

Allan F Mcrae

List of Publications by Year in descending order

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Version: 2024-02-01

123
papers

13,678
citations

34105

52
h-index

27406

106
g-index

151
all docs

151
docs citations

151
times ranked

20457
citing authors

#	ARTICLE	IF	CITATIONS
1	DNA methylation age of blood predicts all-cause mortality in later life. <i>Genome Biology</i> , 2015, 16, 25.	8.8	928
2	A Versatile Gene-Based Test for Genome-wide Association Studies. <i>American Journal of Human Genetics</i> , 2010, 87, 139-145.	6.2	809
3	DNA methylation-based measures of biological age: meta-analysis predicting time to death. <i>Aging</i> , 2016, 8, 1844-1865.	3.1	786
4	Epigenetic Signatures of Cigarette Smoking. <i>Circulation: Cardiovascular Genetics</i> , 2016, 9, 436-447.	5.1	678
5	DNA methylation profiles in monozygotic and dizygotic twins. <i>Nature Genetics</i> , 2009, 41, 240-245.	21.4	634
6	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. <i>Nature Communications</i> , 2018, 9, 2941.	12.8	570
7	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , 2015, 6, 8570.	12.8	533
8	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.	1.9	472
9	GWAS on family history of Alzheimer's disease. <i>Translational Psychiatry</i> , 2018, 8, 99.	4.8	406
10	Signatures of negative selection in the genetic architecture of human complex traits. <i>Nature Genetics</i> , 2018, 50, 746-753.	21.4	304
11	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. <i>Nature Communications</i> , 2018, 9, 2282.	12.8	294
12	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. <i>Genome Biology</i> , 2016, 17, 255.	8.8	251
13	Integrative analysis of omics summary data reveals putative mechanisms underlying complex traits. <i>Nature Communications</i> , 2018, 9, 918.	12.8	250
14	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.	8.4	246
15	Contribution of genetic variation to transgenerational inheritance of DNA methylation. <i>Genome Biology</i> , 2014, 15, R73.	9.6	231
16	Common Variants in the Trichohyalin Gene Are Associated with Straight Hair in Europeans. <i>American Journal of Human Genetics</i> , 2009, 85, 750-755.	6.2	230
17	The epigenetic clock and telomere length are independently associated with chronological age and mortality. <i>International Journal of Epidemiology</i> , 2016, 45, 424-432.	1.9	227
18	Common and rare variant association analyses in amyotrophic lateral sclerosis identify 15 risk loci with distinct genetic architectures and neuron-specific biology. <i>Nature Genetics</i> , 2021, 53, 1636-1648.	21.4	223

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19	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	21.4	218
20	Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. <i>Genome Medicine</i> , 2019, 11, 54.	8.2	191
21	Identification of 55,000 Replicated DNA Methylation QTL. <i>Scientific Reports</i> , 2018, 8, 17605.	3.3	157
22	Variants in TF and HFE Explain $\hat{\approx}$ 44% of Genetic Variation in Serum-Transferrin Levels. <i>American Journal of Human Genetics</i> , 2009, 84, 60-65.	6.2	155
23	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , 2017, 101, 888-902.	6.2	154
24	Genetic and environmental exposures constrain epigenetic drift over the human life course. <i>Genome Research</i> , 2014, 24, 1725-1733.	5.5	152
25	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. <i>Nature Communications</i> , 2018, 9, 387.	12.8	151
26	Epigenetic prediction of complex traits and death. <i>Genome Biology</i> , 2018, 19, 136.	8.8	146
27	Fast set-based association analysis using summary data from GWAS identifies novel gene loci for human complex traits. <i>Scientific Reports</i> , 2016, 6, 32894.	3.3	138
28	Genotype-by-environment interactions inferred from genetic effects on phenotypic variability in the UK Biobank. <i>Science Advances</i> , 2019, 5, eaaw3538.	10.3	123
29	Compelling evidence that a single nucleotide substitution in TYRP1 is responsible for coat-colour polymorphism in a free-living population of Soay sheep. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2007, 274, 619-626.	2.6	116
30	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. <i>American Journal of Human Genetics</i> , 2015, 97, 75-85.	6.2	116
31	Risk prediction of late-onset Alzheimer's disease implies an oligogenic architecture. <i>Nature Communications</i> , 2020, 11, 4799.	12.8	110
32	Association between ORMDL3, IL1RL1 and a deletion on chromosome 17q21 with asthma risk in Australia. <i>European Journal of Human Genetics</i> , 2011, 19, 458-464.	2.8	105
33	OSCA: a tool for omic-data-based complex trait analysis. <i>Genome Biology</i> , 2019, 20, 107.	8.8	105
34	A Cytogenetic Abnormality and Rare Coding Variants Identify ABCA13 as a Candidate Gene in Schizophrenia, Bipolar Disorder, and Depression. <i>American Journal of Human Genetics</i> , 2009, 85, 833-846.	6.2	102
35	A Localized Negative Genetic Correlation Constrains Microevolution of Coat Color in Wild Sheep. <i>Science</i> , 2008, 319, 318-320.	12.6	97
36	Predicting gene targets from integrative analyses of summary data from GWAS and eQTL studies for 28 human complex traits. <i>Genome Medicine</i> , 2016, 8, 84.	8.2	91

