Allan F Mcrae

List of Publications by Year
in descending order

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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	Effects of copy number variations on brain structure and risk for psychiatric illness: Largeâ€scale studies from the<scp>ENIGMA</scp>working groups on<scp>CNVs</scp>. Human Brain Mapping, 2022, 43, 300-328.	3.6	30
2	Polygenic risk score analysis for amyotrophic lateral sclerosis leveraging cognitive performance, educational attainment and schizophrenia. European Journal of Human Genetics, 2022, 30, 532-539.	2.8	16
3	Epigenetic scores for the circulating proteome as tools for disease prediction. ELife, 2022, 11, .	6.0	37
4	Functional characterisation of the amyotrophic lateral sclerosis risk locus GPX3/TNIP1. Genome Medicine, 2022, 14, 7.	8.2	12
5	Genome-wide study of DNA methylation shows alterations in metabolic, inflammatory, and cholesterol pathways in ALS. Science Translational Medicine, 2022, 14, eabj0264.	12.4	38
6	The role of critical immune genes in brain disorders: insights from neuroimaging immunogenetics. Brain Communications, 2022, 4, fcac078.	3.3	6
7	Epigenome-wide meta-analysis of blood DNA methylation and its association with subcortical volumes: findings from the ENIGMA Epigenetics Working Group. Molecular Psychiatry, 2021, 26, 3884-3895.	7.9	34
8	Epigenome-Wide Association Study of Thyroid Function Traits Identifies Novel Associations of fT3 With KLF9 and DOT1L. Journal of Clinical Endocrinology and Metabolism, 2021, 106, e2191-e2202.	3.6	14
9	Creating and Validating a DNA Methylation-Based Proxy for Interleukin-6. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2021, 76, 2284-2292.	3.6	16
10	Meta-analysis of genome-wide DNA methylation identifies shared associations across neurodegenerative disorders. Genome Biology, 2021, 22, 90.	8.8	49
11	1q21.1 distal copy number variants are associated with cerebral and cognitive alterations in humans. Translational Psychiatry, 2021, 11, 182.	4.8	24
12	Phantom epistasis between unlinked loci. Nature, 2021, 596, E1-E3.	27.8	16
13	Identical twins carry a persistent epigenetic signature of early genome programming. Nature Communications, 2021, 12, 5618.	12.8	26
14	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	21.4	218
15	Common and rare variant association analyses in amyotrophic lateral sclerosis identify 15 risk loci with distinct genetic architectures and neuron-specific biology. Nature Genetics, 2021, 53, 1636-1648.	21.4	223
16	Association of Copy Number Variation of the 15q11.2 BP1-BP2 Region With Cortical and Subcortical Morphology and Cognition. JAMA Psychiatry, 2020, 77, 420.	11.0	54
17	Characterisation of an inflammation-related epigenetic score and its association with cognitive ability. Clinical Epigenetics, 2020, 12, 113.	4.1	38
18	Risk prediction of late-onset Alzheimerâ€™s disease implies an oligogenic architecture. Nature Communications, 2020, 11, 4799.	12.8	110

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19	Bayesian reassessment of the epigenetic architecture of complex traits. Nature Communications, 2020, 11, 2865.	12.8	43
20	Analysis of DNA methylation associates the cystineâ€“glutamate antiporter SLC7A11 with risk of Parkinsonâ€™s disease. Nature Communications, 2020, 11, 1238.	12.8	85
21	Significant out-of-sample classification from methylation profile scoring for amyotrophic lateral sclerosis. Npj Genomic Medicine, 2020, 5, 10.	3.8	25
22	Multi-method genome- and epigenome-wide studies of inflammatory protein levels in healthy older adults. Genome Medicine, 2020, 12, 60.	8.2	30
23	Promoter-anchored chromatin interactions predicted from genetic analysis of epigenomic data. Nature Communications, 2020, 11, 2061.	12.8	8
24	Blood DNA methylation sites predict death risk in a longitudinal study of 12, 300 individuals. Aging, 2020, 12, 14092-14124.	3.1	15
25	Genotype-by-environment interactions inferred from genetic effects on phenotypic variability in the UK Biobank. Science Advances, 2019, 5, eaaw3538.	10.3	123
26	Genome and epigenome wide studies of neurological protein biomarkers in the Lothian Birth Cohort 1936. Nature Communications, 2019, 10, 3160.	12.8	42
27	Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. Genome Medicine, 2019, 11, 54.	8.2	191
28	OSCA: a tool for omic-data-based complex trait analysis. Genome Biology, 2019, 20, 107.	8.8	105
29	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
30	Tissue-specific sex differences in human gene expression. Human Molecular Genetics, 2019, 28, 2976-2986.	2.9	41
31	An epigenetic score for BMI based on DNA methylation correlates with poor physical health and major disease in the Lothian Birth Cohort. International Journal of Obesity, 2019, 43, 1795-1802.	3.4	25
32	Genetic regulation of methylation in human endometrium and blood and gene targets for reproductive diseases. Clinical Epigenetics, 2019, 11, 49.	4.1	26
33	Childhood intelligence attenuates the association between biological ageing and health outcomes in later life. Translational Psychiatry, 2019, 9, 323.	4.8	15
34	Integrative analysis of omics summary data reveals putative mechanisms underlying complex traits. Nature Communications, 2018, 9, 918.	12.8	250
35	Signatures of negative selection in the genetic architecture of human complex traits. Nature Genetics, 2018, 50, 746-753.	21.4	304
36	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. Nature Communications, 2018, 9, 387.	12.8	151

