

Riccardo E Marioni

List of Publications by Year in Descending Order

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

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	A proteomic survival predictor for COVID-19 patients in intensive care 2022 , 1, e0000007		6
195	Blood-based epigenome-wide analyses of cognitive abilities.. <i>Genome Biology</i> , 2022 , 23, 26	18.3	1
194	Epigenetic scores for the circulating proteome as tools for disease prediction.. <i>ELife</i> , 2022 , 11,	8.9	2
193	Epigenetic biomarkers of ageing are predictive of mortality risk in a longitudinal clinical cohort of individuals diagnosed with oropharyngeal cancer.. <i>Clinical Epigenetics</i> , 2022 , 14, 1	7.7	0
192	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals.. <i>Nature Genetics</i> , 2022 ,	36.3	7
191	DNA methylation in relation to gestational age and brain dysmaturation in preterm infants.. <i>Brain Communications</i> , 2022 , 4, fcac056	4.5	1
190	DNA methylome-wide association study of genetic risk for depression implicates antigen processing and immune responses.. <i>Genome Medicine</i> , 2022 , 14, 36	14.4	1
189	Association between anticholinergic burden and dementia in UK Biobank.. <i>Alzheimer's and Dementia: Translational Research and Clinical Interventions</i> , 2022 , 8, e12290	6	1
188	Genome- and epigenome-wide studies of plasma protein biomarkers for Alzheimer's disease implicate TBCA and TREM2 in disease risk.. <i>Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring</i> , 2022 , 14, e12280	5.2	
187	DNA methylation signature of chronic low-grade inflammation and its role in cardio-respiratory diseases.. <i>Nature Communications</i> , 2022 , 13, 2408	17.4	1
186	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> , 2022 , 18, e1010208	6	0
185	Epigenetic prediction of major depressive disorder. <i>Molecular Psychiatry</i> , 2021 , 26, 5112-5123	15.1	18
184	Association of low-frequency and rare coding variants with information processing speed. <i>Translational Psychiatry</i> , 2021 , 11, 613	8.6	0
183	The genetic and epigenetic profile of serum IL10 in the Lothian Birth Cohort 1936 and its relationship to Alzheimer's disease.. <i>Wellcome Open Research</i> , 2021 , 6, 306	4.8	
182	DNA Methylation and Protein Markers of Chronic Inflammation and Their Associations With Brain and Cognitive Aging. <i>Neurology</i> , 2021 , 97, e2340-e2352	6.5	3
181	Associations between alcohol use and accelerated biological ageing. <i>Addiction Biology</i> , 2021 , 27, e131004.6		0
180	Birth weight associations with DNA methylation differences in an adult population. <i>Epigenetics</i> , 2021 , 16, 783-796	5.7	7

179	Meta-analysis of genome-wide DNA methylation identifies shared associations across neurodegenerative disorders. <i>Genome Biology</i> , 2021 , 22, 90	18.3	6
178	Epigenome-wide association study of kidney function identifies trans-ethnic and ethnic-specific loci. <i>Genome Medicine</i> , 2021 , 13, 74	14.4	3
177	Epigenetic predictors of lifestyle traits applied to the blood and brain. <i>Brain Communications</i> , 2021 , 3, fcab082	4.5	1
176	Variation in VKORC1 Is Associated with Vascular Dementia. <i>Journal of Alzheimer's Disease</i> , 2021 , 80, 1329-1337	4.3	0
175	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021 , 22, 194	18.3	14
174	An epigenetic predictor of death captures multi-modal measures of brain health. <i>Molecular Psychiatry</i> , 2021 , 26, 3806-3816	15.1	31
173	Structural brain correlates of serum and epigenetic markers of inflammation in major depressive disorder. <i>Brain, Behavior, and Immunity</i> , 2021 , 92, 39-48	16.6	14
172	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. <i>Human Molecular Genetics</i> , 2021 , 30, 393-409	5.6	6
171	Creating and Validating a DNA Methylation-Based Proxy for Interleukin-6. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2021 , 76, 2284-2292	6.4	1
170	DNA methylation of blood cells is associated with prevalent type 2 diabetes in a meta-analysis of four European cohorts. <i>Clinical Epigenetics</i> , 2021 , 13, 40	7.7	8
169	A time-resolved proteomic and prognostic map of COVID-19. <i>Cell Systems</i> , 2021 , 12, 780-794.e7	10.6	32
168	Increase in anticholinergic burden from 1990 to 2015: Age-period-cohort analysis in UK biobank. <i>British Journal of Clinical Pharmacology</i> , 2021 ,	3.8	1
167	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021 , 53, 1311-1321	36.3	27
166	Identification of epigenome-wide DNA methylation differences between carriers of APOE ϵ 4 and APOE ϵ 2 alleles. <i>Genome Medicine</i> , 2021 , 13, 1	14.4	11
165	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. <i>Nature Communications</i> , 2021 , 12, 7173	17.4	1
164	Meta-analyses identify DNA methylation associated with kidney function and damage. <i>Nature Communications</i> , 2021 , 12, 7174	17.4	0
163	DNA methylation in APOE: The relationship with Alzheimer's and with cardiovascular health. <i>Alzheimer's and Dementia: Translational Research and Clinical Interventions</i> , 2020 , 6, e12026	6	5
162	Exploratory analysis of age and sex dependent DNA methylation patterns on the X-chromosome in whole blood samples. <i>Genome Medicine</i> , 2020 , 12, 39	14.4	13