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37	Monozygotic twins affected with major depressive disorder have greater variance in methylation than their unaffected co-twin. <i>Translational Psychiatry</i> , 2013, 3, e269-e269.	4.8	89
38	Identification of Common Genetic Variants Influencing Spontaneous Dizygotic Twinning and Female Fertility. <i>American Journal of Human Genetics</i> , 2016, 98, 898-908.	6.2	89
39	Quantitative trait loci (QTL) mapping of resistance to strongyles and coccidia in the free-living Soay sheep (<i>Ovis aries</i>). <i>International Journal for Parasitology</i> , 2007, 37, 121-129.	3.1	87
40	Analysis of DNA methylation associates the cystine-glutamate antiporter SLC7A11 with risk of Parkinson's disease. <i>Nature Communications</i> , 2020, 11, 1238.	12.8	85
41	The Brisbane Systems Genetics Study: Genetical Genomics Meets Complex Trait Genetics. <i>PLoS ONE</i> , 2012, 7, e35430.	2.5	83
42	Congruence of Additive and Non-Additive Effects on Gene Expression Estimated from Pedigree and SNP Data. <i>PLoS Genetics</i> , 2013, 9, e1003502.	3.5	79
43	DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons. <i>JAMA Psychiatry</i> , 2018, 75, 949.	11.0	78
44	Geographical structure and differential natural selection among North European populations. <i>Genome Research</i> , 2009, 19, 804-814.	5.5	75
45	Genetic control of gene expression in whole blood and lymphoblastoid cell lines is largely independent. <i>Genome Research</i> , 2012, 22, 456-466.	5.5	75
46	A Genome-Wide Association Study of Caffeine-Related Sleep Disturbance: Confirmation of a Role for a Common Variant in the Adenosine Receptor. <i>Sleep</i> , 2012, 35, 967-975.	1.1	75
47	Family-based genome-wide association studies. <i>Pharmacogenomics</i> , 2009, 10, 181-190.	1.3	69
48	Meta-analysis of epigenome-wide association studies of cognitive abilities. <i>Molecular Psychiatry</i> , 2018, 23, 2133-2144.	7.9	68
49	Epigenetic influences on aging: a longitudinal genome-wide methylation study in old Swedish twins. <i>Epigenetics</i> , 2018, 13, 975-987.	2.7	65
50	Genome-wide autozygosity is associated with lower general cognitive ability. <i>Molecular Psychiatry</i> , 2016, 21, 837-843.	7.9	62
51	CWAS Findings for Human Iris Patterns: Associations with Variants in Genes that Influence Normal Neuronal Pattern Development. <i>American Journal of Human Genetics</i> , 2011, 89, 334-343.	6.2	59
52	708 Common and 2010 rare DISC1 locus variants identified in 1542 subjects: analysis for association with psychiatric disorder and cognitive traits. <i>Molecular Psychiatry</i> , 2014, 19, 668-675.	7.9	59
53	Development of a Linkage Map and Mapping of Phenotypic Polymorphisms in a Free-Living Population of Soay Sheep (<i>Ovis aries</i>). <i>Genetics</i> , 2006, 173, 1521-1537.	2.9	57
54	Genome-Wide Association Study of Height and Body Mass Index in Australian Twin Families. <i>Twin Research and Human Genetics</i> , 2010, 13, 179-193.	0.6	56