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37	Meta-analysis of epigenome-wide association studies of cognitive abilities. Molecular Psychiatry, 2018, 23, 2133-2144.	7.9	68
38	Identification of 55,000 Replicated DNA Methylation QTL. Scientific Reports, 2018, 8, 17605.	3.3	157
39	Trajectories of inflammatory biomarkers over the eighth decade and their associations with immune cell profiles and epigenetic ageing. Clinical Epigenetics, 2018, 10, 159.	4.1	30
40	Epigenetic prediction of complex traits and death. Genome Biology, 2018, 19, 136.	8.8	146
41	Epigenetic influences on aging: a longitudinal genome-wide methylation study in old Swedish twins. Epigenetics, 2018, 13, 975-987.	2.7	65
42	Genotype effects contribute to variation in longitudinal methylome patterns in older people. Genome Medicine, 2018, 10, 75.	8.2	37
43	Genome-wide average DNA methylation is determined in utero. International Journal of Epidemiology, 2018, 47, 908-916.	1.9	38
44	Genome-wide DNA methylation profiling in whole blood reveals epigenetic signatures associated with migraine. BMC Genomics, 2018, 19, 69.	2.8	41
45	GWAS on family history of Alzheimerâ€™s disease. Translational Psychiatry, 2018, 8, 99.	4.8	406
46	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. Nature Communications, 2018, 9, 2941.	12.8	570
47	DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons. JAMA Psychiatry, 2018, 75, 949.	11.0	78
48	Genome-wide survey of parent-of-origin effects on DNA methylation identifies candidate imprinted loci in humans. Human Molecular Genetics, 2018, 27, 2927-2939.	2.9	22
49	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. Nature Communications, 2018, 9, 2282.	12.8	294
50	Role of DNA Methylation in Type 2 Diabetes Etiology: Using Genotype as a Causal Anchor. Diabetes, 2017, 66, 1713-1722.	0.6	32
51	Analysis of Genome-Wide Association Data. Methods in Molecular Biology, 2017, 1526, 161-173.	0.9	11
52	Testing Two Evolutionary Theories of Human Aging with DNA Methylation Data. Genetics, 2017, 207, 1547-1560.	2.9	12
53	Whole exome sequencing and <scp>DNA</scp> methylation analysis in a clinical amyotrophic lateral sclerosis cohort. Molecular Genetics & Genomic Medicine, 2017, 5, 418-428.	1.2	14
54	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. American Journal of Human Genetics, 2017, 101, 888-902.	6.2	154

