

Riccardo E Marioni

List of Publications by Year in descending order

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Version: 2024-02-01

168
papers

20,544
citations

18436

62
h-index

15218

126
g-index

235
all docs

235
docs citations

235
times ranked

26196
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	7.1	1,589
2	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016, 533, 539-542.	13.7	1,204
3	DNA methylation age of blood predicts all-cause mortality in later life. <i>Genome Biology</i> , 2015, 16, 25.	3.8	928
4	Age-associated cognitive decline. <i>British Medical Bulletin</i> , 2009, 92, 135-152.	2.7	857
5	DNA methylation-based measures of biological age: meta-analysis predicting time to death. <i>Aging</i> , 2016, 8, 1844-1865.	1.4	786
6	Epigenetic Signatures of Cigarette Smoking. <i>Circulation: Cardiovascular Genetics</i> , 2016, 9, 436-447.	5.1	678
7	DNA methylation aging clocks: challenges and recommendations. <i>Genome Biology</i> , 2019, 20, 249.	3.8	552
8	Genomic structural equation modelling provides insights into the multivariate genetic architecture of complex traits. <i>Nature Human Behaviour</i> , 2019, 3, 513-525.	6.2	511
9	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. <i>Nature Communications</i> , 2018, 9, 2098.	5.8	484
10	The epigenetic clock is correlated with physical and cognitive fitness in the Lothian Birth Cohort 1936. <i>International Journal of Epidemiology</i> , 2015, 44, 1388-1396.	0.9	472
11	Ultra-High-Throughput Clinical Proteomics Reveals Classifiers of COVID-19 Infection. <i>Cell Systems</i> , 2020, 11, 11-24.e4.	2.9	439
12	Genome-wide association study of depression phenotypes in UK Biobank identifies variants in excitatory synaptic pathways. <i>Nature Communications</i> , 2018, 9, 1470.	5.8	415
13	GWAS on family history of Alzheimer's disease. <i>Translational Psychiatry</i> , 2018, 8, 99.	2.4	406
14	Association analysis in over 329,000 individuals identifies 116 independent variants influencing neuroticism. <i>Nature Genetics</i> , 2018, 50, 6-11.	9.4	327
15	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.	2.6	326
16	Cognitive function, dementia and type 2 diabetes mellitus in the elderly. <i>Nature Reviews Endocrinology</i> , 2011, 7, 108-114.	4.3	317
17	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. <i>Nature Communications</i> , 2018, 9, 2282.	5.8	294
18	Brain age and other bodily "ages": implications for neuropsychiatry. <i>Molecular Psychiatry</i> , 2019, 24, 266-281.	4.1	291

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19	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, 223-232.	2.6	287
20	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. <i>Nature Genetics</i> , 2016, 48, 1151-1161.	9.4	261
21	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. <i>Genome Biology</i> , 2016, 17, 255.	3.8	251
22	Integrative analysis of omics summary data reveals putative mechanisms underlying complex traits. <i>Nature Communications</i> , 2018, 9, 918.	5.8	250
23	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.	3.9	246
24	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, 13790-13794.	3.3	244
25	The epigenetic clock and telomere length are independently associated with chronological age and mortality. <i>International Journal of Epidemiology</i> , 2016, 45, 424-432.	0.9	227
26	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	9.4	218
27	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. <i>Nature Genetics</i> , 2022, 54, 437-449.	9.4	215
28	DNA methylation-based estimator of telomere length. <i>Aging</i> , 2019, 11, 5895-5923.	1.4	198
29	Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. <i>Genome Medicine</i> , 2019, 11, 54.	3.6	191
30	Social adversity and epigenetic aging: a multi-cohort study on socioeconomic differences in peripheral blood DNA methylation. <i>Scientific Reports</i> , 2017, 7, 16266.	1.6	181
31	Molecular Genetic Contributions to Social Deprivation and Household Income in UK Biobank. <i>Current Biology</i> , 2016, 26, 3083-3089.	1.8	177
32	Identification of 55,000 Replicated DNA Methylation QTL. <i>Scientific Reports</i> , 2018, 8, 17605.	1.6	157
33	Molecular genetic contributions to socioeconomic status and intelligence. <i>Intelligence</i> , 2014, 44, 26-32.	1.6	156
34	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , 2017, 101, 888-902.	2.6	154
35	Association Between Raised Inflammatory Markers and Cognitive Decline in Elderly People With Type 2 Diabetes. <i>Diabetes</i> , 2010, 59, 710-713.	0.3	152
36	Genetic and environmental exposures constrain epigenetic drift over the human life course. <i>Genome Research</i> , 2014, 24, 1725-1733.	2.4	152

