## Sarah E Harris

List of Publications by Year in descending order

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SADAH F HADDIS

#	Article	IF	CITATIONS
1	Gene-mapping study of extremes of cerebral small vessel disease reveals TRIM47 as a strong candidate. Brain, 2022, 145, 1992-2007.	3.7	6
2	Blood-based epigenome-wide analyses of cognitive abilities. Genome Biology, 2022, 23, 26.	3.8	20
3	Epigenetic scores for the circulating proteome as tools for disease prediction. ELife, 2022, 11, .	2.8	37
4	Circulating Metabolome and White Matter Hyperintensities in Women and Men. Circulation, 2022, 145, 1040-1052.	1.6	17
5	Meta-GWAS Reveals Novel Genetic Variants Associated with Urinary Excretion of Uromodulin. Journal of the American Society of Nephrology: JASN, 2022, 33, 511-529.	3.0	14
6	DNA methylome-wide association study of genetic risk for depression implicates antigen processing and immune responses. Genome Medicine, 2022, 14, 36.	3.6	16
7	A comparison of blood and brainâ€derived ageing and inflammationâ€related DNA methylation signatures and their association with microglial burdens. European Journal of Neuroscience, 2022, 56, 5637-5649.	1.2	9
8	Longitudinal dynamics of clonal hematopoiesis identifies gene-specific fitness effects. Nature Medicine, 2022, 28, 1439-1446.	15.2	36
9	An epigenetic predictor of death captures multi-modal measures of brain health. Molecular Psychiatry, 2021, 26, 3806-3816.	4.1	77
10	Pulmonary Function and Risk of Alzheimer Dementia. Chest, 2021, 160, 274-276.	0.4	3
11	Multi-ancestry genome-wide association study accounting for gene-psychosocial factor interactions identifies novel loci for blood pressure traits. Human Genetics and Genomics Advances, 2021, 2, 100013.	1.0	2
12	Three major dimensions of human brain cortical ageing in relation to cognitive decline across the eighth decade of life. Molecular Psychiatry, 2021, 26, 2651-2662.	4.1	29
13	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. Human Molecular Genetics, 2021, 30, 393-409.	1.4	32
14	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.	1.7	16
15	Meta-analysis of genome-wide DNA methylation identifies shared associations across neurodegenerative disorders. Genome Biology, 2021, 22, 90.	3.8	49
16	Epigenetic predictors of lifestyle traits applied to the blood and brain. Brain Communications, 2021, 3, fcab082.	1.5	6
17	Multi-ancestry genome-wide gene–sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	4.1	13
18	Rare Missense Functional Variants at <i>COL4A1</i> and <i>COL4A2</i> in Sporadic Intracerebral Hemorrhage. Neurology, 2021, 97, .	1.5	6

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19	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	3.8	90
20	Rare and low-frequency exonic variants and gene-by-smoking interactions in pulmonary function. Scientific Reports, 2021, 11, 19365.	1.6	2
21	Genome-wide analysis of gene dosage in 24,092 individuals estimates that 10,000 genes modulate cognitive ability. Molecular Psychiatry, 2021, 26, 2663-2676.	4.1	33
22	The genetic and epigenetic profile of serumÂS100β in the Lothian Birth Cohort 1936 and its relationship to Alzheimer's disease. Wellcome Open Research, 2021, 6, 306.	0.9	1
23	DNA Methylation and Protein Markers of Chronic Inflammation and Their Associations With Brain and Cognitive Aging. Neurology, 2021, 97, e2340-e2352.	1.5	44
24	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. Nature Communications, 2021, 12, 7173.	5.8	8
25	Meta-analyses identify DNA methylation associated with kidney function and damage. Nature Communications, 2021, 12, 7174.	5.8	30
26	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
27	Polygenic predictors of age-related decline in cognitive ability. Molecular Psychiatry, 2020, 25, 2584-2598.	4.1	38
28	Lossâ€ofâ€Function Mutations in the <i>ALPL</i> Gene Presenting with Adult Onset Osteoporosis and Low Serum Concentrations of Total Alkaline Phosphatase. Journal of Bone and Mineral Research, 2020, 35, 657-661.	3.1	23
29	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	9.4	91
30	Attitudes to ageing, biomarkers of ageing and mortality: the Lothian Birth Cohort 1936. Journal of Epidemiology and Community Health, 2020, 74, 377-383.	2.0	5
31	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	4.1	17
32	Multi-method genome- and epigenome-wide studies of inflammatory protein levels in healthy older adults. Genome Medicine, 2020, 12, 60.	3.6	30
33	Generation of twenty four induced pluripotent stem cell lines from twenty four members of the Lothian Birth Cohort 1936. Stem Cell Research, 2020, 46, 101851.	0.3	16
34	Using regulatory variants to detect gene–gene interactions identifies networks of genes linked to cell immortalisation. Nature Communications, 2020, 11, 343.	5.8	7
35	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	0.9	3
36	Neurology-related protein biomarkers are associated with cognitive ability and brain volume in older age. Nature Communications, 2020, 11, 800.	5.8	42

