

Michael E Weale

List of Publications by Citations

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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.

129 papers	14,806 citations	59 h-index	121 g-index
136 ext. papers	17,389 ext. citations	11.9 avg, IF	5.48 L-index

#	Paper	IF	Citations
129	A whole-genome association study of major determinants for host control of HIV-1. <i>Science</i> , 2007 , 317, 944-7	33.3	999
128	A genome-wide association study identifies new psoriasis susceptibility loci and an interaction between HLA-C and ERAP1. <i>Nature Genetics</i> , 2010 , 42, 985-90	36.3	773
127	Identification of 15 new psoriasis susceptibility loci highlights the role of innate immunity. <i>Nature Genetics</i> , 2012 , 44, 1341-8	36.3	681
126	Association of multidrug resistance in epilepsy with a polymorphism in the drug-transporter gene ABCB1. <i>New England Journal of Medicine</i> , 2003 , 348, 1442-8	59.2	611
125	Common genetic variants influence human subcortical brain structures. <i>Nature</i> , 2015 , 520, 224-9	50.4	601
124	Natural selection on EPAS1 (HIF2alpha) associated with low hemoglobin concentration in Tibetan highlanders. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 11459-64	11.5	551
123	The ENIGMA Consortium: large-scale collaborative analyses of neuroimaging and genetic data. <i>Brain Imaging and Behavior</i> , 2014 , 8, 153-82	4.1	539
122	Identification of common variants associated with human hippocampal and intracranial volumes. <i>Nature Genetics</i> , 2012 , 44, 552-61	36.3	498
121	Genetic variability in the regulation of gene expression in ten regions of the human brain. <i>Nature Neuroscience</i> , 2014 , 17, 1418-1428	25.5	483
120	A genome-wide investigation of SNPs and CNVs in schizophrenia. <i>PLoS Genetics</i> , 2009 , 5, e1000373	6	357
119	Rare coding variants in the phospholipase D3 gene confer risk for Alzheimer's disease. <i>Nature</i> , 2014 , 505, 550-554	50.4	345
118	Population genetic structure of variable drug response. <i>Nature Genetics</i> , 2001 , 29, 265-9	36.3	344
117	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , 2015 , 6, 8570	17.4	335
116	Long-range LD can confound genome scans in admixed populations. <i>American Journal of Human Genetics</i> , 2008 , 83, 132-5; author reply 135-9	11	253
115	Novel insights into the genetics of smoking behaviour, lung function, and chronic obstructive pulmonary disease (UK BiLEVE): a genetic association study in UK Biobank. <i>Lancet Respiratory Medicine</i> , 2015 , 3, 769-81	35.1	245
114	Genome-wide association study of obsessive-compulsive disorder. <i>Molecular Psychiatry</i> , 2013 , 18, 788-98	15.1	244
113	Genome-wide association study of major recurrent depression in the U.K. population. <i>American Journal of Psychiatry</i> , 2010 , 167, 949-57	11.9	194