161	Ultra-High-Throughput Clinical Proteomics Reveals Classifiers of COVID-19 Infection. <i>Cell Systems</i> , 2020 , 11, 11-24.e4	10.6	219
160	Bayesian reassessment of the epigenetic architecture of complex traits. <i>Nature Communications</i> , 2020 , 11, 2865	17.4	18
159	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> , 2020 , 75, 2249-2257	6.4	2
158	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> , 2020 , 20, 91	4.2	6
157	Multi-method genome- and epigenome-wide studies of inflammatory protein levels in healthy older adults. <i>Genome Medicine</i> , 2020 , 12, 60	14.4	9
156	DNA methylation outlier burden, health, and ageing in Generation Scotland and the Lothian Birth Cohorts of 1921 and 1936. <i>Clinical Epigenetics</i> , 2020 , 12, 49	7.7	8
155	Blood DNA methylation sites predict death risk in a longitudinal study of 12, 300 individuals. <i>Aging</i> , 2020 , 12, 14092-14124	5.6	6
154	MethylDetectR: a software for methylation-based health profiling. <i>Wellcome Open Research</i> , 2020 , 5, 283	4.8	2
153	Neurology-related protein biomarkers are associated with cognitive ability and brain volume in older age. <i>Nature Communications</i> , 2020 , 11, 800	17.4	8
152	Characterisation of an inflammation-related epigenetic score and its association with cognitive ability. <i>Clinical Epigenetics</i> , 2020 , 12, 113	7.7	15
151	Epigenetic measures of ageing predict the prevalence and incidence of leading causes of death and disease burden. <i>Clinical Epigenetics</i> , 2020 , 12, 115	7.7	40
150	Epigenome-wide analyses identify DNA methylation signatures of dementia risk. <i>Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring</i> , 2020 , 12, e12078	5.2	1
149	Attitudes to ageing, biomarkers of ageing and mortality: the Lothian Birth Cohort 1936. <i>Journal of Epidemiology and Community Health</i> , 2020 , 74, 377-383	5.1	2
148	Risk prediction of late-onset Alzheimer's disease implies an oligogenic architecture. <i>Nature Communications</i> , 2020 , 11, 4799	17.4	41
147	MethylDetectR: a software for methylation-based health profiling. <i>Wellcome Open Research</i> , 2020 , 5, 283	4.8	1
146	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. <i>Molecular Psychiatry</i> , 2020 , 25, 2392-2409	15.1	45
145	Polygenic predictors of age-related decline in cognitive ability. <i>Molecular Psychiatry</i> , 2020 , 25, 2584-2598	5.1	24
144	Age-dependent DNA methylation patterns on the Y chromosome in elderly males. <i>Aging Cell</i> , 2020 , 19, e12907	9.9	13