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37	Social activity, cognitive decline and dementia risk: a 20-year prospective cohort study. BMC Public Health, 2015, 15, 1089.	1.2	152
38	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. Nature Communications, 2018, 9, 387.	5.8	151
39	Investigating the possible causal association of smoking with depression and anxiety using Mendelian randomisation meta-analysis: the CARTA consortium. BMJ Open, 2014, 4, e006141.	0.8	150
40	DNA methylation levels at individual age-associated CpG sites can be indicative for life expectancy. Aging, 2016, 8, 394-401.	1.4	150
41	Epigenetic prediction of complex traits and death. Genome Biology, 2018, 19, 136.	3.8	146
42	Partial reprogramming induces a steady decline in epigenetic age before loss of somatic identity. Aging Cell, 2019, 18, e12877.	3.0	128
43	A time-resolved proteomic and prognostic map of COVID-19. Cell Systems, 2021, 12, 780-794.e7.	2.9	125
44	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. Nature Communications, 2018, 9, 5141.	5.8	119
45	An epigenome-wide association study of sex-specific chronological ageing. Genome Medicine, 2020, 12, 1.	3.6	117
46	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. American Journal of Human Genetics, 2015, 97, 75-85.	2.6	116
47	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	3.3	110
48	Risk prediction of late-onset Alzheimer's disease implies an oligogenic architecture. Nature Communications, 2020, 11, 4799.	5.8	110
49	Epigenetic measures of ageing predict the prevalence and incidence of leading causes of death and disease burden. Clinical Epigenetics, 2020, 12, 115.	1.8	109
50	Effect of Smoking on Blood Pressure and Resting Heart Rate. Circulation: Cardiovascular Genetics, 2015, 8, 832-841.	5.1	105
51	Epigenetic Patterns in Blood Associated With Lipid Traits Predict Incident Coronary Heart Disease Events and Are Enriched for Results From Genome-Wide Association Studies. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	104
52	Investigating the relationship between DNA methylation age acceleration and risk factors for Alzheimer's disease. Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2018, 10, 429-437.	1.2	93
53	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	3.8	90
54	Active Cognitive Lifestyle Is Associated with Positive Cognitive Health Transitions and Compression of Morbidity from Age Sixty-Five. PLoS ONE, 2012, 7, e50940.	1.1	90

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55	Genetic prediction of male pattern baldness. PLoS Genetics, 2017, 13, e1006594.	1.5	89
56	A meta-analysis of genome-wide association studies of epigenetic age acceleration. PLoS Genetics, 2019, 15, e1008104.	1.5	83
57	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular Psychiatry, 2020, 25, 2392-2409.	4.1	83
58	Tracking the Epigenetic Clock Across the Human Life Course: A Meta-analysis of Longitudinal Cohort Data. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2019, 74, 57-61.	1.7	81
59	Cognitive lifestyle jointly predicts longitudinal cognitive decline and mortality risk. European Journal of Epidemiology, 2014, 29, 211-219.	2.5	79
60	DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons. JAMA Psychiatry, 2018, 75, 949.	6.0	78
61	Active Cognitive Lifestyle Associates with Cognitive Recovery and a Reduced Risk of Cognitive Decline. Journal of Alzheimer's Disease, 2012, 28, 223-230.	1.2	77
62	An epigenetic predictor of death captures multi-modal measures of brain health. Molecular Psychiatry, 2021, 26, 3806-3816.	4.1	77
63	Identification of epigenome-wide DNA methylation differences between carriers of APOE ϵ 4 and APOE ϵ 2 alleles. Genome Medicine, 2021, 13, 1.	3.6	76
64	Peripheral Levels of Fibrinogen, C-Reactive Protein, and Plasma Viscosity Predict Future Cognitive Decline in Individuals Without Dementia. Psychosomatic Medicine, 2009, 71, 901-906.	1.3	75
65	Reverse Causation in the Association Between C-Reactive Protein and Fibrinogen Levels and Cognitive Abilities in an Aging Sample. Psychosomatic Medicine, 2009, 71, 404-409.	1.3	74
66	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. Human Molecular Genetics, 2016, 25, 358-370.	1.4	73
67	Meta-analysis of epigenome-wide association studies of cognitive abilities. Molecular Psychiatry, 2018, 23, 2133-2144.	4.1	68
68	Epigenetic signatures of starting and stopping smoking. EBioMedicine, 2018, 37, 214-220.	2.7	67
69	Association of KIBRA and memory. Neuroscience Letters, 2009, 458, 140-143.	1.0	66
70	Epigenetic influences on aging: a longitudinal genome-wide methylation study in old Swedish twins. Epigenetics, 2018, 13, 975-987.	1.3	65
71	DNA methylation and the epigenetic clock in relation to physical frailty in older people: the Lothian Birth Cohort 1936. Clinical Epigenetics, 2018, 10, 101.	1.8	62
72	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. Blood, 2015, 126, e19-e29.	0.6	55

