

Michael E Weale

List of Publications by Year in descending order

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Version: 2024-02-01

128
papers

19,056
citations

19657

61
h-index

16650

123
g-index

136
all docs

136
docs citations

136
times ranked

31484
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrated Polygenic Tool Substantially Enhances Coronary Artery Disease Prediction. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, e003304.	3.6	73
2	Identification of Candidate Parkinson Disease Genes by Integrating Genome-Wide Association Study, Expression, and Epigenetic Data Sets. <i>JAMA Neurology</i> , 2021, 78, 464.	9.0	95
3	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.	1.6	48
4	Dystonia genes functionally converge in specific neurons and share neurobiology with psychiatric disorders. <i>Brain</i> , 2020, 143, 2771-2787.	7.6	50
5	Regulatory sites for splicing in human basal ganglia are enriched for disease-relevant information. <i>Nature Communications</i> , 2020, 11, 1041.	12.8	22
6	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.	2.7	14
7	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.	4.7	13
8	Transcriptomic and genetic analyses reveal potential causal drivers for intractable partial epilepsy. <i>Brain</i> , 2019, 142, 1616-1630.	7.6	47
9	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.	4.7	47
10	The genetic determinants of renal allograft rejection. <i>American Journal of Transplantation</i> , 2018, 18, 2100-2101.	4.7	4
11	Phenome-wide association studies across large population cohorts support drug target validation. <i>Nature Communications</i> , 2018, 9, 4285.	12.8	134
12	Transethnic differences in GWAS signals: A simulation study. <i>Annals of Human Genetics</i> , 2018, 82, 280-286.	0.8	21
13	Characterizing the Relation Between Expression QTLs and Complex Traits: Exploring the Role of Tissue Specificity. <i>Behavior Genetics</i> , 2018, 48, 374-385.	2.1	12
14	Abstract O21: ARHGEF26 is a Novel Genetic Risk Factor for Vascular Inflammation and Coronary Artery Disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2018, 38, .	2.4	0
15	Novel genetic loci associated with hippocampal volume. <i>Nature Communications</i> , 2017, 8, 13624.	12.8	250
16	693. Identification, Regulation and Characterisation of Transcribed Intergenic Regions in Human Substantia Nigra and Putamen. <i>Biological Psychiatry</i> , 2017, 81, S281.	1.3	0
17	Mutations in the vesicular trafficking protein annexin A11 are associated with amyotrophic lateral sclerosis. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	129
18	Genome-wide Pleiotropy Between Parkinson Disease and Autoimmune Diseases. <i>JAMA Neurology</i> , 2017, 74, 780.	9.0	245

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19	Cost-effectiveness of pharmacogenetic-guided treatment: are we there yet?. <i>Pharmacogenomics Journal</i> , 2017, 17, 395-402.	2.0	173
20	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.	6.2	19
21	Genetic analysis in UK Biobank links insulin resistance and transendothelial migration pathways to coronary artery disease. <i>Nature Genetics</i> , 2017, 49, 1392-1397.	21.4	190
22	An additional k-means clustering step improves the biological features of WGCNA gene co-expression networks. <i>BMC Systems Biology</i> , 2017, 11, 47.	3.0	253
23	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.	3.7	84
24	Novel genetic loci underlying human intracranial volume identified through genome-wide association. <i>Nature Neuroscience</i> , 2016, 19, 1569-1582.	14.8	213
25	Genetic influences on schizophrenia and subcortical brain volumes: large-scale proof of concept. <i>Nature Neuroscience</i> , 2016, 19, 420-431.	14.8	204
26	Frontotemporal dementia: insights into the biological underpinnings of disease through gene co-expression network analysis. <i>Molecular Neurodegeneration</i> , 2016, 11, 21.	10.8	39
27	Systematic assessment of the influence of complement gene polymorphisms on kidney transplant outcome. <i>Immunobiology</i> , 2016, 221, 528-534.	1.9	10
28	Smoking Gun or Circumstantial Evidence? Comparison of Statistical Learning Methods using Functional Annotations for Prioritizing Risk Variants. <i>Scientific Reports</i> , 2015, 5, 13373.	3.3	7
29	Network-Informed Gene Ranking Tackles Genetic Heterogeneity in Exome-Sequencing Studies of Monogenic Disease. <i>Human Mutation</i> , 2015, 36, 1135-1144.	2.5	7
30	Patrick Matthew's law of natural selection. <i>Biological Journal of the Linnean Society</i> , 2015, 115, 785-791.	1.6	62
31	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.	7.2	117
32	Common genetic variants influence human subcortical brain structures. <i>Nature</i> , 2015, 520, 224-229.	27.8	772
33	Pooled Sequencing of 531 Genes in Inflammatory Bowel Disease Identifies an Associated Rare Variant in <i>BTNL2</i> and Implicates Other Immune Related Genes. <i>PLoS Genetics</i> , 2015, 11, e1004955.	3.5	59
34	Recursive splicing in long vertebrate genes. <i>Nature</i> , 2015, 521, 371-375.	27.8	128
35	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, 769-781.	10.7	346
36	Assessing models for genetic prediction of complex traits: a comparison of visualization and quantitative methods. <i>BMC Genomics</i> , 2015, 16, 405.	2.8	0