143	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> , 2020 , 75, 473-480	6.4	7
142	Epigenetic prediction of complex traits and mortality in a cohort of individuals with oropharyngeal cancer. <i>Clinical Epigenetics</i> , 2020 , 12, 58	7.7	3
141	Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. <i>Genome Medicine</i> , 2019 , 11, 54	14.4	81
140	Age-related clonal haemopoiesis is associated with increased epigenetic age. <i>Current Biology</i> , 2019 , 29, R786-R787	6.3	20
139	Examining the Impact of Imputation Errors on Fine-Mapping Using DNA Methylation QTL as a Model Trait. <i>Genetics</i> , 2019 , 212, 577-586	4	1
138	Parent of origin genetic effects on methylation in humans are common and influence complex trait variation. <i>Nature Communications</i> , 2019 , 10, 1383	17.4	21
137	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> , 2019 , 43, 1795-1802	5.5	12
136	Genomic structural equation modelling provides insights into the multivariate genetic architecture of complex traits. <i>Nature Human Behaviour</i> , 2019 , 3, 513-525	12.8	209
135	Identification of novel differentially methylated sites with potential as clinical predictors of impaired respiratory function and COPD. <i>EBioMedicine</i> , 2019 , 43, 576-586	8.8	13
134	DNA methylome profiling of all-cause mortality in comparison with age-associated methylation patterns. <i>Clinical Epigenetics</i> , 2019 , 11, 23	7.7	11
133	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> , 2019 , 35, 181-188	7.2	3
132	Brain age and other bodily 'ages': implications for neuropsychiatry. <i>Molecular Psychiatry</i> , 2019 , 24, 266-281	11.1	146
131	Genome and epigenome wide studies of neurological protein biomarkers in the Lothian Birth Cohort 1936. <i>Nature Communications</i> , 2019 , 10, 3160	17.4	21
130	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> , 2019 , 9, 248	8.6	17
129	DNA methylation-based estimator of telomere length. <i>Aging</i> , 2019 , 11, 5895-5923	5.6	69
128	Epigenome-wide association study of leukocyte telomere length. <i>Aging</i> , 2019 , 11, 5876-5894	5.6	4
127	Genome-wide meta-analysis of depression identifies 102 independent variants and highlights the importance of the prefrontal brain regions. <i>Nature Neuroscience</i> , 2019 , 22, 343-352	25.5	639
126	An epigenome-wide association study of sex-specific chronological ageing. <i>Genome Medicine</i> , 2019 , 12, 1	14.4	43

125	A meta-analysis of genome-wide association studies of epigenetic age acceleration. <i>PLoS Genetics</i> , 2019 , 15, e1008104	6	38
124	Childhood intelligence attenuates the association between biological ageing and health outcomes in later life. <i>Translational Psychiatry</i> , 2019 , 9, 323	8.6	8
123	DNA methylation aging clocks: challenges and recommendations. <i>Genome Biology</i> , 2019 , 20, 249	18.3	248
122	Partial reprogramming induces a steady decline in epigenetic age before loss of somatic identity. <i>Aging Cell</i> , 2019 , 18, e12877	9.9	62
121	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	6.4	45
120	Integrative analysis of omics summary data reveals putative mechanisms underlying complex traits. <i>Nature Communications</i> , 2018 , 9, 918	17.4	110
119	Genome-wide association study of depression phenotypes in UK Biobank identifies variants in excitatory synaptic pathways. <i>Nature Communications</i> , 2018 , 9, 1470	17.4	226
118	Association of Methylation Signals With Incident Coronary Heart Disease in an Epigenome-Wide Assessment of Circulating Tumor Necrosis Factor α . <i>JAMA Cardiology</i> , 2018 , 3, 463-472	16.2	17
117	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. <i>Nature Communications</i> , 2018 , 9, 387	17.4	106
116	Association analysis in over 329,000 individuals identifies 116 independent variants influencing neuroticism. <i>Nature Genetics</i> , 2018 , 50, 6-11	36.3	202
115	Meta-analysis of epigenome-wide association studies of cognitive abilities. <i>Molecular Psychiatry</i> , 2018 , 23, 2133-2144	15.1	46
114	Phenotypic and genetic analysis of cognitive performance in Major Depressive Disorder in the Generation Scotland: Scottish Family Health Study. <i>Translational Psychiatry</i> , 2018 , 8, 63	8.6	7
113	Altered DNA methylation associated with a translocation linked to major mental illness. <i>NPJ Schizophrenia</i> , 2018 , 4, 5	5.5	9
112	The epigenetic clock and telomere length are independently associated with chronological age and mortality. <i>International Journal of Epidemiology</i> , 2018 , 45, 424-432	7.8	153
111	DNA methylation and the epigenetic clock in relation to physical frailty in older people: the Lothian Birth Cohort 1936. <i>Clinical Epigenetics</i> , 2018 , 10, 101	7.7	36
110	DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons: Meta-analysis of Multiethnic Epigenome-wide Studies. <i>JAMA Psychiatry</i> , 2018 , 75, 949-959	14.5	51
109	The epigenetic clock and objectively measured sedentary and walking behavior in older adults: the Lothian Birth Cohort 1936. <i>Clinical Epigenetics</i> , 2018 , 10, 4	7.7	18
108	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. <i>Nature Communications</i> , 2018 , 9, 2282	17.4	147