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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, 919-923.	1.4	54
74	Multiethnic Exome-Wide Association Study of Subclinical Atherosclerosis. <i>Circulation: Cardiovascular Genetics</i> , 2016, 9, 511-520.	5.1	54
75	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: Table A1. <i>BMJ Open</i> , 2015, 5, e008808.	0.8	53
76	Structural brain correlates of serum and epigenetic markers of inflammation in major depressive disorder. <i>Brain, Behavior, and Immunity</i> , 2021, 92, 39-48.	2.0	53
77	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.	1.1	51
78	Meta-analysis of genome-wide DNA methylation identifies shared associations across neurodegenerative disorders. <i>Genome Biology</i> , 2021, 22, 90.	3.8	49
79	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.	1.4	48
80	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.	1.5	45
81	Epigenetic prediction of major depressive disorder. <i>Molecular Psychiatry</i> , 2021, 26, 5112-5123.	4.1	44
82	DNA Methylation and Protein Markers of Chronic Inflammation and Their Associations With Brain and Cognitive Aging. <i>Neurology</i> , 2021, 97, e2340-e2352.	1.5	44
83	Bayesian reassessment of the epigenetic architecture of complex traits. <i>Nature Communications</i> , 2020, 11, 2865.	5.8	43
84	Genome and epigenome wide studies of neurological protein biomarkers in the Lothian Birth Cohort 1936. <i>Nature Communications</i> , 2019, 10, 3160.	5.8	42
85	Neurology-related protein biomarkers are associated with cognitive ability and brain volume in older age. <i>Nature Communications</i> , 2020, 11, 800.	5.8	42
86	C-reactive protein, APOE genotype and longitudinal cognitive change in an older population. <i>Age and Ageing</i> , 2014, 43, 289-292.	0.7	41
87	Common Genetic Variants Explain the Majority of the Correlation Between Height and Intelligence: The Generation Scotland Study. <i>Behavior Genetics</i> , 2014, 44, 91-96.	1.4	41
88	Molecular genetic contributions to self-rated health. <i>International Journal of Epidemiology</i> , 2017, 46, dyw219.	0.9	39
89	Polygenic predictors of age-related decline in cognitive ability. <i>Molecular Psychiatry</i> , 2020, 25, 2584-2598.	4.1	38
90	Characterisation of an inflammation-related epigenetic score and its association with cognitive ability. <i>Clinical Epigenetics</i> , 2020, 12, 113.	1.8	38

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91	Association Between Polymorphisms of the Dopamine Receptor D2 and Catechol-o-Methyl Transferase Genes and Cognitive Function. <i>Behavior Genetics</i> , 2010, 40, 630-638.	1.4	37
92	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, 43-48.	2.2	37
93	Genotype effects contribute to variation in longitudinal methylome patterns in older people. <i>Genome Medicine</i> , 2018, 10, 75.	3.6	37
94	Age-related clonal haemopoiesis is associated with increased epigenetic age. <i>Current Biology</i> , 2019, 29, R786-R787.	1.8	37
95	Parent of origin genetic effects on methylation in humans are common and influence complex trait variation. <i>Nature Communications</i> , 2019, 10, 1383.	5.8	37
96	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.	1.8	37
97	Epigenetic scores for the circulating proteome as tools for disease prediction. <i>ELife</i> , 2022, 11, .	2.8	37
98	Longitudinal dynamics of clonal hematopoiesis identifies gene-specific fitness effects. <i>Nature Medicine</i> , 2022, 28, 1439-1446.	15.2	36
99	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.	2.4	34
100	Variation in the uric acid transporter gene (SLC2A9) and memory performance. <i>Human Molecular Genetics</i> , 2010, 19, 2321-2330.	1.4	33
101	Genetic Stratification to Identify Risk Groups for Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2017, 57, 275-283.	1.2	33
102	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.	1.4	33
103	Association of Methylation Signals With Incident Coronary Heart Disease in an Epigenome-Wide Assessment of Circulating Tumor Necrosis Factor \pm . <i>JAMA Cardiology</i> , 2018, 3, 463.	3.0	33
104	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. <i>Human Molecular Genetics</i> , 2021, 30, 393-409.	1.4	32
105	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.	1.8	30
106	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.	1.8	30
107	Multi-method genome- and epigenome-wide studies of inflammatory protein levels in healthy older adults. <i>Genome Medicine</i> , 2020, 12, 60.	3.6	30
108	Meta-analyses identify DNA methylation associated with kidney function and damage. <i>Nature Communications</i> , 2021, 12, 7174.	5.8	30