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55	Association of Copy Number Variation of the 15q11.2 BP1-BP2 Region With Cortical and Subcortical Morphology and Cognition. <i>JAMA Psychiatry</i> , 2020, 77, 420.	11.0	54
56	Clustered Coding Variants in the Glutamate Receptor Complexes of Individuals with Schizophrenia and Bipolar Disorder. <i>PLoS ONE</i> , 2011, 6, e19011.	2.5	54
57	Horn type and horn length genes map to the same chromosomal region in Soay sheep. <i>Heredity</i> , 2010, 104, 196-205.	2.6	49
58	Meta-analysis of genome-wide DNA methylation identifies shared associations across neurodegenerative disorders. <i>Genome Biology</i> , 2021, 22, 90.	8.8	49
59	MAPPING QUANTITATIVE TRAIT LOCI UNDERLYING FITNESS-RELATED TRAITS IN A FREE-LIVING SHEEP POPULATION. <i>Evolution; International Journal of Organic Evolution</i> , 2007, 61, 1403-1416.	2.3	48
60	Seasonal Effects on Gene Expression. <i>PLoS ONE</i> , 2015, 10, e0126995.	2.5	48
61	Inflammation-driven bone formation in a mouse model of ankylosing spondylitis: sequential not parallel processes. <i>Arthritis Research and Therapy</i> , 2016, 18, 35.	3.5	46
62	Bayesian reassessment of the epigenetic architecture of complex traits. <i>Nature Communications</i> , 2020, 11, 2865.	12.8	43
63	Genome and epigenome wide studies of neurological protein biomarkers in the Lothian Birth Cohort 1936. <i>Nature Communications</i> , 2019, 10, 3160.	12.8	42
64	Genome-wide DNA methylation profiling in whole blood reveals epigenetic signatures associated with migraine. <i>BMC Genomics</i> , 2018, 19, 69.	2.8	41
65	Tissue-specific sex differences in human gene expression. <i>Human Molecular Genetics</i> , 2019, 28, 2976-2986.	2.9	41
66	Genome-wide average DNA methylation is determined in utero. <i>International Journal of Epidemiology</i> , 2018, 47, 908-916.	1.9	38
67	Characterisation of an inflammation-related epigenetic score and its association with cognitive ability. <i>Clinical Epigenetics</i> , 2020, 12, 113.	4.1	38
68	Genome-wide study of DNA methylation shows alterations in metabolic, inflammatory, and cholesterol pathways in ALS. <i>Science Translational Medicine</i> , 2022, 14, eabj0264.	12.4	38
69	Bone density in sheep: genetic variation and quantitative trait loci localisation. <i>Bone</i> , 2003, 33, 540-548.	2.9	37
70	Divergence between Human Populations Estimated from Linkage Disequilibrium. <i>American Journal of Human Genetics</i> , 2008, 83, 737-743.	6.2	37
71	Genotype effects contribute to variation in longitudinal methylome patterns in older people. <i>Genome Medicine</i> , 2018, 10, 75.	8.2	37
72	Epigenetic scores for the circulating proteome as tools for disease prediction. <i>ELife</i> , 2022, 11, .	6.0	37