107	Identification of 55,000 Replicated DNA Methylation QTL. <i>Scientific Reports</i> , 2018 , 8, 17605	4.9	78
106	Epigenetic signatures of starting and stopping smoking. <i>EBioMedicine</i> , 2018 , 37, 214-220	8.8	36
105	Association of facial ageing with DNA methylation and epigenetic age predictions. <i>Clinical Epigenetics</i> , 2018 , 10, 140	7.7	6
104	Trajectories of inflammatory biomarkers over the eighth decade and their associations with immune cell profiles and epigenetic ageing. <i>Clinical Epigenetics</i> , 2018 , 10, 159	7.7	17
103	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. <i>Nature Communications</i> , 2018 , 9, 5141	17.4	64
102	Epigenetic prediction of complex traits and death. <i>Genome Biology</i> , 2018 , 19, 136	18.3	77
101	Epigenetic influences on aging: a longitudinal genome-wide methylation study in old Swedish twins. <i>Epigenetics</i> , 2018 , 13, 975-987	5.7	37
100	Genotype effects contribute to variation in longitudinal methylome patterns in older people. <i>Genome Medicine</i> , 2018 , 10, 75	14.4	21
99	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> , 2018 , 103, 691-706	11	151
98	Addendum: Genome-wide association study of depression phenotypes in UK Biobank identifies variants in excitatory synaptic pathways. <i>Nature Communications</i> , 2018 , 9, 3578	17.4	3
97	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. <i>Nature Communications</i> , 2018 , 9, 2098	17.4	254
96	GWAS on family history of Alzheimer's disease. <i>Translational Psychiatry</i> , 2018 , 8, 99	8.6	238
95	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> , 2018 , 10, 429-437	5.2	57
94	Misestimation of heritability and prediction accuracy of male-pattern baldness. <i>Nature Communications</i> , 2018 , 9, 2537	17.4	14
93	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> , 2017 , 10,		72
92	Identification, replication and characterization of epigenetic remodelling in the aging genome: a cross population analysis. <i>Scientific Reports</i> , 2017 , 7, 8183	4.9	23
91	Genetic prediction of male pattern baldness. <i>PLoS Genetics</i> , 2017 , 13, e1006594	6	59
90	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> , 2017 , 14, e1002215	11.6	162

89	Molecular genetic contributions to self-rated health. <i>International Journal of Epidemiology</i> , 2017 , 46, 994-1009	7.8	30
88	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , 2017 , 101, 888-902	11	83
87	Social adversity and epigenetic aging: a multi-cohort study on socioeconomic differences in peripheral blood DNA methylation. <i>Scientific Reports</i> , 2017 , 7, 16266	4.9	118
86	Markers of Psychological Differences and Social and Health Inequalities: Possible Genetic and Phenotypic Overlaps. <i>Journal of Personality</i> , 2017 , 85, 104-117	4.4	6
85	Genetic Stratification to Identify Risk Groups for Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2017 , 57, 275-283	4.3	21
84	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> , 2017 , 9, 2489-2503	5.6	20
83	Comparison of HapMap and 1000 Genomes Reference Panels in a Large-Scale Genome-Wide Association Study. <i>PLoS ONE</i> , 2017 , 12, e0167742	3.7	21
82	Molecular Genetic Contributions to Social Deprivation and Household Income in UK Biobank. <i>Current Biology</i> , 2016 , 26, 3083-3089	6.3	126
81	Multiethnic Exome-Wide Association Study of Subclinical Atherosclerosis. <i>Circulation: Cardiovascular Genetics</i> , 2016 , 9, 511-520		34
80	Epigenetic Signatures of Cigarette Smoking. <i>Circulation: Cardiovascular Genetics</i> , 2016 , 9, 436-447		442
79	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. <i>Nature Genetics</i> , 2016 , 48, 1151-1161	36.3	181
78	Genetic variants linked to education predict longevity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 13366-13371	11.5	90
77	Polygenic risk of ischemic stroke is associated with cognitive ability. <i>Neurology</i> , 2016 , 86, 611-8	6.5	13
76	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. <i>Human Molecular Genetics</i> , 2016 , 25, 358-70	5.6	54
75	DNA methylation levels at individual age-associated CpG sites can be indicative for life expectancy. <i>Aging</i> , 2016 , 8, 394-401	5.6	99
74	DNA methylation-based measures of biological age: meta-analysis predicting time to death. <i>Aging</i> , 2016 , 8, 1844-1865	5.6	531
73	Differential effects of the APOE e4 allele on different domains of cognitive ability across the life-course. <i>European Journal of Human Genetics</i> , 2016 , 24, 919-23	5.3	47
72	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. <i>Genome Biology</i> , 2016 , 17, 255	18.3	171