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37	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	0.9	4
38	Brain age and other bodily â€~ages': implications for neuropsychiatry. Molecular Psychiatry, 2019, 24, 266-281.	4.1	291
39	What genome-wide association studies reveal about the association between intelligence and physical health, illness, and mortality. Current Opinion in Psychology, 2019, 27, 6-12.	2.5	45
40	What genome-wide association studies reveal about the association between intelligence and mental health. Current Opinion in Psychology, 2019, 27, 25-30.	2.5	36
41	Genome and epigenome wide studies of neurological protein biomarkers in the Lothian Birth Cohort 1936. Nature Communications, 2019, 10, 3160.	5.8	42
42	Epigenome-wide association study of lung function level and its change. European Respiratory Journal, 2019, 54, 1900457.	3.1	49
43	Epigenetic signatures of smoking associate with cognitive function, brain structure, and mental and physical health outcomes in the Lothian Birth Cohort 1936. Translational Psychiatry, 2019, 9, 248.	2.4	34
44	Novel Genetic Locus Influencing Retinal Venular Tortuosity Is Also Associated With Risk of Coronary Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2019, 39, 2542-2552.	1.1	23
45	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
46	Predicting incident dementia 3â€8 years after brief cognitive tests in the UK Biobank prospective study of 500,000 people. Alzheimer's and Dementia, 2019, 15, 1546-1557.	0.4	28
47	Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. Genome Medicine, 2019, 11, 54.	3.6	191
48	Sex-specific moderation by lifestyle and psychosocial factors on the genetic contributions to adiposity in 112,151 individuals from UK Biobank. Scientific Reports, 2019, 9, 363.	1.6	6
49	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	1.6	85
50	Sleep and cognitive aging in the eighth decade of life. Sleep, 2019, 42, .	0.6	32
51	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	5.8	64
52	Linked Mutations at Adjacent Nucleotides Have Shaped Human Population Differentiation and Protein Evolution. Genome Biology and Evolution, 2019, 11, 759-775.	1.1	9
53	Smoking does not accelerate leucocyte telomere attrition: a meta-analysis of 18 longitudinal cohorts. Royal Society Open Science, 2019, 6, 190420.	1.1	33
54	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. Nature Communications, 2019, 10, 2154.	5.8	172

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55	A multi-ancestry genome-wide study incorporating gene–smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	1.4	31
56	Multi-ancestry genome-wide gene–smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	9.4	112
57	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. Nature Genetics, 2019, 51, 481-493.	9.4	350
58	Increased ultra-rare variant load in an isolated Scottish population impacts exonic and regulatory regions. PLoS Genetics, 2019, 15, e1008480.	1.5	17
59	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. American Journal of Human Genetics, 2019, 104, 112-138.	2.6	106
60	DNA methylation-based estimator of telomere length. Aging, 2019, 11, 5895-5923.	1.4	198
61	Epigenome-wide association study of leukocyte telomere length. Aging, 2019, 11, 5876-5894.	1.4	19
62	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. American Journal of Human Genetics, 2018, 102, 375-400.	2.6	123
63	Association analysis in over 329,000 individuals identifies 116 independent variants influencing neuroticism. Nature Genetics, 2018, 50, 6-11.	9.4	327
64	Meta-analysis of epigenome-wide association studies of cognitive abilities. Molecular Psychiatry, 2018, 23, 2133-2144.	4.1	68
65	Brain age predicts mortality. Molecular Psychiatry, 2018, 23, 1385-1392.	4.1	513
66	Genetic contributions to self-reported tiredness. Molecular Psychiatry, 2018, 23, 609-620.	4.1	45
67	Genome-Wide Meta-Analysis Unravels Interactions between Magnesium Homeostasis and Metabolic Phenotypes. Journal of the American Society of Nephrology: JASN, 2018, 29, 335-348.	3.0	34
68	Identification of 55,000 Replicated DNA Methylation QTL. Scientific Reports, 2018, 8, 17605.	1.6	157
69	Trajectories of inflammatory biomarkers over the eighth decade and their associations with immune cell profiles and epigenetic ageing. Clinical Epigenetics, 2018, 10, 159.	1.8	30
70	Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. Nature Communications, 2018, 9, 4455.	5.8	181
71	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	9.4	924
72	Body mass index is negatively associated with telomere length: a collaborative cross-sectional meta-analysis of 87 observational studies. American Journal of Clinical Nutrition, 2018, 108, 453-475.	2.2	137

