genome-Wide Association Studies. <i>Circulation: Cardiovascular Genetics</i> , <b>2017</b> , 10,		72
155	Effect of Smoking on Blood Pressure and Resting Heart Rate: A Mendelian Randomization Meta-Analysis in the CARTA Consortium. <i>Circulation: Cardiovascular Genetics</i> , <b>2015</b> , 8, 832-41		70
154	Active cognitive lifestyle is associated with positive cognitive health transitions and compression of morbidity from age sixty-five. <i>PLoS ONE</i> , <b>2012</b> , 7, e50940	3.7	69
153	DNA methylation-based estimator of telomere length. <i>Aging</i> , <b>2019</b> , 11, 5895-5923	5.6	69
152	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. <i>Nature Communications</i> , <b>2018</b> , 9, 5141	17.4	64
151	Active cognitive lifestyle associates with cognitive recovery and a reduced risk of cognitive decline. <i>Journal of Alzheimer's Disease</i> , <b>2012</b> , 28, 223-30	4.3	62
150	Partial reprogramming induces a steady decline in epigenetic age before loss of somatic identity. <i>Aging Cell</i> , <b>2019</b> , 18, e12877	9.9	62
149	Peripheral levels of fibrinogen, C-reactive protein, and plasma viscosity predict future cognitive decline in individuals without dementia. <i>Psychosomatic Medicine</i> , <b>2009</b> , 71, 901-6	3.7	61
148	Genetic prediction of male pattern baldness. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006594	6	59
147	Cognitive lifestyle jointly predicts longitudinal cognitive decline and mortality risk. <i>European Journal of Epidemiology</i> , <b>2014</b> , 29, 211-9	12.1	59
146	Investigating the relationship between DNA methylation age acceleration and risk factors for Alzheimer's disease. <i>Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring</i> , <b>2018</b> , 10, 429-437	5.2	57
145	Reverse causation in the association between C-reactive protein and fibrinogen levels and cognitive abilities in an aging sample. <i>Psychosomatic Medicine</i> , <b>2009</b> , 71, 404-9	3.7	56
144	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. <i>Human Molecular Genetics</i> , <b>2016</b> , 25, 358-70	5.6	54

143	Association of KIBRA and memory. <i>Neuroscience Letters</i> , <b>2009</b> , 458, 140-3	3.3	52
142	DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons: Meta-analysis of Multiethnic Epigenome-wide Studies. <i>JAMA Psychiatry</i> , <b>2018</b> , 75, 949-959	14.5	51
141	Differential effects of the APOE e4 allele on different domains of cognitive ability across the life-course. <i>European Journal of Human Genetics</i> , <b>2016</b> , 24, 919-23	5.3	47
140	Meta-analysis of epigenome-wide association studies of cognitive abilities. <i>Molecular Psychiatry</i> , <b>2018</b> , 23, 2133-2144	15.1	46
139	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. <i>Blood</i> , <b>2015</b> , 126, e19-29	2.2	45
138	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> , <b>2019</b> , 74, 57-61	6.4	45
137	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. <i>Molecular Psychiatry</i> , <b>2020</b> , 25, 2392-2409	15.1	45
136	An epigenome-wide association study of sex-specific chronological ageing. <i>Genome Medicine</i> , <b>2019</b> , 12, 1	14.4	43
135	Risk prediction of late-onset Alzheimer's disease implies an oligogenic architecture. <i>Nature Communications</i> , <b>2020</b> , 11, 4799	17.4	41
134	Stratification by smoking status reveals an association of CHRNA5-A3-B4 genotype with body mass index in never smokers. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004799	6	40
133	Epigenetic measures of ageing predict the prevalence and incidence of leading causes of death and disease burden. <i>Clinical Epigenetics</i> , <b>2020</b> , 12, 115	7.7	40
132	Heavier smoking may lead to a relative increase in waist circumference: evidence for a causal relationship from a Mendelian randomisation meta-analysis. The CARTA consortium. <i>BMJ Open</i> , <b>2015</b> , 5, e008808	3	39