71	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> , 2016 , 154, 43-8	5.6	34
70	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016 , 533, 539-42	50.4	850
69	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. <i>American Journal of Human Genetics</i> , 2015 , 97, 75-85	11	85
68	Exome sequencing to detect rare variants associated with general cognitive ability: a pilot study. <i>Twin Research and Human Genetics</i> , 2015 , 18, 117-25	2.2	6
67	DNA methylation age of blood predicts all-cause mortality in later life. <i>Genome Biology</i> , 2015 , 16, 25	18.3	670
66	The epigenetic clock is correlated with physical and cognitive fitness in the Lothian Birth Cohort 1936. <i>International Journal of Epidemiology</i> , 2015 , 44, 1388-96	7.8	357
65	Effect of Smoking on Blood Pressure and Resting Heart Rate: A Mendelian Randomization Meta-Analysis in the CARTA Consortium. <i>Circulation: Cardiovascular Genetics</i> , 2015 , 8, 832-41		70
64	Structural Brain MRI Trait Polygenic Score Prediction of Cognitive Abilities. <i>Twin Research and Human Genetics</i> , 2015 , 18, 738-45	2.2	3
63	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. <i>Blood</i> , 2015 , 126, e19-29	2.2	45
62	Social activity, cognitive decline and dementia risk: a 20-year prospective cohort study. <i>BMC Public Health</i> , 2015 , 15, 1089	4.1	99
61	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> , 2015 , 5, e008808	3	39
60	S2-01-01: Epigenetic considerations in cognitive decline 2015 , 11, P162-P162		
59	Common genetic variants explain the majority of the correlation between height and intelligence: the generation Scotland study. <i>Behavior Genetics</i> , 2014 , 44, 91-6	3.2	30
58	Cognitive lifestyle jointly predicts longitudinal cognitive decline and mortality risk. <i>European Journal of Epidemiology</i> , 2014 , 29, 211-9	12.1	59
57	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> , 2014 , 94, 223-32	11	233
56	Genetic and environmental exposures constrain epigenetic drift over the human life course. <i>Genome Research</i> , 2014 , 24, 1725-33	9.7	123
55	Molecular genetic contributions to socioeconomic status and intelligence. <i>Intelligence</i> , 2014 , 44, 26-32	3	131
54	Improving access to psychological therapies and older people: findings from the Eastern Region. <i>Behaviour Research and Therapy</i> , 2014 , 56, 75-81	5.2	18

53	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> , 2014 , 281, 20140117	4.4	17
52	Investigating the possible causal association of smoking with depression and anxiety using Mendelian randomisation meta-analysis: the CARTA consortium. <i>BMJ Open</i> , 2014 , 4, e006141	3	115
51	Stratification by smoking status reveals an association of CHRNA5-A3-B4 genotype with body mass index in never smokers. <i>PLoS Genetics</i> , 2014 , 10, e1004799	6	40
50	C-reactive protein, APOE genotype and longitudinal cognitive change in an older population. <i>Age and Ageing</i> , 2014 , 43, 289-92	3	26
49	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> , 2014 , 111, 13790-4	11.5	181
48	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> , 2012 , 12, 45	4.1	35
47	Active cognitive lifestyle associates with cognitive recovery and a reduced risk of cognitive decline. <i>Journal of Alzheimer's Disease</i> , 2012 , 28, 223-30	4.3	62
46	Active cognitive lifestyle is associated with positive cognitive health transitions and compression of morbidity from age sixty-five. <i>PLoS ONE</i> , 2012 , 7, e50940	3.7	69
45	Cognitive function, dementia and type 2 diabetes mellitus in the elderly. <i>Nature Reviews Endocrinology</i> , 2011 , 7, 108-14	15.2	265
44	The association between late-life cognitive test scores and retrospective informant interview data. <i>International Psychogeriatrics</i> , 2011 , 23, 274-9	3.4	7
43	Genetic associations between fibrinogen and cognitive performance in three Scottish cohorts. <i>Behavior Genetics</i> , 2011 , 41, 691-9	3.2	13
42	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> , 2011 , 11, 127	4.7	31
41	Association between raised inflammatory markers and cognitive decline in elderly people with type 2 diabetes: the Edinburgh Type 2 Diabetes Study. <i>Diabetes</i> , 2010 , 59, 710-3	0.9	123
40	Blood rheology and cognition in the Edinburgh Type 2 Diabetes Study. <i>Age and Ageing</i> , 2010 , 39, 354-9	3	13
39	Variation in the uric acid transporter gene (SLC2A9) and memory performance. <i>Human Molecular Genetics</i> , 2010 , 19, 2321-30	5.6	29
38	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> , 2010 , 40, 3-11	3.2	16
37	Association between polymorphisms of the dopamine receptor D2 and catechol-o-methyl transferase genes and cognitive function. <i>Behavior Genetics</i> , 2010 , 40, 630-8	3.2	31
36	Association of KIBRA and memory. <i>Neuroscience Letters</i> , 2009 , 458, 140-3	3.3	52