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37	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , 2015, 6, 8570.	12.8	533
38	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. <i>Molecular Psychiatry</i> , 2015, 20, 647-656.	7.9	235
39	A Bayesian Method to Incorporate Hundreds of Functional Characteristics with Association Evidence to Improve Variant Prioritization. <i>PLoS ONE</i> , 2014, 9, e98122.	2.5	29
40	Genome-Scale Methods Converge on Key Mitochondrial Genes for the Survival of Human Cardiomyocytes in Hypoxia. <i>Circulation: Cardiovascular Genetics</i> , 2014, 7, 407-415.	5.1	7
41	Rare coding variants in the phospholipase D3 gene confer risk for Alzheimer's disease. <i>Nature</i> , 2014, 505, 550-554.	27.8	425
42	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, 2220-2231.	2.9	123
43	The ENIGMA Consortium: large-scale collaborative analyses of neuroimaging and genetic data. <i>Brain Imaging and Behavior</i> , 2014, 8, 153-182.	2.1	696
44	Genetic variability in the regulation of gene expression in ten regions of the human brain. <i>Nature Neuroscience</i> , 2014, 17, 1418-1428.	14.8	620
45	Genome-wide association study identifies three novel susceptibility loci for severe Acne vulgaris. <i>Nature Communications</i> , 2014, 5, 4020.	12.8	68
46	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.e1-1514.e12.	3.1	33
47	Genetic evidence for a pathogenic role for the vitamin D3 metabolizing enzyme CYP24A1 in multiple sclerosis. <i>Multiple Sclerosis and Related Disorders</i> , 2014, 3, 211-219.	2.0	44
48	Insights into TREM2 biology by network analysis of human brain gene expression data. <i>Neurobiology of Aging</i> , 2013, 34, 2699-2714.	3.1	145
49	Genome-wide association study of obsessive-compulsive disorder. <i>Molecular Psychiatry</i> , 2013, 18, 788-798.	7.9	312
50	Tapping into success and collaboration. <i>Nature</i> , 2013, 498, 299-299.	27.8	1
51	Epilepsy, hippocampal sclerosis and febrile seizures linked by common genetic variation around SCN1A. <i>Brain</i> , 2013, 136, 3140-3150.	7.6	168
52	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, 102-108.	2.8	201
53	Genetic Signatures Reveal High-Altitude Adaptation in a Set of Ethiopian Populations. <i>Molecular Biology and Evolution</i> , 2013, 30, 1877-1888.	8.9	173
54	Widespread sex differences in gene expression and splicing in the adult human brain. <i>Nature Communications</i> , 2013, 4, 2771.	12.8	255