131	A meta-analysis of genome-wide association studies of epigenetic age acceleration. <i>PLoS Genetics</i> , <b>2019</b> , 15, e1008104	6	38
130	Epigenetic influences on aging: a longitudinal genome-wide methylation study in old Swedish twins. <i>Epigenetics</i> , <b>2018</b> , 13, 975-987	5.7	37
129	DNA methylation and the epigenetic clock in relation to physical frailty in older people: the Lothian Birth Cohort 1936. <i>Clinical Epigenetics</i> , <b>2018</b> , 10, 101	7.7	36
128	Epigenetic signatures of starting and stopping smoking. <i>EBioMedicine</i> , <b>2018</b> , 37, 214-220	8.8	36
127	Examining the influence of gender, education, social class and birth cohort on MMSE tracking over time: a population-based prospective cohort study. <i>BMC Geriatrics</i> , <b>2012</b> , 12, 45	4.1	35
126	Multiethnic Exome-Wide Association Study of Subclinical Atherosclerosis. <i>Circulation: Cardiovascular Genetics</i> , <b>2016</b> , 9, 511-520		34

125	Longitudinal telomere length shortening and cognitive and physical decline in later life: The Lothian Birth Cohorts 1936 and 1921. <i>Mechanisms of Ageing and Development</i> , <b>2016</b> , 154, 43-8	5.6	34
124	A time-resolved proteomic and prognostic map of COVID-19. <i>Cell Systems</i> , <b>2021</b> , 12, 780-794.e7	10.6	32
123	The reliability of assigning individuals to cognitive states using the Mini Mental-State Examination: a population-based prospective cohort study. <i>BMC Medical Research Methodology</i> , <b>2011</b> , 11, 127	4.7	31
122	Association between polymorphisms of the dopamine receptor D2 and catechol-o-methyl transferase genes and cognitive function. <i>Behavior Genetics</i> , <b>2010</b> , 40, 630-8	3.2	31
121	An epigenetic predictor of death captures multi-modal measures of brain health. <i>Molecular Psychiatry</i> , <b>2021</b> , 26, 3806-3816	15.1	31
120	Molecular genetic contributions to self-rated health. <i>International Journal of Epidemiology</i> , <b>2017</b> , 46, 994-1009	7.8	30
119	Common genetic variants explain the majority of the correlation between height and intelligence: the generation Scotland study. <i>Behavior Genetics</i> , <b>2014</b> , 44, 91-6	3.2	30
118	Variation in the uric acid transporter gene (SLC2A9) and memory performance. <i>Human Molecular Genetics</i> , <b>2010</b> , 19, 2321-30	5.6	29
117	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , <b>2021</b> , 53, 1311-1321	36.3	27
116	C-reactive protein, APOE genotype and longitudinal cognitive change in an older population. <i>Age and Ageing</i> , <b>2014</b> , 43, 289-92	3	26
115	Polygenic predictors of age-related decline in cognitive ability. <i>Molecular Psychiatry</i> , <b>2020</b> , 25, 2584-2598	5.1	24
114	Identification, replication and characterization of epigenetic remodelling in the aging genome: a cross population analysis. <i>Scientific Reports</i> , <b>2017</b> , 7, 8183	4.9	23
113	Parent of origin genetic effects on methylation in humans are common and influence complex trait variation. <i>Nature Communications</i> , <b>2019</b> , 10, 1383	17.4	21
112	Genome and epigenome wide studies of neurological protein biomarkers in the Lothian Birth Cohort 1936. <i>Nature Communications</i> , <b>2019</b> , 10, 3160	17.4	21
111	Genetic Stratification to Identify Risk Groups for Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , <b>2017</b> , 57, 275-283	4.3	21
110	Comparison of HapMap and 1000 Genomes Reference Panels in a Large-Scale Genome-Wide Association Study. <i>PLoS ONE</i> , <b>2017</b> , 12, e0167742	3.7	21
109	Genotype effects contribute to variation in longitudinal methylome patterns in older people. <i>Genome Medicine</i> , <b>2018</b> , 10, 75	14.4	21