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73	Epigenome-wide meta-analysis of blood DNA methylation and its association with subcortical volumes: findings from the ENIGMA Epigenetics Working Group. <i>Molecular Psychiatry</i> , 2021, 26, 3884-3895.	7.9	34
74	Role of DNA Methylation in Type 2 Diabetes Etiology: Using Genotype as a Causal Anchor. <i>Diabetes</i> , 2017, 66, 1713-1722.	0.6	32
75	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.	4.1	30
76	Multi-method genome- and epigenome-wide studies of inflammatory protein levels in healthy older adults. <i>Genome Medicine</i> , 2020, 12, 60.	8.2	30
77	Effects of copy number variations on brain structure and risk for psychiatric illness: Large-scale studies from the ENIGMA working groups on CNVs. <i>Human Brain Mapping</i> , 2022, 43, 300-328.	3.6	30
78	Mapping of multiple quantitative trait loci for growth and carcass traits in a complex commercial sheep pedigree. <i>Animal Science</i> , 2005, 80, 135-141.	1.3	28
79	Power and SNP tagging in whole mitochondrial genome association studies. <i>Genome Research</i> , 2008, 18, 911-917.	5.5	27
80	Genetic Influences on Life Span and Its Relationship to Personality. <i>Psychosomatic Medicine</i> , 2012, 74, 16-22.	2.0	27
81	Genetic regulation of methylation in human endometrium and blood and gene targets for reproductive diseases. <i>Clinical Epigenetics</i> , 2019, 11, 49.	4.1	26
82	Identical twins carry a persistent epigenetic signature of early genome programming. <i>Nature Communications</i> , 2021, 12, 5618.	12.8	26
83	Replicated effects of sex and genotype on gene expression in human lymphoblastoid cell lines. <i>Human Molecular Genetics</i> , 2007, 16, 364-373.	2.9	25
84	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.	3.4	25
85	Significant out-of-sample classification from methylation profile scoring for amyotrophic lateral sclerosis. <i>Npj Genomic Medicine</i> , 2020, 5, 10.	3.8	25
86	Variation in BMPR1B, TGFRB1 and BMPR2 and Control of Dizygotic Twinning. <i>Twin Research and Human Genetics</i> , 2011, 14, 408-416.	0.6	24
87	1q21.1 distal copy number variants are associated with cerebral and cognitive alterations in humans. <i>Translational Psychiatry</i> , 2021, 11, 182.	4.8	24
88	Genetic and Nongenetic Variation Revealed for the Principal Components of Human Gene Expression. <i>Genetics</i> , 2013, 195, 1117-1128.	2.9	23
89	Genome-wide survey of parent-of-origin effects on DNA methylation identifies candidate imprinted loci in humans. <i>Human Molecular Genetics</i> , 2018, 27, 2927-2939.	2.9	22
90	Promoter polymorphisms in two overlapping 6p25 genes implicate mitochondrial proteins in cognitive deficit in schizophrenia. <i>Molecular Psychiatry</i> , 2012, 17, 1328-1339.	7.9	19