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55	Gene expression changes with age in skin, adipose tissue, blood and brain. <i>Genome Biology</i> , 2013, 14, R75.	9.6	263
56	Resolving the polymorphism-in-probe problem is critical for correct interpretation of expression QTL studies. <i>Nucleic Acids Research</i> , 2013, 41, e88-e88.	14.5	39
57	Initial Assessment of the Pathogenic Mechanisms of the Recently Identified Alzheimer Risk Loci. <i>Annals of Human Genetics</i> , 2013, 77, 85-105.	0.8	41
58	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, 666-673.	1.9	43
59	Fine-Mapping, Gene Expression and Splicing Analysis of the Disease Associated LRRK2 Locus. <i>PLoS ONE</i> , 2013, 8, e70724.	2.5	45
60	Inferring separate parental admixture components in unknown DNA samples using autosomal SNPs. <i>European Journal of Human Genetics</i> , 2012, 20, 1283-1289.	2.8	5
61	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, 341-346.	2.1	11
62	Conditional analysis identifies three novel major histocompatibility complex loci associated with psoriasis. <i>Human Molecular Genetics</i> , 2012, 21, 5185-5192.	2.9	58
63	Identification of common variants associated with human hippocampal and intracranial volumes. <i>Nature Genetics</i> , 2012, 44, 552-561.	21.4	594
64	MAPT expression and splicing is differentially regulated by brain region: relation to genotype and implication for tauopathies. <i>Human Molecular Genetics</i> , 2012, 21, 4094-4103.	2.9	191
65	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, 738-751.	3.9	48
66	Identification of 15 new psoriasis susceptibility loci highlights the role of innate immunity. <i>Nature Genetics</i> , 2012, 44, 1341-1348.	21.4	848
67	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.	3.9	4
68	Common genetic variants in complement genes other than CFH, CD46 and the CFHRs are not associated with aHUS. <i>Molecular Immunology</i> , 2012, 49, 640-648.	2.2	37
69	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, 20-28.	4.4	121
70	Using Functional Annotation for the Empirical Determination of Bayes Factors for Genome-Wide Association Study Analysis. <i>PLoS ONE</i> , 2011, 6, e14808.	2.5	26
71	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, 275-282.	3.9	214
72	Chromosome 9p21 in sporadic amyotrophic lateral sclerosis in the UK and seven other countries: a genome-wide association study. <i>Lancet Neurology</i> , The, 2010, 9, 986-994.	10.2	205

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73	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.	3.2	57
74	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, 3059-3063.	6.7	43
75	Genetic and isotopic analysis and the UK Border Agency. <i>Significance</i> , 2010, 7, 58-61.	0.4	2
76	Genes predict village of origin in rural Europe. <i>European Journal of Human Genetics</i> , 2010, 18, 1269-1270.	2.8	22
77	A genome-wide association study identifies new psoriasis susceptibility loci and an interaction between HLA-C and ERAP1. <i>Nature Genetics</i> , 2010, 42, 985-990.	21.4	918
78	Genome-Wide Association Study of Major Recurrent Depression in the U.K. Population. <i>American Journal of Psychiatry</i> , 2010, 167, 949-957.	7.2	221
79	Delta-Centralization Fails to Control for Population Stratification in Genetic Association Studies. <i>Human Heredity</i> , 2010, 69, 285-294.	0.8	5
80	Endless possibility. <i>New Scientist</i> , 2010, 208, 27.	0.0	0
81	Natural selection on <i>EPAS1</i> (<i>HIF2L</i>) 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, 11459-11464.	7.1	708
82	Quality Control for Genome-Wide Association Studies. <i>Methods in Molecular Biology</i> , 2010, 628, 341-372.	0.9	106
83	Concepts of Population Genomics. , 2009, , 22-32.		0
84	A Genome-Wide Investigation of SNPs and CNVs in Schizophrenia. <i>PLoS Genetics</i> , 2009, 5, e1000373.	3.5	383
85	A critical evaluation of genomic control methods for genetic association studies. <i>Genetic Epidemiology</i> , 2009, 33, 290-298.	1.3	46
86	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, 579-588.	1.8	89
87	No major role of common SV2A variation for predisposition or levetiracetam response in epilepsy. <i>Epilepsy Research</i> , 2009, 83, 44-51.	1.6	32
88	A genome-wide study of common SNPs and CNVs in cognitive performance in the CANTAB. <i>Human Molecular Genetics</i> , 2009, 18, 4650-4661.	2.9	131
89	Genomics software: The view from 10,000 feet. <i>Human Genomics</i> , 2009, 4, 56-8.	2.9	0
90	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, 667-668.	1.7	62