112	Gene expression changes with age in skin, adipose tissue, blood and brain. <i>Genome Biology</i> , 2013 , 14, R75	18.3	185
111	Positive selection on a high-sensitivity allele of the human bitter-taste receptor TAS2R16. <i>Current Biology</i> , 2005 , 15, 1257-65	6.3	180
110	Inferences from DNA data: population histories, evolutionary processes and forensic match probabilities. <i>Journal of the Royal Statistical Society Series A: Statistics in Society</i> , 2003 , 166, 155-188	2.1	179
109	Quality control parameters on a large dataset of regionally dissected human control brains for whole genome expression studies. <i>Journal of Neurochemistry</i> , 2011 , 119, 275-82	6	178
108	A novel polymorphism associated with lactose tolerance in Africa: multiple causes for lactase persistence?. <i>Human Genetics</i> , 2007 , 120, 779-88	6.3	178
107	Novel genetic loci associated with hippocampal volume. <i>Nature Communications</i> , 2017 , 8, 13624	17.4	173
106	Chromosome 9p21 in sporadic amyotrophic lateral sclerosis in the UK and seven other countries: a genome-wide association study. <i>Lancet Neurology, The</i> , 2010 , 9, 986-94	24.1	171
105	Selection and evaluation of tagging SNPs in the neuronal-sodium-channel gene SCN1A: implications for linkage-disequilibrium gene mapping. <i>American Journal of Human Genetics</i> , 2003 , 73, 551-65	11	171
104	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. <i>Molecular Psychiatry</i> , 2015 , 20, 647-656	15.1	167
103	Widespread sex differences in gene expression and splicing in the adult human brain. <i>Nature Communications</i> , 2013 , 4, 2771	17.4	166
102	Genetic influences on schizophrenia and subcortical brain volumes: large-scale proof of concept. <i>Nature Neuroscience</i> , 2016 , 19, 420-431	25.5	163
101	The C9ORF72 expansion mutation is a common cause of ALS+/-FTD in Europe and has a single founder. <i>European Journal of Human Genetics</i> , 2013 , 21, 102-8	5.3	159
100	Multicentre search for genetic susceptibility loci in sporadic epilepsy syndrome and seizure types: a case-control study. <i>Lancet Neurology, The</i> , 2007 , 6, 970-80	24.1	152
99	Genome-wide Pleiotropy Between Parkinson Disease and Autoimmune Diseases. <i>JAMA Neurology</i> , 2017 , 74, 780-792	17.2	150
98	Novel genetic loci underlying human intracranial volume identified through genome-wide association. <i>Nature Neuroscience</i> , 2016 , 19, 1569-1582	25.5	147
97	Epilepsy, hippocampal sclerosis and febrile seizures linked by common genetic variation around SCN1A. <i>Brain</i> , 2013 , 136, 3140-50	11.2	144
96	The T allele of a single-nucleotide polymorphism 13.9 kb upstream of the lactase gene (LCT) (C-13.9kbT) does not predict or cause the lactase-persistence phenotype in Africans. <i>American Journal of Human Genetics</i> , 2004 , 74, 1102-10	11	140
95	Genetic signatures reveal high-altitude adaptation in a set of ethiopian populations. <i>Molecular Biology and Evolution</i> , 2013 , 30, 1877-88	8.3	137

94	Genome scans and candidate gene approaches in the study of common diseases and variable drug responses. <i>Trends in Genetics</i> , 2003 , 19, 615-22	8.5	136
93	An additional k-means clustering step improves the biological features of WGCNA gene co-expression networks. <i>BMC Systems Biology</i> , 2017 , 11, 47	3.5	134
92	MAPT expression and splicing is differentially regulated by brain region: relation to genotype and implication for tauopathies. <i>Human Molecular Genetics</i> , 2012 , 21, 4094-103	5.6	134
91	A single-nucleotide polymorphism tagging set for human drug metabolism and transport. <i>Nature Genetics</i> , 2005 , 37, 84-9	36.3	134
90	Genetic analysis in UK Biobank links insulin resistance and transendothelial migration pathways to coronary artery disease. <i>Nature Genetics</i> , 2017 , 49, 1392-1397	36.3	127
89	Insights into TREM2 biology by network analysis of human brain gene expression data. <i>Neurobiology of Aging</i> , 2013 , 34, 2699-714	5.6	119
88	Y chromosome evidence for Anglo-Saxon mass migration. <i>Molecular Biology and Evolution</i> , 2002 , 19, 1008-21	3.1	119
87	Cost-effectiveness of pharmacogenetic-guided treatment: are we there yet?. <i>Pharmacogenomics Journal</i> , 2017 , 17, 395-402	3.5	118
86	A genome-wide study of common SNPs and CNVs in cognitive performance in the CANTAB. <i>Human Molecular Genetics</i> , 2009 , 18, 4650-61	5.6	117
85	Founding mothers of Jewish communities: geographically separated Jewish groups were independently founded by very few female ancestors. <i>American Journal of Human Genetics</i> , 2002 , 70, 1411-20	11	113
84	Cross-disorder genome-wide analyses suggest a complex genetic relationship between Tourette's syndrome and OCD. <i>American Journal of Psychiatry</i> , 2015 , 172, 82-93	11.9	101
83	Integration of GWAS SNPs and tissue specific expression profiling reveal discrete eQTLs for human traits in blood and brain. <i>Neurobiology of Disease</i> , 2012 , 47, 20-8	7.5	100
82	Population genomics: linkage disequilibrium holds the key. <i>Current Biology</i> , 2001 , 11, R576-9	6.3	98
81	A genome-wide association meta-analysis identifies a novel locus at 17q11.2 associated with sporadic amyotrophic lateral sclerosis. <i>Human Molecular Genetics</i> , 2014 , 23, 2220-31	5.6	95
80	Genetic intra-tumour heterogeneity in epithelial ovarian cancer and its implications for molecular diagnosis of tumours. <i>Journal of Pathology</i> , 2007 , 211, 286-95	9.4	94
79	Identifying candidate causal variants responsible for altered activity of the ABCB1 multidrug resistance gene. <i>Genome Research</i> , 2004 , 14, 1333-44	9.7	94
78	Recursive splicing in long vertebrate genes. <i>Nature</i> , 2015 , 521, 371-375	50.4	88
77	Quality control for genome-wide association studies. <i>Methods in Molecular Biology</i> , 2010 , 628, 341-72	1.4	83