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91	No Association Between General Cognitive Ability and Rare Copy Number Variation. <i>Behavior Genetics</i> , 2013, 43, 202-207.	2.1	17
92	Large Autosomal Copy-Number Differences within Unselected Monozygotic Twin Pairs are Rare. <i>Twin Research and Human Genetics</i> , 2015, 18, 13-18.	0.6	17
93	A genome wide survey supports the involvement of large copy number variants in schizophrenia with and without intellectual disability. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2013, 162, 847-854.	1.7	16
94	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.	3.6	16
95	Polygenic risk score analysis for amyotrophic lateral sclerosis leveraging cognitive performance, educational attainment and schizophrenia. <i>European Journal of Human Genetics</i> , 2022, 30, 532-539.	2.8	16
96	Phantom epistasis between unlinked loci. <i>Nature</i> , 2021, 596, E1-E3.	27.8	16
97	Autosomal genetic control of human gene expression does not differ across the sexes. <i>Genome Biology</i> , 2016, 17, 248.	8.8	15
98	Childhood intelligence attenuates the association between biological ageing and health outcomes in later life. <i>Translational Psychiatry</i> , 2019, 9, 323.	4.8	15
99	Blood DNA methylation sites predict death risk in a longitudinal study of 12, 300 individuals. <i>Aging</i> , 2020, 12, 14092-14124.	3.1	15
100	Modeling Linkage Disequilibrium in Natural Populations: The Example of the Soay Sheep Population of St. Kilda, Scotland. <i>Genetics</i> , 2005, 171, 251-258.	2.9	14
101	Whole exome sequencing and DNA methylation analysis in a clinical amyotrophic lateral sclerosis cohort. <i>Molecular Genetics & Genomic Medicine</i> , 2017, 5, 418-428.	1.2	14
102	Epigenome-Wide Association Study of Thyroid Function Traits Identifies Novel Associations of <i>FT3</i> With <i>KLF9</i> and <i>DOT1L</i> . <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021, 106, e2191-e2202.	3.6	14
103	Congenital Sensorineural Deafness in Australian Stumpy-Tail Cattle Dogs Is an Autosomal Recessive Trait That Maps to CFA10. <i>PLoS ONE</i> , 2010, 5, e13364.	2.5	13
104	Hemani et al. reply. <i>Nature</i> , 2014, 514, E5-E6.	27.8	12
105	Testing Two Evolutionary Theories of Human Aging with DNA Methylation Data. <i>Genetics</i> , 2017, 207, 1547-1560.	2.9	12
106	Functional characterisation of the amyotrophic lateral sclerosis risk locus <i>GPX3/TNIP1</i> . <i>Genome Medicine</i> , 2022, 14, 7.	8.2	12
107	Analysis of Genome-Wide Association Data. <i>Methods in Molecular Biology</i> , 2017, 1526, 161-173.	0.9	11
108	Shared genetic control of expression and methylation in peripheral blood. <i>BMC Genomics</i> , 2016, 17, 278.	2.8	10

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109	Genetically defined elevated homocysteine levels do not result in widespread changes of DNA methylation in leukocytes. PLoS ONE, 2017, 12, e0182472.	2.5	10
110	Promoter-anchored chromatin interactions predicted from genetic analysis of epigenomic data. Nature Communications, 2020, 11, 2061.	12.8	8
111	Examination of a region showing linkage map discrepancies across sheep breeds. Mammalian Genome, 2006, 17, 346-353.	2.2	7
112	The use of common mitochondrial variants to detect and characterise population structure in the Australian population: implications for genome-wide association studies. European Journal of Human Genetics, 2008, 16, 1396-1403.	2.8	6
113	Association Study of Common Mitochondrial Variants and Cognitive Ability. Behavior Genetics, 2009, 39, 504-512.	2.1	6
114	No evidence for warming climate theory of coat colour change in Soay sheep: a comment on Maloney et al.. Biology Letters, 2010, 6, 678-679.	2.3	6
115	Sharing a Placenta is Associated With a Greater Similarity in DNA Methylation in Monochorionic Versus Dichorionic Twin Pairs in Blood at Age 14. Twin Research and Human Genetics, 2015, 18, 680-685.	0.6	6
116	Evidence for mitochondrial genetic control of autosomal gene expression. Human Molecular Genetics, 2016, 25, ddd347.	2.9	6
117	The role of critical immune genes in brain disorders: insights from neuroimaging immunogenetics. Brain Communications, 2022, 4, fcac078.	3.3	6
118	Calculation of IBD probabilities with dense SNP or sequence data. Genetic Epidemiology, 2008, 32, 513-519.	1.3	5
119	A Simple Linear Regression Method for Quantitative Trait Loci Linkage Analysis With Censored Observations. Genetics, 2006, 173, 1735-1745.	2.9	4
120	Family-based mitochondrial association study of traits related to type 2 diabetes and the metabolic syndrome in adolescents. Diabetologia, 2009, 52, 2359-2368.	6.3	4
121	The autosomal genetic control of sexually dimorphic traits in humans is largely the same across the sexes. Genome Biology, 2016, 17, 169.	8.8	4
122	Examining the Impact of Imputation Errors on Fine-Mapping Using DNA Methylation QTL as a Model Trait. Genetics, 2019, 212, 577-586.	2.9	2
123	Case-Control Association Testing of Common Variants from Sequencing of DNA Pools. PLoS ONE, 2013, 8, e65410.	2.5	0