108	Age-related clonal haemopoiesis is associated with increased epigenetic age. <i>Current Biology</i> , <b>2019</b> , 29, R786-R787	6.3	20

107	Age-related gene expression changes, and transcriptome wide association study of physical and cognitive aging traits, in the Lothian Birth Cohort 1936. <i>Aging</i> , <b>2017</b> , 9, 2489-2503	5.6	20
106	Bayesian reassessment of the epigenetic architecture of complex traits. <i>Nature Communications</i> , <b>2020</b> , 11, 2865	17.4	18
105	Epigenetic prediction of major depressive disorder. <i>Molecular Psychiatry</i> , <b>2021</b> , 26, 5112-5123	15.1	18
104	The epigenetic clock and objectively measured sedentary and walking behavior in older adults: the Lothian Birth Cohort 1936. <i>Clinical Epigenetics</i> , <b>2018</b> , 10, 4	7.7	18
103	Improving access to psychological therapies and older people: findings from the Eastern Region. <i>Behaviour Research and Therapy</i> , <b>2014</b> , 56, 75-81	5.2	18
102	Association of Methylation Signals With Incident Coronary Heart Disease in an Epigenome-Wide Assessment of Circulating Tumor Necrosis Factor $\square$ <i>JAMA Cardiology</i> , <b>2018</b> , 3, 463-472	16.2	17
101	Epigenetic signatures of smoking associate with cognitive function, brain structure, and mental and physical health outcomes in the Lothian Birth Cohort 1936. <i>Translational Psychiatry</i> , <b>2019</b> , 9, 248	8.6	17
100	The total burden of rare, non-synonymous exome genetic variants is not associated with childhood or late-life cognitive ability. <i>Proceedings of the Royal Society B: Biological Sciences</i> , <b>2014</b> , 281, 20140117	4.4	17
99	Trajectories of inflammatory biomarkers over the eighth decade and their associations with immune cell profiles and epigenetic ageing. <i>Clinical Epigenetics</i> , <b>2018</b> , 10, 159	7.7	17
98	Genetic variants associated with altered plasma levels of C-reactive protein are not associated with late-life cognitive ability in four Scottish samples. <i>Behavior Genetics</i> , <b>2010</b> , 40, 3-11	3.2	16
97	Characterisation of an inflammation-related epigenetic score and its association with cognitive ability. <i>Clinical Epigenetics</i> , <b>2020</b> , 12, 113	7.7	15
96	Identification of 55,000 Replicated DNA Methylation QTL		14
95	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , <b>2021</b> , 22, 194	18.3	14
94	Structural brain correlates of serum and epigenetic markers of inflammation in major depressive disorder. <i>Brain, Behavior, and Immunity</i> , <b>2021</b> , 92, 39-48	16.6	14
93	Misestimation of heritability and prediction accuracy of male-pattern baldness. <i>Nature Communications</i> , <b>2018</b> , 9, 2537	17.4	14
92	Identification of novel differentially methylated sites with potential as clinical predictors of impaired respiratory function and COPD. <i>EBioMedicine</i> , <b>2019</b> , 43, 576-586	8.8	13
91	Exploratory analysis of age and sex dependent DNA methylation patterns on the X-chromosome in whole blood samples. <i>Genome Medicine</i> , <b>2020</b> , 12, 39	14.4	13
90	Polygenic risk of ischemic stroke is associated with cognitive ability. <i>Neurology</i> , <b>2016</b> , 86, 611-8	6.5	13

89	Genetic associations between fibrinogen and cognitive performance in three Scottish cohorts. <i>Behavior Genetics</i> , <b>2011</b> , 41, 691-9	3.2	13
88	Blood rheology and cognition in the Edinburgh Type 2 Diabetes Study. <i>Age and Ageing</i> , <b>2010</b> , 39, 354-9	3	13
87	Age-dependent DNA methylation patterns on the Y chromosome in elderly males. <i>Aging Cell</i> , <b>2020</b> , 19, e12907	9.9	13
86	An epigenetic score for BMI based on DNA methylation correlates with poor physical health and major disease in the Lothian Birth Cohort. <i>International Journal of Obesity</i> , <b>2019</b> , 43, 1795-1802	5.5	12