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55	Association of Body Mass Index with DNA Methylation and Gene Expression in Blood Cells and Relations to Cardiometabolic Disease: A Mendelian Randomization Approach. PLoS Medicine, 2017, 14, e1002215.	8.4	246
56	Genetically defined elevated homocysteine levels do not result in widespread changes of DNA methylation in leukocytes. PLoS ONE, 2017, 12, e0182472.	2.5	10
57	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
58	Predicting gene targets from integrative analyses of summary data from GWAS and eQTL studies for 28 human complex traits. Genome Medicine, 2016, 8, 84.	8.2	91
59	Fast set-based association analysis using summary data from GWAS identifies novel gene loci for human complex traits. Scientific Reports, 2016, 6, 32894.	3.3	138
60	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. Genome Biology, 2016, 17, 255.	8.8	251
61	Inflammation-driven bone formation in a mouse model of ankylosing spondylitis: sequential not parallel processes. Arthritis Research and Therapy, 2016, 18, 35.	3.5	46
62	Identification of Common Genetic Variants Influencing Spontaneous Dizygotic Twinning and Female Fertility. American Journal of Human Genetics, 2016, 98, 898-908.	6.2	89
63	Epigenetic Signatures of Cigarette Smoking. Circulation: Cardiovascular Genetics, 2016, 9, 436-447.	5.1	678
64	Evidence for mitochondrial genetic control of autosomal gene expression. Human Molecular Genetics, 2016, 25, ddw347.	2.9	6
65	Autosomal genetic control of human gene expression does not differ across the sexes. Genome Biology, 2016, 17, 248.	8.8	15
66	Shared genetic control of expression and methylation in peripheral blood. BMC Genomics, 2016, 17, 278.	2.8	10
67	The epigenetic clock and telomere length are independently associated with chronological age and mortality. International Journal of Epidemiology, 2016, 45, 424-432.	1.9	227
68	Genome-wide autozygosity is associated with lower general cognitive ability. Molecular Psychiatry, 2016, 21, 837-843.	7.9	62
69	DNA methylation-based measures of biological age: meta-analysis predicting time to death. Aging, 2016, 8, 1844-1865.	3.1	786
70	Sharing a Placenta is Associated With a Greater Similarity in DNA Methylation in Monochorionic Versus Dichorionic Twin Pars in Blood at Age 14. Twin Research and Human Genetics, 2015, 18, 680-685.	0.6	6
71	Large Autosomal Copy-Number Differences within Unselected Monozygotic Twin Pairs are Rare. Twin Research and Human Genetics, 2015, 18, 13-18.	0.6	17
72	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. American Journal of Human Genetics, 2015, 97, 75-85.	6.2	116

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73	DNA methylation age of blood predicts all-cause mortality in later life. Genome Biology, 2015, 16, 25.	8.8	928
74	The epigenetic clock is correlated with physical and cognitive fitness in the Lothian Birth Cohort 1936. International Journal of Epidemiology, 2015, 44, 1388-1396.	1.9	472
75	The transcriptional landscape of age in human peripheral blood. Nature Communications, 2015, 6, 8570.	12.8	533
76	Seasonal Effects on Gene Expression. PLoS ONE, 2015, 10, e0126995.	2.5	48
77	Hemani et al. reply. Nature, 2014, 514, E5-E6.	27.8	12
78	Contribution of genetic variation to transgenerational inheritance of DNA methylation. Genome Biology, 2014, 15, R73.	9.6	231
79	Genetic and environmental exposures constrain epigenetic drift over the human life course. Genome Research, 2014, 24, 1725-1733.	5.5	152
80	708 Common and 2010 rare DISC1 locus variants identified in 1542 subjects: analysis for association with psychiatric disorder and cognitive traits. Molecular Psychiatry, 2014, 19, 668-675.	7.9	59
81	A genome wide survey supports the involvement of large copy number variants in schizophrenia with and without intellectual disability. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2013, 162, 847-854.	1.7	16
82	No Association Between General Cognitive Ability and Rare Copy Number Variation. Behavior Genetics, 2013, 43, 202-207.	2.1	17
83	Congruence of Additive and Non-Additive Effects on Gene Expression Estimated from Pedigree and SNP Data. PLoS Genetics, 2013, 9, e1003502.	3.5	79
84	Genetic and Nongenetic Variation Revealed for the Principal Components of Human Gene Expression. Genetics, 2013, 195, 1117-1128.	2.9	23
85	Monozygotic twins affected with major depressive disorder have greater variance in methylation than their unaffected co-twin. Translational Psychiatry, 2013, 3, e269-e269.	4.8	89
86	Case-Control Association Testing of Common Variants from Sequencing of DNA Pools. PLoS ONE, 2013, 8, e65410.	2.5	0
87	Genetic control of gene expression in whole blood and lymphoblastoid cell lines is largely independent. Genome Research, 2012, 22, 456-466.	5.5	75
88	A Genome-Wide Association Study of Caffeine-Related Sleep Disturbance: Confirmation of a Role for a Common Variant in the Adenosine Receptor. Sleep, 2012, 35, 967-975.	1.1	75
89	Promoter polymorphisms in two overlapping 6p25 genes implicate mitochondrial proteins in cognitive deficit in schizophrenia. Molecular Psychiatry, 2012, 17, 1328-1339.	7.9	19
90	The Brisbane Systems Genetics Study: Genetical Genomics Meets Complex Trait Genetics. PLoS ONE, 2012, 7, e35430.	2.5	83