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73	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	5.8	484
74	GWAS on family history of Alzheimer's disease. Translational Psychiatry, 2018, 8, 99.	2.4	406
75	Reversal of endothelial dysfunction reduces white matter vulnerability in cerebral small vessel disease in rats. Science Translational Medicine, 2018, 10, .	5.8	129
76	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
77	Genetic risk for neurodegenerative disorders, and its overlap with cognitive ability and physical function. PLoS ONE, 2018, 13, e0198187.	1.1	17
78	Exploring causality in the association between circulating 25-hydroxyvitamin D and colorectal cancer risk: a large Mendelian randomisation study. BMC Medicine, 2018, 16, 142.	2.3	62
79	Longitudinal serum S100β and brain aging in the Lothian Birth Cohort 1936. Neurobiology of Aging, 2018, 69, 274-282.	1.5	13
80	Apolipoprotein E genotype does not moderate the associations of depressive symptoms, neuroticism and allostatic load with cognitive ability and cognitive aging in the Lothian Birth Cohort 1936. PLoS ONE, 2018, 13, e0192604.	1.1	7
81	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	1.1	94
82	Genetic contributions to Trail Making Test performance in UK Biobank. Molecular Psychiatry, 2018, 23, 1575-1583.	4.1	21
83	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 2018, 3, 4.	0.9	19
84	Molecular genetic contributions to self-rated health. International Journal of Epidemiology, 2017, 46, dyw219.	0.9	39
85	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. International Journal of Epidemiology, 2017, 46, dyw318.	0.9	36
86	Genome-wide association analyses for lung function and chronic obstructive pulmonary disease identify new loci and potential druggable targets. Nature Genetics, 2017, 49, 416-425.	9.4	257
87	Short telomere length is associated with impaired cognitive performance in European ancestry cohorts. Translational Psychiatry, 2017, 7, e1100-e1100.	2.4	61
88	Common variants in CLDN14 are associated with differential excretion of magnesium over calcium in urine. Pflugers Archiv European Journal of Physiology, 2017, 469, 91-103.	1.3	27
89	Interaction of APOE e4 and poor glycemic control predicts white matter hyperintensity growth from 73 to 76. Neurobiology of Aging, 2017, 54, 54-58.	1.5	20
90	Klotho, APOEε4, cognitive ability, brain size, atrophy, and survival: a study in the Aberdeen Birth Cohort of 1936. Neurobiology of Aging, 2017, 55, 91-98.	1.5	22