85	DNA methylome profiling of all-cause mortality in comparison with age-associated methylation patterns. <i>Clinical Epigenetics</i> , <b>2019</b> , 11, 23	7.7	11
84	Identification of epigenome-wide DNA methylation differences between carriers of APOE $\epsilon$ 4 and APOE $\epsilon$ 2 alleles. <i>Genome Medicine</i> , <b>2021</b> , 13, 1	14.4	11
83	Multi-method genome- and epigenome-wide studies of inflammatory protein levels in healthy older adults. <i>Genome Medicine</i> , <b>2020</b> , 12, 60	14.4	9
82	Altered DNA methylation associated with a translocation linked to major mental illness. <i>NPJ Schizophrenia</i> , <b>2018</b> , 4, 5	5.5	9
81	DNA methylation outlier burden, health, and ageing in Generation Scotland and the Lothian Birth Cohorts of 1921 and 1936. <i>Clinical Epigenetics</i> , <b>2020</b> , 12, 49	7.7	8
80	Neurology-related protein biomarkers are associated with cognitive ability and brain volume in older age. <i>Nature Communications</i> , <b>2020</b> , 11, 800	17.4	8
79	Epigenetic clocks predict prevalence and incidence of leading causes of death and disease burden		8
78	Genome-wide association studies identify 137 loci for DNA methylation biomarkers of ageing		8
77	Accelerated Epigenetic Ageing in Major Depressive Disorder		8
76	Genome-wide meta-analysis of depression identifies 102 independent variants and highlights the importance of the prefrontal brain regions		8
75	An epigenetic predictor of death captures multi-modal measures of brain health		8
74	Childhood intelligence attenuates the association between biological ageing and health outcomes in later life. <i>Translational Psychiatry</i> , <b>2019</b> , 9, 323	8.6	8
73	DNA methylation of blood cells is associated with prevalent type 2 diabetes in a meta-analysis of four European cohorts. <i>Clinical Epigenetics</i> , <b>2021</b> , 13, 40	7.7	8
72	Phenotypic and genetic analysis of cognitive performance in Major Depressive Disorder in the Generation Scotland: Scottish Family Health Study. <i>Translational Psychiatry</i> , <b>2018</b> , 8, 63	8.6	7



71	The association between late-life cognitive test scores and retrospective informant interview data. <i>International Psychogeriatrics</i> , <b>2011</b> , 23, 274-9	3.4	7
70	Birth weight associations with DNA methylation differences in an adult population. <i>Epigenetics</i> , <b>2021</b> , 16, 783-796	5.7	7
69	Epigenetic Age Acceleration and Cognitive Function in African American Adults in Midlife: The Atherosclerosis Risk in Communities Study. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , <b>2020</b> , 75, 473-480	6.4	7
68	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals.. <i>Nature Genetics</i> , <b>2022</b> ,	36.3	7
67	Exome sequencing to detect rare variants associated with general cognitive ability: a pilot study. <i>Twin Research and Human Genetics</i> , <b>2015</b> , 18, 117-25	2.2	6
66	DNA methylation-based measures of accelerated biological ageing and the risk of dementia in the oldest-old: a study of the Lothian Birth Cohort 1921. <i>BMC Psychiatry</i> , <b>2020</b> , 20, 91	4.2	6
65	Markers of Psychological Differences and Social and Health Inequalities: Possible Genetic and Phenotypic Overlaps. <i>Journal of Personality</i> , <b>2017</b> , 85, 104-117	4.4	6
64	A proteomic survival predictor for COVID-19 patients in intensive care <b>2022</b> , 1, e0000007		6
63	Blood DNA methylation sites predict death risk in a longitudinal study of 12, 300 individuals. <i>Aging</i> , <b>2020</b> , 12, 14092-14124	5.6	6
62	Ninety-nine independent genetic loci influencing general cognitive function include genes associated with brain health and structure (N = 280,360)		6
61	Improved prediction of chronological age from DNA methylation limits it as a biomarker of ageing		6