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91	Genetic Influences on Life Span and Its Relationship to Personality. Psychosomatic Medicine, 2012, 74, 16-22.	2.0	27
92	Association between ORMDL3, IL1RL1 and a deletion on chromosome 17q21 with asthma risk in Australia. European Journal of Human Genetics, 2011, 19, 458-464.	2.8	105
93	GWAS Findings for Human Iris Patterns: Associations with Variants in Genes that Influence Normal Neuronal Pattern Development. American Journal of Human Genetics, 2011, 89, 334-343.	6.2	59
94	Variation in BMPR1B, TGFRB1 and BMPR2 and Control of Dizygotic Twinning. Twin Research and Human Genetics, 2011, 14, 408-416.	0.6	24
95	Clustered Coding Variants in the Glutamate Receptor Complexes of Individuals with Schizophrenia and Bipolar Disorder. PLoS ONE, 2011, 6, e19011.	2.5	54
96	A Versatile Gene-Based Test for Genome-wide Association Studies. American Journal of Human Genetics, 2010, 87, 139-145.	6.2	809
97	Horn type and horn length genes map to the same chromosomal region in Soay sheep. Heredity, 2010, 104, 196-205.	2.6	49
98	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
99	Genome-Wide Association Study of Height and Body Mass Index in Australian Twin Families. Twin Research and Human Genetics, 2010, 13, 179-193.	0.6	56
100	Congenital Sensorineural Deafness in Australian Stumpy-Tail Cattle Dogs Is an Autosomal Recessive Trait That Maps to CFA10. PLoS ONE, 2010, 5, e13364.	2.5	13
101	Family-based genome-wide association studies. Pharmacogenomics, 2009, 10, 181-190.	1.3	69
102	Geographical structure and differential natural selection among North European populations. Genome Research, 2009, 19, 804-814.	5.5	75
103	Association Study of Common Mitochondrial Variants and Cognitive Ability. Behavior Genetics, 2009, 39, 504-512.	2.1	6
104	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
105	DNA methylation profiles in monozygotic and dizygotic twins. Nature Genetics, 2009, 41, 240-245.	21.4	634
106	Variants in TF and HFE Explain â^¼40% of Genetic Variation in Serum-Transferrin Levels. American Journal of Human Genetics, 2009, 84, 60-65.	6.2	155
107	Common Variants in the Trichohyalin Gene Are Associated with Straight Hair in Europeans. American Journal of Human Genetics, 2009, 85, 750-755.	6.2	230
108	A Cytogenetic Abnormality and Rare Coding Variants Identify ABCA13 as a Candidate Gene in Schizophrenia, Bipolar Disorder, and Depression. American Journal of Human Genetics, 2009, 85, 833-846.	6.2	102

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109	Calculation of IBD probabilities with dense SNP or sequence data. Genetic Epidemiology, 2008, 32, 513-519.	1.3	5
110	Divergence between Human Populations Estimated from Linkage Disequilibrium. American Journal of Human Genetics, 2008, 83, 737-743.	6.2	37
111	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
112	A Localized Negative Genetic Correlation Constrains Microevolution of Coat Color in Wild Sheep. Science, 2008, 319, 318-320.	12.6	97
113	Power and SNP tagging in whole mitochondrial genome association studies. Genome Research, 2008, 18, 911-917.	5.5	27
114	Compelling evidence that a single nucleotide substitution in TYRP1 is responsible for coat-colour polymorphism in a free-living population of Soay sheep. Proceedings of the Royal Society B: Biological Sciences, 2007, 274, 619-626.	2.6	116
115	Replicated effects of sex and genotype on gene expression in human lymphoblastoid cell lines. Human Molecular Genetics, 2007, 16, 364-373.	2.9	25
116	MAPPING QUANTITATIVE TRAIT LOCI UNDERLYING FITNESS-RELATED TRAITS IN A FREE-LIVING SHEEP POPULATION. Evolution; International Journal of Organic Evolution, 2007, 61, 1403-1416.	2.3	48
117	Quantitative trait loci (QTL) mapping of resistance to strongyles and coccidia in the free-living Soay sheep (Ovis aries). International Journal for Parasitology, 2007, 37, 121-129.	3.1	87
118	Development of a Linkage Map and Mapping of Phenotypic Polymorphisms in a Free-Living Population of Soay Sheep (Ovis aries). Genetics, 2006, 173, 1521-1537.	2.9	57
119	Examination of a region showing linkage map discrepancies across sheep breeds. Mammalian Genome, 2006, 17, 346-353.	2.2	7
120	A Simple Linear Regression Method for Quantitative Trait Loci Linkage Analysis With Censored Observations. Genetics, 2006, 173, 1735-1745.	2.9	4
121	Modeling Linkage Disequilibrium in Natural Populations: The Example of the Soay Sheep Population of St. Kilda, Scotland. Genetics, 2005, 171, 251-258.	2.9	14
122	Mapping of multiple quantitative trait loci for growth and carcass traits in a complex commercial sheep pedigree. Animal Science, 2005, 80, 135-141.	1.3	28
123	Bone density in sheep: genetic variation and quantitative trait loci localisation. Bone, 2003, 33, 540-548.	2.9	37