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91	Single Nucleotide Polymorphisms Associated with Reading Ability Show Connection to Socio-Economic Outcomes. Behavior Genetics, 2017, 47, 469-479.	1.4	13
92	Cognitive ability and physical health: a Mendelian randomization study. Scientific Reports, 2017, 7, 2651.	1.6	34
93	An epigenome-wide association study meta-analysis of educational attainment. Molecular Psychiatry, 2017, 22, 1680-1690.	4.1	70
94	Age-related gene expression changes, and transcriptome wide association study of physical and cognitive aging traits, in the Lothian Birth Cohort 1936. Aging, 2017, 9, 2489-2503.	1.4	33
95	Genetic prediction of male pattern baldness. PLoS Genetics, 2017, 13, e1006594.	1.5	89
96	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.	3.9	246
97	Molecular genetic aetiology of general cognitive function is enriched in evolutionarily conserved regions. Translational Psychiatry, 2016, 6, e980-e980.	2.4	41
98	Personality Polygenes, Positive Affect, and Life Satisfaction. Twin Research and Human Genetics, 2016, 19, 407-417.	0.3	16
99	Genome-wide association study of cognitive functions and educational attainment in UK Biobank (N=112 151). Molecular Psychiatry, 2016, 21, 758-767.	4.1	317
100	Longitudinal telomere length shortening and cognitive and physical decline in later life: The Lothian Birth Cohorts 1936 and 1921. Mechanisms of Ageing and Development, 2016, 154, 43-48.	2.2	37
101	Pleiotropy between neuroticism and physical and mental health: findings from 108 038 men and women in UK Biobank. Translational Psychiatry, 2016, 6, e791-e791.	2.4	135
102	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	13.7	1,204
103	Molecular Genetic Contributions to Social Deprivation and Household Income in UK Biobank. Current Biology, 2016, 26, 3083-3089.	1.8	177
104	<i>KLB</i> is associated with alcohol drinking, and its gene product β-Klotho is necessary for FGF21 regulation of alcohol preference. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14372-14377.	3.3	208
105	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	9.4	261
106	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
107	The epigenetic clock and telomere length are independently associated with chronological age and mortality. International Journal of Epidemiology, 2016, 45, 424-432.	0.9	227
108	Shared genetic aetiology between cognitive functions and physical and mental health in UK Biobank (N=112 151) and 24 GWAS consortia. Molecular Psychiatry, 2016, 21, 1624-1632.	4.1	340

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109	Polygenic risk for coronary artery disease is associated with cognitive ability in older adults. International Journal of Epidemiology, 2016, 45, 433-440.	0.9	16
110	Systems genetics identifies a convergent gene network for cognition and neurodevelopmental disease. Nature Neuroscience, 2016, 19, 223-232.	7.1	131
111	Polygenic risk of ischemic stroke is associated with cognitive ability. Neurology, 2016, 86, 611-618.	1.5	14
112	Genome-wide autozygosity is associated with lower general cognitive ability. Molecular Psychiatry, 2016, 21, 837-843.	4.1	62
113	<i>APOE/TOMM40</i> Genetic Loci, White Matter Hyperintensities, and Cerebral Microbleeds. International Journal of Stroke, 2015, 10, 1297-1300.	2.9	15
114	Recurrent Coding Sequence Variation Explains Only A Small Fraction of the Genetic Architecture of Colorectal Cancer. Scientific Reports, 2015, 5, 16286.	1.6	24
115	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
116	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. Nature Communications, 2015, 6, 8658.	5.8	108
117	Genetic contributions to variation in general cognitive function: a meta-analysis of genome-wide association studies in the CHARGE consortium (N=53 949). Molecular Psychiatry, 2015, 20, 183-192.	4.1	344
118	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
119	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. American Journal of Human Genetics, 2015, 97, 75-85.	2.6	116
120	DNA methylation age of blood predicts all-cause mortality in later life. Genome Biology, 2015, 16, 25.	3.8	928
121	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. Nature Genetics, 2015, 47, 1282-1293.	9.4	294
122	The epigenetic clock is correlated with physical and cognitive fitness in the Lothian Birth Cohort 1936. International Journal of Epidemiology, 2015, 44, 1388-1396.	0.9	472
123	Genes From a Translational Analysis Support a Multifactorial Nature of White Matter Hyperintensities. Stroke, 2015, 46, 341-347.	1.0	33
124	Post-mortem brain analyses of the Lothian Birth Cohort 1936: extending lifetime cognitive and brain phenotyping to the level of the synapse. Acta Neuropathologica Communications, 2015, 3, 53.	2.4	25
125	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	1.1	64
126	Genetic Basis of a Cognitive Complexity Metric. PLoS ONE, 2015, 10, e0123886.	1.1	22