60	Meta-analysis of genome-wide DNA methylation identifies shared associations across neurodegenerative disorders. <i>Genome Biology</i> , <b>2021</b> , 22, 90	18.3	6
59	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. <i>Human Molecular Genetics</i> , <b>2021</b> , 30, 393-409	5.6	6
58	Association of facial ageing with DNA methylation and epigenetic age predictions. <i>Clinical Epigenetics</i> , <b>2018</b> , 10, 140	7.7	6
57	DNA methylation in APOE: The relationship with Alzheimer's and with cardiovascular health. <i>Alzheimer's and Dementia: Translational Research and Clinical Interventions</i> , <b>2020</b> , 6, e12026	6	5
56	Birth weight associations with psychiatric and physical health, cognitive function, and DNA methylation differences in an adult population		5
55	Epigenome-wide association study of leukocyte telomere length. <i>Aging</i> , <b>2019</b> , 11, 5876-5894	5.6	4
54	An epigenetic score for BMI based on DNA methylation correlates with poor physical health and major disease in the Lothian Birth Cohort 1936		4

53	Using tree-based methods for detection of gene-gene interactions in the presence of a polygenic signal: simulation study with application to educational attainment in the Generation Scotland Cohort Study. <i>Bioinformatics</i> , <b>2019</b> , 35, 181-188	7.2	3
52	Structural Brain MRI Trait Polygenic Score Prediction of Cognitive Abilities. <i>Twin Research and Human Genetics</i> , <b>2015</b> , 18, 738-45	2.2	3
51	DNA Methylation and Protein Markers of Chronic Inflammation and Their Associations With Brain and Cognitive Aging. <i>Neurology</i> , <b>2021</b> , 97, e2340-e2352	6.5	3
50	Epigenome-wide association study of kidney function identifies trans-ethnic and ethnic-specific loci. <i>Genome Medicine</i> , <b>2021</b> , 13, 74	14.4	3
49	Epigenetic prediction of complex traits and mortality in a cohort of individuals with oropharyngeal cancer. <i>Clinical Epigenetics</i> , <b>2020</b> , 12, 58	7.7	3
48	Addendum: Genome-wide association study of depression phenotypes in UK Biobank identifies variants in excitatory synaptic pathways. <i>Nature Communications</i> , <b>2018</b> , 9, 3578	17.4	3
47	Weighted Gene Coregulation Network Analysis of Promoter DNA Methylation on All-Cause Mortality in Old-Aged Birth Cohorts Finds Modules of High-Risk Associated Biomarkers. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , <b>2020</b> , 75, 2249-2257	6.4	2
46	Epigenetic scores for the circulating proteome as tools for disease prediction.. <i>ELife</i> , <b>2022</b> , 11,	8.9	2
45	Associations between alcohol use and accelerated biological ageing		2
44	Childhood intelligence attenuates the association between biological ageing and health outcomes in later		2
43	Creating and validating a DNA methylation-based proxy for Interleukin-6		2
42	MethylDetectR: a software for methylation-based health profiling. <i>Wellcome Open Research</i> , <b>2020</b> , 5, 283	4.8	2
41	Methylation-Based Age Estimation in a Wild Mouse		2
40	An epigenetic proxy of chronic inflammation outperforms serum levels as a biomarker of brain ageing		2
39	Epigenetic scores for the circulating proteome as tools for disease prediction		2
38	Bayesian reassessment of the epigenetic architecture of complex traits		2
37	A meta-analysis of genome-wide association studies of epigenetic age acceleration		2
36	Attitudes to ageing, biomarkers of ageing and mortality: the Lothian Birth Cohort 1936. <i>Journal of Epidemiology and Community Health</i> , <b>2020</b> , 74, 377-383	5.1	2

35	Blood-based epigenome-wide analyses of cognitive abilities		2
34	Examining the Impact of Imputation Errors on Fine-Mapping Using DNA Methylation QTL as a Model Trait. <i>Genetics</i> , <b>2019</b> , 212, 577-586	4	1
33	Blood-based epigenome-wide analyses of cognitive abilities.. <i>Genome Biology</i> , <b>2022</b> , 23, 26	18.3	1