76	Multiple rare variants as a cause of a common phenotype: several different lactase persistence associated alleles in a single ethnic group. <i>Journal of Molecular Evolution</i> , 2009 , 69, 579-88	3.1	80
75	Multiple origins of Ashkenazi Levites: Y chromosome evidence for both Near Eastern and European ancestries. <i>American Journal of Human Genetics</i> , 2003 , 73, 768-79	11	78
74	Phenome-wide association studies across large population cohorts support drug target validation. <i>Nature Communications</i> , 2018 , 9, 4285	17.4	76
73	Mutations in the vesicular trafficking protein annexin A11 are associated with amyotrophic lateral sclerosis. <i>Science Translational Medicine</i> , 2017 , 9,	17.5	74
72	High-resolution Y chromosome haplotypes of Israeli and Palestinian Arabs reveal geographic substructure and substantial overlap with haplotypes of Jews. <i>Human Genetics</i> , 2000 , 107, 630-41	6.3	64
71	Genomics implicates adaptive and innate immunity in Alzheimer's and Parkinson's diseases. <i>Annals of Clinical and Translational Neurology</i> , 2016 , 3, 924-933	5.3	62
70	Evolution of a length polymorphism in the human PER3 gene, a component of the circadian system. <i>Journal of Biological Rhythms</i> , 2005 , 20, 490-9	3.2	59
69	Failure to replicate effect of Kibra on human memory in two large cohorts of European origin. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2008 , 147B, 667-8	3.5	57
68	Armenian Y chromosome haplotypes reveal strong regional structure within a single ethno-national group. <i>Human Genetics</i> , 2001 , 109, 659-74	6.3	51
67	Little genetic differentiation as assessed by uniparental markers in the presence of substantial language variation in peoples of the Cross River region of Nigeria. <i>BMC Evolutionary Biology</i> , 2010 , 10, 92	3	49
66	Genome-wide association study identifies three novel susceptibility loci for severe Acne vulgaris. <i>Nature Communications</i> , 2014 , 5, 4020	17.4	48
65	Pooled sequencing of 531 genes in inflammatory bowel disease identifies an associated rare variant in BTNL2 and implicates other immune related genes. <i>PLoS Genetics</i> , 2015 , 11, e1004955	6	43
64	Investigating the utility of human embryonic stem cell-derived neurons to model ageing and neurodegenerative disease using whole-genome gene expression and splicing analysis. <i>Journal of Neurochemistry</i> , 2012 , 122, 738-51	6	41
63	Initial assessment of the pathogenic mechanisms of the recently identified Alzheimer risk Loci. <i>Annals of Human Genetics</i> , 2013 , 77, 85-105	2.2	40
62	The Val158Met COMT polymorphism is a modifier of the age at onset in Parkinson's disease with a sexual dimorphism. <i>Journal of Neurology, Neurosurgery and Psychiatry</i> , 2013 , 84, 666-73	5.5	40
61	Fine-mapping, gene expression and splicing analysis of the disease associated LRRK2 locus. <i>PLoS ONE</i> , 2013 , 8, e70724	3.7	40
60	A critical evaluation of genomic control methods for genetic association studies. <i>Genetic Epidemiology</i> , 2009 , 33, 290-8	2.6	40
59	Genetic determinants of variable metabolism have little impact on the clinical use of leading antipsychotics in the CATIE study. <i>Genetics in Medicine</i> , 2008 , 10, 720-9	8.1	40