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127	Polygenic Risk for Alzheimer's Disease is not Associated with Cognitive Ability or Cognitive Aging in Non-Demented Older People. Journal of Alzheimer's Disease, 2014, 39, 565-574.	1.2	63
128	Are APOE É <sup>,</sup> genotype and TOMM40 poly-T repeat length associations with cognitive ageing mediated by brain white matter tract integrity?. Translational Psychiatry, 2014, 4, e449-e449.	2.4	20
129	Predicting cognitive ability in ageing cohorts using Type 2 diabetes genetic risk. Diabetic Medicine, 2014, 31, 714-720.	1.2	13
130	A genome-wide association study implicates the APOE locus in nonpathological cognitive ageing. Molecular Psychiatry, 2014, 19, 76-87.	4.1	142
131	Childhood intelligence is heritable, highly polygenic and associated with FNBP1L. Molecular Psychiatry, 2014, 19, 253-258.	4.1	241
132	Gender and telomere length: Systematic review and meta-analysis. Experimental Gerontology, 2014, 51, 15-27.	1.2	394
133	Genetic and environmental exposures constrain epigenetic drift over the human life course. Genome Research, 2014, 24, 1725-1733.	2.4	152
134	Alzheimer's disease susceptibility genes APOE and TOMM40, and brain white matter integrity in the Lothian Birth Cohort 1936. Neurobiology of Aging, 2014, 35, 1513.e25-1513.e33.	1.5	58
135	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.	4.1	59
136	Polygenic Risk for Schizophrenia Is Associated with Cognitive Change Between Childhood and Old Age. Biological Psychiatry, 2013, 73, 938-943.	0.7	118
137	Telomere Length and Physical Performance at Older Ages: An Individual Participant Meta-Analysis. PLoS ONE, 2013, 8, e69526.	1.1	35
138	Complex Variation in Measures of General Intelligence and Cognitive Change. PLoS ONE, 2013, 8, e81189.	1.1	7
139	The Role of Variation at AβPP, PSEN1, PSEN2, and MAPT in Late Onset Alzheimer's Disease. Journal of Alzheimer's Disease, 2012, 28, 377-387.	1.2	53
140	Telomere length and aging biomarkers in 70-year-olds: the Lothian Birth Cohort 1936. Neurobiology of Aging, 2012, 33, 1486.e3-1486.e8.	1.5	64
141	Genetic contributions to stability and change in intelligence from childhood to old age. Nature, 2012, 482, 212-215.	13.7	228
142	APOE E4 status predicts age-related cognitive decline in the ninth decade: longitudinal follow-up of the Lothian Birth Cohort 1921. Molecular Psychiatry, 2012, 17, 315-324.	4.1	143
143	Genome-wide association studies establish that human intelligence is highly heritable and polygenic. Molecular Psychiatry, 2011, 16, 996-1005.	4.1	571
144	The genetics of cognitive ability and cognitive ageing in healthy older people. Trends in Cognitive Sciences, 2011, 15, 388-94.	4.0	99

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145	Genetic Predictors of Fibrin D-Dimer Levels in Healthy Adults. Circulation, 2011, 123, 1864-1872.	1.6	60
146	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. Nature Genetics, 2011, 43, 1082-1090.	9.4	367
147	Genetic Variants Associated With Altered Plasma Levels of C-Reactive Protein are not Associated With Late-Life Cognitive Ability in Four Scottish Samples. Behavior Genetics, 2010, 40, 3-11.	1.4	18
148	A genetic association analysis of cognitive ability and cognitive ageing using 325 markers for 109 genes associated with oxidative stress or cognition. BMC Genetics, 2007, 8, 43.	2.7	69
149	The association between telomere length, physical health, cognitive ageing, and mortality in non-demented older people. Neuroscience Letters, 2006, 406, 260-264.	1.0	172
150	The brain-derived neurotrophic factor Val66Met polymorphism is associated with age-related change in reasoning skills. Molecular Psychiatry, 2006, 11, 505-513.	4.1	146
151	The functional COMT polymorphism, Val158Met, is associated with logical memory and the personality trait intellect/imagination in a cohort of healthy 79 year olds. Neuroscience Letters, 2005, 385, 1-6.	1.0	81
152	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	0.9	11
153	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	0.9	1
154	The genetic and epigenetic profile of serumÂS100β in the Lothian Birth Cohort 1936 and its relationship to Alzheimer's disease. Wellcome Open Research, 0, 6, 306.	0.9	0