35	Age-associated cognitive decline. <i>British Medical Bulletin</i> , 2009 , 92, 135-52	5.4	616
34	Reverse causation in the association between C-reactive protein and fibrinogen levels and cognitive abilities in an aging sample. <i>Psychosomatic Medicine</i> , 2009 , 71, 404-9	3.7	56
33	Peripheral levels of fibrinogen, C-reactive protein, and plasma viscosity predict future cognitive decline in individuals without dementia. <i>Psychosomatic Medicine</i> , 2009 , 71, 901-6	3.7	61
32	The genetic and epigenetic profile of serum IL-10 in the Lothian Birth Cohort 1936 and its relationship to Alzheimer's disease. <i>Wellcome Open Research</i> , 2019 , 6, 306	4.8	
31	Associations between alcohol use and accelerated biological ageing		2
30	Polygenic predictors of age-related decline in cognitive ability		1
29	Identification of novel differentially methylated sites with potential as clinical predictors of impaired respiratory function and COPD		1
28	Childhood intelligence attenuates the association between biological ageing and health outcomes in later life		2
27	An epigenome-wide association study of sex-specific chronological ageing		1
26	Epigenetic prediction of major depressive disorder		1
25	Creating and validating a DNA methylation-based proxy for Interleukin-6		2
24	A comparison of blood and brain-derived ageing and inflammation-related DNA methylation signatures and their association with microglial burdens		1
23	Characterisation of an inflammation-related epigenetic score and its association with cognitive ability		1
22	Identification of 55,000 Replicated DNA Methylation QTL		14
21	Ninety-nine independent genetic loci influencing general cognitive function include genes associated with brain health and structure (N = 280,360)		6
20	Epigenetic clocks predict prevalence and incidence of leading causes of death and disease burden		8
19	Integrative omics approach to identify the molecular architecture of inflammatory protein levels in healthy older adults		1
18	Genome-wide association studies identify 137 loci for DNA methylation biomarkers of ageing		8

17	Methylation-Based Age Estimation in a Wild Mouse	2
16	An epigenetic proxy of chronic inflammation outperforms serum levels as a biomarker of brain ageing	2
15	Epigenetic scores for the circulating proteome as tools for disease prediction	2
14	Accelerated Epigenetic Ageing in Major Depressive Disorder	8
13	An epigenetic score for BMI based on DNA methylation correlates with poor physical health and major disease in the Lothian Birth Cohort 1936	4
12	Partial reprogramming induces a steady decline in epigenetic age before loss of somatic identity	1
11	Improved prediction of chronological age from DNA methylation limits it as a biomarker of ageing	6
10	Trajectories of inflammatory biomarkers over the eighth decade and their associations with immune cell counts and epigenetic ageing	1
9	Genome-wide meta-analysis of depression identifies 102 independent variants and highlights the importance of the prefrontal brain regions	8
8	Bayesian reassessment of the epigenetic architecture of complex traits	2
7	A meta-analysis of genome-wide association studies of epigenetic age acceleration	2
6	Birth weight associations with psychiatric and physical health, cognitive function, and DNA methylation differences in an adult population	5
5	An epigenetic predictor of death captures multi-modal measures of brain health	8
4	GWAS of epigenetic ageing rates in blood reveals a critical role for TERT	1
3	DNA methylation and brain dysmaturation in preterm infants	1
2	Blood-based epigenome-wide analyses of cognitive abilities	2
1	Multivariate Modeling of Direct and Proxy GWAS Indicates Substantial Common Variant Heritability of Alzheimer's Disease	1