58	Conditional analysis identifies three novel major histocompatibility complex loci associated with psoriasis. <i>Human Molecular Genetics</i> , 2012 , 21, 5185-92	5.6	39
57	Resolving the polymorphism-in-probe problem is critical for correct interpretation of expression QTL studies. <i>Nucleic Acids Research</i> , 2013 , 41, e88	20.1	38
56	The potentially deleterious functional variant flavin-containing monooxygenase 2*1 is at high frequency throughout sub-Saharan Africa. <i>Pharmacogenetics and Genomics</i> , 2008 , 18, 877-86	1.9	37
55	Common genetic variants in complement genes other than CFH, CD46 and the CFHRs are not associated with aHUS. <i>Molecular Immunology</i> , 2012 , 49, 640-8	4.3	33
54	Long- and short-term outcomes in renal allografts with deceased donors: A large recipient and donor genome-wide association study. <i>American Journal of Transplantation</i> , 2018 , 18, 1370-1379	8.7	32
53	Genetic evidence for a pathogenic role for the vitamin D3 metabolizing enzyme in multiple sclerosis. <i>Multiple Sclerosis and Related Disorders</i> , 2014 , 3, 211-219	4	32
52	Increased prevalence of M694V in patients with ankylosing spondylitis: additional evidence for a link with familial mediterranean fever. <i>Arthritis and Rheumatism</i> , 2010 , 62, 3059-63		31
51	Frontotemporal dementia: insights into the biological underpinnings of disease through gene co-expression network analysis. <i>Molecular Neurodegeneration</i> , 2016 , 11, 21	19	30
50	Large-scale pathways-based association study in amyotrophic lateral sclerosis. <i>Brain</i> , 2007 , 130, 2292-301	11.2	29
49	Transcriptomic and genetic analyses reveal potential causal drivers for intractable partial epilepsy. <i>Brain</i> , 2019 , 142, 1616-1630	11.2	28
48	Alternative ion channel splicing in mesial temporal lobe epilepsy and Alzheimer's disease. <i>Genome Biology</i> , 2007 , 8, R32	18.3	28
47	The influence of density on frequency-dependent selection by wild birds feeding on artificial prey. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1998 , 265, 1031-1035	4.4	28
46	No major role of common SV2A variation for predisposition or levetiracetam response in epilepsy. <i>Epilepsy Research</i> , 2009 , 83, 44-51	3	27
45	Rare deep-rooting Y chromosome lineages in humans: lessons for phylogeography. <i>Genetics</i> , 2003 , 165, 229-34	4	25
44	A Bayesian method to incorporate hundreds of functional characteristics with association evidence to improve variant prioritization. <i>PLoS ONE</i> , 2014 , 9, e98122	3.7	24
43	Using functional annotation for the empirical determination of Bayes Factors for genome-wide association study analysis. <i>PLoS ONE</i> , 2011 , 6, e14808	3.7	24
42	Reply to 'Haplotype block structure of the cytochrome P450 CYP2C gene cluster on chromosome 10'. <i>Nature Genetics</i> , 2005 , 37, 916-916	36.3	24
41	Promoter polymorphisms and allelic imbalance in ABCB1 expression. <i>Pharmacogenetics and Genomics</i> , 2007 , 17, 951-9	1.9	22

40	Assessment of common variability and expression quantitative trait loci for genome-wide associations for progressive supranuclear palsy. <i>Neurobiology of Aging</i> , 2014 , 35, 1514.e1-12	5.6	21
39	Dystonia genes functionally converge in specific neurons and share neurobiology with psychiatric disorders. <i>Brain</i> , 2020 , 143, 2771-2787	11.2	20
38	Genes predict village of origin in rural Europe. <i>European Journal of Human Genetics</i> , 2010 , 18, 1269-70	5.3	19
37	Integrated Polygenic Tool Substantially Enhances Coronary Artery Disease Prediction. <i>Circulation Genomic and Precision Medicine</i> , 2021 , 14, e003304	5.2	19
36	Genetic enhancement of cognition in a kindred with cone-rod dystrophy due to RIMS1 mutation. <i>Journal of Medical Genetics</i> , 2007 , 44, 373-80	5.8	18
35	Anti-apostatic selection by wild birds on quasi-natural morphs of the land snail <i>Cepaea hortensis</i> : a generalised linear mixed models approach. <i>Oikos</i> , 2005 , 108, 335-343	4	17
34	Identification of Candidate Parkinson Disease Genes by Integrating Genome-Wide Association Study, Expression, and Epigenetic Data Sets. <i>JAMA Neurology</i> , 2021 , 78, 464-472	17.2	17
33	New genetic evidence supports isolation and drift in the Ladin communities of the South Tyrolean Alps but not an ancient origin in the Middle East. <i>European Journal of Human Genetics</i> , 2008 , 16, 124-34	5.3	16
32	Systematic assessment of the influence of complement gene polymorphisms on kidney transplant outcome. <i>Immunobiology</i> , 2016 , 221, 528-34	3.4	10
31	Transethnic differences in GWAS signals: A simulation study. <i>Annals of Human Genetics</i> , 2018 , 82, 280-286	6.2	10
30	The Genetic Legacy of Zoroastrianism in Iran and India: Insights into Population Structure, Gene Flow, and Selection. <i>American Journal of Human Genetics</i> , 2017 , 101, 353-368	11	10
29	Validation of an Integrated Risk Tool, Including Polygenic Risk Score, for Atherosclerotic Cardiovascular Disease in Multiple Ethnicities and Ancestries. <i>American Journal of Cardiology</i> , 2021 , 148, 157-164	3	10
28	Analysis of European case-control studies suggests that common inherited variation in mitochondrial DNA is not involved in susceptibility to amyotrophic lateral sclerosis. <i>Amyotrophic Lateral Sclerosis and Other Motor Neuron Disorders</i> , 2012 , 13, 341-6		9
27	High-throughput analysis of informative CYP2D6 compound haplotypes. <i>Genomics</i> , 2003 , 81, 166-74	4.3	9
26	Characterizing the Relation Between Expression QTLs and Complex Traits: Exploring the Role of Tissue Specificity. <i>Behavior Genetics</i> , 2018 , 48, 374-385	3.2	8
25	Gene Variants at Loci Related to Blood Pressure Account for Variation in Response to Antihypertensive Drugs Between Black and White Individuals. <i>Hypertension</i> , 2019 , 74, 614-622	8.5	8
24	Sex-Specific Genetic Data Support One of Two Alternative Versions of the Foundation of the Ruling Dynasty of the Nso' in Cameroon. <i>Current Anthropology</i> , 2008 , 49, 707-714	2.1	8
23	Network-Informed Gene Ranking Tackles Genetic Heterogeneity in Exome-Sequencing Studies of Monogenic Disease. <i>Human Mutation</i> , 2015 , 36, 1135-44	4.7	7