32	Polygenic predictors of age-related decline in cognitive ability		1
31	Identification of novel differentially methylated sites with potential as clinical predictors of impaired respiratory function and COPD		1
30	An epigenome-wide association study of sex-specific chronological ageing		1
29	Epigenetic prediction of major depressive disorder		1
28	A comparison of blood and brain-derived ageing and inflammation-related DNA methylation signatures and their association with microglial burdens		1
27	Characterisation of an inflammation-related epigenetic score and its association with cognitive ability		1
26	Integrative omics approach to identify the molecular architecture of inflammatory protein levels in healthy older adults		1
25	Partial reprogramming induces a steady decline in epigenetic age before loss of somatic identity		1
24	Trajectories of inflammatory biomarkers over the eighth decade and their associations with immune cell counts and epigenetic ageing		1
23	GWAS of epigenetic ageing rates in blood reveals a critical role forTERT		1
22	Epigenome-wide analyses identify DNA methylation signatures of dementia risk. <i>Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring</i> , <b>2020</b> , 12, e12078	5.2	1
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20	Epigenetic predictors of lifestyle traits applied to the blood and brain. <i>Brain Communications</i> , <b>2021</b> , 3, fcab082	4.5	1
19	DNA methylation and brain dysmaturation in preterm infants		1
18	Multivariate Modeling of Direct and Proxy GWAS Indicates Substantial Common Variant Heritability of Alzheimer's Disease		1

17	Creating and Validating a DNA Methylation-Based Proxy for Interleukin-6. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , <b>2021</b> , 76, 2284-2292	6.4	1
16	Increase in anticholinergic burden from 1990 to 2015: Age-period-cohort analysis in UK biobank. <i>British Journal of Clinical Pharmacology</i> , <b>2021</b> ,	3.8	1
15	DNA methylation in relation to gestational age and brain dysmaturation in preterm infants.. <i>Brain Communications</i> , <b>2022</b> , 4, fcac056	4.5	1
14	DNA methylome-wide association study of genetic risk for depression implicates antigen processing and immune responses.. <i>Genome Medicine</i> , <b>2022</b> , 14, 36	14.4	1
13	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. <i>Nature Communications</i> , <b>2021</b> , 12, 7173	17.4	1
12	Association between anticholinergic burden and dementia in UK Biobank.. <i>Alzheimer's and Dementia: Translational Research and Clinical Interventions</i> , <b>2022</b> , 8, e12290	6	1
11	DNA methylation signature of chronic low-grade inflammation and its role in cardio-respiratory diseases.. <i>Nature Communications</i> , <b>2022</b> , 13, 2408	17.4	1
10	Epigenetic biomarkers of ageing are predictive of mortality risk in a longitudinal clinical cohort of individuals diagnosed with oropharyngeal cancer.. <i>Clinical Epigenetics</i> , <b>2022</b> , 14, 1	7.7	0
9	Association of low-frequency and rare coding variants with information processing speed. <i>Translational Psychiatry</i> , <b>2021</b> , 11, 613	8.6	0
8	Associations between alcohol use and accelerated biological ageing. <i>Addiction Biology</i> , <b>2021</b> , 27, e131004.6	4.6	0
7	Variation in VKORC1 Is Associated with Vascular Dementia. <i>Journal of Alzheimer's Disease</i> , <b>2021</b> , 80, 1329-1337	4.3	0
6	Meta-analyses identify DNA methylation associated with kidney function and damage. <i>Nature Communications</i> , <b>2021</b> , 12, 7174	17.4	0
5	Integrated analysis of direct and proxy genome wide association studies highlights polygenicity of Alzheimer's disease outside of the APOE region. <i>PLoS Genetics</i> , <b>2022</b> , 18, e1010208	6	0
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