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109	Improving access to psychological therapies and older people: Findings from the Eastern Region. <i>Behaviour Research and Therapy</i> , 2014, 56, 75-81.	1.6	29
110	Comparison of HapMap and 1000 Genomes Reference Panels in a Large-Scale Genome-Wide Association Study. <i>PLoS ONE</i> , 2017, 12, e0167742.	1.1	29
111	A proteomic survival predictor for COVID-19 patients in intensive care. , 2022, 1, e0000007.		28
112	Identification, replication and characterization of epigenetic remodelling in the aging genome: a cross population analysis. <i>Scientific Reports</i> , 2017, 7, 8183.	1.6	27
113	Age-dependent DNA methylation patterns on the Y chromosome in elderly males. <i>Aging Cell</i> , 2020, 19, e12907.	3.0	27
114	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.	3.6	26
115	DNA methylation signature of chronic low-grade inflammation and its role in cardio-respiratory diseases. <i>Nature Communications</i> , 2022, 13, 2408.	5.8	26
116	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.	1.6	25
117	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.	1.1	24
118	Misestimation of heritability and prediction accuracy of male-pattern baldness. <i>Nature Communications</i> , 2018, 9, 2537.	5.8	22
119	Identification of novel differentially methylated sites with potential as clinical predictors of impaired respiratory function and COPD. <i>EBioMedicine</i> , 2019, 43, 576-586.	2.7	21
120	Epigenome-wide association study of kidney function identifies trans-ethnic and ethnic-specific loci. <i>Genome Medicine</i> , 2021, 13, 74.	3.6	20
121	Blood-based epigenome-wide analyses of cognitive abilities. <i>Genome Biology</i> , 2022, 23, 26.	3.8	20
122	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.	1.2	19
123	Epigenome-wide association study of leukocyte telomere length. <i>Aging</i> , 2019, 11, 5876-5894.	1.4	19
124	Associations between alcohol use and accelerated biological ageing. <i>Addiction Biology</i> , 2022, 27, e13100.	1.4	19
125	Assessing the causal role of epigenetic clocks in the development of multiple cancers: a Mendelian randomization study. <i>ELife</i> , 2022, 11, .	2.8	19
126	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.	1.4	18

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127	Birth weight associations with DNA methylation differences in an adult population. <i>Epigenetics</i> , 2021, 16, 783-796.	1.3	18
128	MethylDetectR: a software for methylation-based health profiling. <i>Wellcome Open Research</i> , 2020, 5, 283.	0.9	18
129	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.	1.8	17
130	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.	1.8	17
131	Addendum: Genome-wide association study of depression phenotypes in UK Biobank identifies variants in excitatory synaptic pathways. <i>Nature Communications</i> , 2018, 9, 3578.	5.8	16
132	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.	1.7	16
133	DNA methylome-wide association study of genetic risk for depression implicates antigen processing and immune responses. <i>Genome Medicine</i> , 2022, 14, 36.	3.6	16
134	Blood rheology and cognition in the Edinburgh Type 2 Diabetes Study. <i>Age and Ageing</i> , 2010, 39, 354-359.	0.7	15
135	Childhood intelligence attenuates the association between biological ageing and health outcomes in later life. <i>Translational Psychiatry</i> , 2019, 9, 323.	2.4	15
136	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.	1.7	15
137	Blood DNA methylation sites predict death risk in a longitudinal study of 12, 300 individuals. <i>Aging</i> , 2020, 12, 14092-14124.	1.4	15
138	Polygenic risk of ischemic stroke is associated with cognitive ability. <i>Neurology</i> , 2016, 86, 611-618.	1.5	14
139	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.	1.8	14
140	MethylDetectR: a software for methylation-based health profiling. <i>Wellcome Open Research</i> , 2020, 5, 283.	0.9	14
141	DNA methylation in relation to gestational age and brain dysmaturation in preterm infants. <i>Brain Communications</i> , 2022, 4, fcac056.	1.5	14
142	Genetic Associations Between Fibrinogen and Cognitive Performance in Three Scottish Cohorts. <i>Behavior Genetics</i> , 2011, 41, 691-699.	1.4	13
143	DNA methylome profiling of all-cause mortality in comparison with age-associated methylation patterns. <i>Clinical Epigenetics</i> , 2019, 11, 23.	1.8	13
144	Association between anticholinergic burden and dementia in UK Biobank. <i>Alzheimer's and Dementia: Translational Research and Clinical Interventions</i> , 2022, 8, e12290.	1.8	12