22	Regulatory sites for splicing in human basal ganglia are enriched for disease-relevant information. <i>Nature Communications</i> , 2020 , 11, 1041	17.4	6
21	Genome-scale methods converge on key mitochondrial genes for the survival of human cardiomyocytes in hypoxia. <i>Circulation: Cardiovascular Genetics</i> , 2014 , 7, 407-15		6
20	Smoking Gun or Circumstantial Evidence? Comparison of Statistical Learning Methods using Functional Annotations for Prioritizing Risk Variants. <i>Scientific Reports</i> , 2015 , 5, 13373	4.9	5
19	The impact of donor and recipient common clinical and genetic variation on estimated glomerular filtration rate in a European renal transplant population. <i>American Journal of Transplantation</i> , 2019 , 19, 2262-2273	8.7	4
18	Delta-centralization fails to control for population stratification in genetic association studies. <i>Human Heredity</i> , 2010 , 69, 285-94	1.1	4
17	Density- and frequency-dependent predation of artificial bird nests. <i>Biological Journal of the Linnean Society</i> , 1997 , 62, 195-208	1.9	4
16	An assessment of the Irish population for large-scale genetic mapping studies involving epilepsy and other complex diseases. <i>European Journal of Human Genetics</i> , 2008 , 16, 176-83	5.3	4
15	The genetic determinants of renal allograft rejection. <i>American Journal of Transplantation</i> , 2018 , 18, 2100-2101	8.7	3
14	Patrick Matthew's law of natural selection. <i>Biological Journal of the Linnean Society</i> , 2015 , 115, 785-791	1.9	3
13	Quality control parameters on a large dataset of regionally dissected human control brains for whole genome expression studies. <i>Journal of Neurochemistry</i> , 2012 , 120, 473-473	6	3
12	Population genetic approaches to neurological disease: Parkinson's disease as an example. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2005 , 360, 1573-8	5.8	3
11	Genetic and isotopic analysis and the UK Border Agency. <i>Significance</i> , 2010 , 7, 58-61	0.5	2
10	Inferring separate parental admixture components in unknown DNA samples using autosomal SNPs. <i>European Journal of Human Genetics</i> , 2012 , 20, 1283-9	5.3	2
9	Scientific community: Tapping into success and collaboration. <i>Nature</i> , 2013 , 498, 299	50.4	1
8	Regulatory sites for known and novel splicing in human basal ganglia are enriched for disease-relevant information		1
7	The genetic legacy of Zoroastrianism in Iran and India: Insights into population structure, gene flow and selection		1
6	Transcriptomic analysis of dystonia-associated genes reveals functional convergence within specific cell types and shared neurobiology with psychiatric disorders		1
5	Genomics implicates adaptive and innate immunity in Alzheimer's and Parkinson's		1

- 4 Assessing models for genetic prediction of complex traits: a comparison of visualization and quantitative methods. *BMC Genomics*, **2015**, 16, 405 4.5
- 3 Genomics software: The view from 10,000 feet. *Human Genomics*, **2009**, 4, 56-8 6.8
- 2 Concepts of Population Genomics **2009**, 22-32
- 1 Darwinism not tautological. *Nature*, **1991**, 351, 600-600 50.4