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91	Long-Range LD Can Confound Genome Scans in Admixed Populations. <i>American Journal of Human Genetics</i> , 2008, 83, 132-135.	6.2	366
92	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, 124-134.	2.8	17
93	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, 176-183.	2.8	5
94	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.	1.6	8
95	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, 720-729.	2.4	48
96	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, 877-886.	1.5	43
97	Large-scale pathways-based association study in amyotrophic lateral sclerosis. <i>Brain</i> , 2007, 130, 2292-2301.	7.6	32
98	Promoter polymorphisms and allelic imbalance in ABCB1 expression. <i>Pharmacogenetics and Genomics</i> , 2007, 17, 951-959.	1.5	23
99	Alternative ion channel splicing in mesial temporal lobe epilepsy and Alzheimer's disease. <i>Genome Biology</i> , 2007, 8, R32.	9.6	38
100	A Whole-Genome Association Study of Major Determinants for Host Control of HIV-1. <i>Science</i> , 2007, 317, 944-947.	12.6	1,136
101	Genetic enhancement of cognition in a kindred with cone-rod dystrophy due to RIMS1 mutation. <i>Journal of Medical Genetics</i> , 2007, 44, 373-380.	3.2	29
102	Genetic intra-tumour heterogeneity in epithelial ovarian cancer and its implications for molecular diagnosis of tumours. <i>Journal of Pathology</i> , 2007, 211, 286-295.	4.5	108
103	Multicentre search for genetic susceptibility loci in sporadic epilepsy syndrome and seizure types: a case-control study. <i>Lancet Neurology</i> , The, 2007, 6, 970-980.	10.2	175
104	A novel polymorphism associated with lactose tolerance in Africa: multiple causes for lactase persistence?. <i>Human Genetics</i> , 2007, 120, 779-788.	3.8	247
105	Reply to 'Haplotype block structure of the cytochrome P450 CYP2C gene cluster on chromosome 10'. <i>Nature Genetics</i> , 2005, 37, 916-916.	21.4	25
106	A single-nucleotide polymorphism tagging set for human drug metabolism and transport. <i>Nature Genetics</i> , 2005, 37, 84-89.	21.4	142
107	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.	2.7	19
108	Positive Selection on a High-Sensitivity Allele of the Human Bitter-Taste Receptor TAS2R16. <i>Current Biology</i> , 2005, 15, 1257-1265.	3.9	224

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109	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, 1573-1578.	4.0	4
110	Evolution of a Length Polymorphism in the Human PER3 Gene, a Component of the Circadian System. <i>Journal of Biological Rhythms</i> , 2005, 20, 490-499.	2.6	64
111	Identifying Candidate Causal Variants Responsible for Altered Activity of the ABCB1 Multidrug Resistance Gene. <i>Genome Research</i> , 2004, 14, 1333-1344.	5.5	107
112	The T Allele of a Single-Nucleotide Polymorphism 13.9 kb Upstream of the Lactase Gene (LCT) (Câ [~] 13.9kbT) Does Not Predict or Cause the Lactase-Persistence Phenotype in Africans. <i>American Journal of Human Genetics</i> , 2004, 74, 1102-1110.	6.2	196
113	Genome scans and candidate gene approaches in the study of common diseases and variable drug responses. <i>Trends in Genetics</i> , 2003, 19, 615-622.	6.7	151
114	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.	1.1	232
115	Association of Multidrug Resistance in Epilepsy with a Polymorphism in the Drug-Transporter Gene <i><i>ABCB1</i></i> . <i>New England Journal of Medicine</i> , 2003, 348, 1442-1448.	27.0	690
116	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, 551-565.	6.2	181
117	Multiple Origins of Ashkenazi Levites: Y Chromosome Evidence for Both Near Eastern and European Ancestries. <i>American Journal of Human Genetics</i> , 2003, 73, 768-779.	6.2	90
118	High-throughput analysis of informative CYP2D6 compound haplotypes. <i>Genomics</i> , 2003, 81, 166-174.	2.9	9
119	Rare Deep-Rooting Y Chromosome Lineages in Humans: Lessons for Phylogeography. <i>Genetics</i> , 2003, 165, 229-234.	2.9	29
120	Y Chromosome Evidence for Anglo-Saxon Mass Migration. <i>Molecular Biology and Evolution</i> , 2002, 19, 1008-1021.	8.9	148
121	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, 1411-1420.	6.2	126
122	Armenian Y chromosome haplotypes reveal strong regional structure within a single ethno-national group. <i>Human Genetics</i> , 2001, 109, 659-674.	3.8	58
123	Population genetic structure of variable drug response. <i>Nature Genetics</i> , 2001, 29, 265-269.	21.4	425
124	Population genomics: Linkage disequilibrium holds the key. <i>Current Biology</i> , 2001, 11, R576-R579.	3.9	119
125	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, 630-641.	3.8	69
126	The influence of density on frequencyâ€“dependent selection by wild birds feeding on artificial prey. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1998, 265, 1031-1035.	2.6	35

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127	Density- and frequency-dependent predation of artificial bird nests. <i>Biological Journal of the Linnean Society</i> , 1997, 62, 195-208.	1.6	8
128	Darwinism not tautological. <i>Nature</i> , 1991, 351, 600-600.	27.8	1