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145	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.	2.4	11
146	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.	1.8	10
147	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.	1.5	10
148	The association between late-life cognitive test scores and retrospective informant interview data. <i>International Psychogeriatrics</i> , 2011, 23, 274-279.	0.6	9
149	Markers of Psychological Differences and Social and Health Inequalities: Possible Genetic and Phenotypic Overlaps. <i>Journal of Personality</i> , 2017, 85, 104-117.	1.8	9
150	Altered DNA methylation associated with a translocation linked to major mental illness. <i>NPI Schizophrenia</i> , 2018, 4, 5.	2.0	9
151	Association of facial ageing with DNA methylation and epigenetic age predictions. <i>Clinical Epigenetics</i> , 2018, 10, 140.	1.8	9
152	A comparison of blood and brain-derived ageing and inflammation-related DNA methylation signatures and their association with microglial burdens. <i>European Journal of Neuroscience</i> , 2022, 56, 5637-5649.	1.2	9
153	Epigenome-wide analyses identify DNA methylation signatures of dementia risk. <i>Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring</i> , 2020, 12, e12078.	1.2	8
154	Epigenetic prediction of complex traits and mortality in a cohort of individuals with oropharyngeal cancer. <i>Clinical Epigenetics</i> , 2020, 12, 58.	1.8	8
155	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. <i>Nature Communications</i> , 2021, 12, 7173.	5.8	8
156	Exome Sequencing to Detect Rare Variants Associated With General Cognitive Ability: A Pilot Study. <i>Twin Research and Human Genetics</i> , 2015, 18, 117-125.	0.3	7
157	Increase in anticholinergic burden from 1990 to 2015: Age-period-cohort analysis in UK biobank. <i>British Journal of Clinical Pharmacology</i> , 2022, 88, 983-993.	1.1	7
158	Epigenetic predictors of lifestyle traits applied to the blood and brain. <i>Brain Communications</i> , 2021, 3, fcb0082.	1.5	6
159	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.	2.0	5
160	Variation in VKORC1 Is Associated with Vascular Dementia. <i>Journal of Alzheimer's Disease</i> , 2021, 80, 1329-1337.	1.2	5
161	Structural Brain MRI Trait Polygenic Score Prediction of Cognitive Abilities. <i>Twin Research and Human Genetics</i> , 2015, 18, 738-745.	0.3	4
162	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.	1.2	4

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163	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. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2020, 75, 2249-2257.	1.7	3
164	Examining the Impact of Imputation Errors on Fine-Mapping Using DNA Methylation QTL as a Model Trait. Genetics, 2019, 212, 577-586.	1.2	2
165	Association of low-frequency and rare coding variants with information processing speed. Translational Psychiatry, 2021, 11, 613.	2.4	2
166	The genetic and epigenetic profile of serum β -microglobulin in the Lothian Birth Cohort 1936 and its relationship to Alzheimer's disease. Wellcome Open Research, 2021, 6, 306.	0.9	1
167	S2-01-01: Epigenetic considerations in cognitive decline. , 2015, 11, P162-P162.		0
168	The genetic and epigenetic profile of serum β -microglobulin in the Lothian Birth Cohort 1936 and its relationship to Alzheimer's disease. Wellcome Open Research, 0, 6, 306.	0.9	0