

Michael E Weale

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/9380379/michael-e-weale-publications-by-year.pdf>

Version: 2024-04-10

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	Integrated Polygenic Tool Substantially Enhances Coronary Artery Disease Prediction. <i>Circulation Genomic and Precision Medicine</i> , 2021 , 14, e003304	5.2	19
128	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
127	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
126	Regulatory sites for splicing in human basal ganglia are enriched for disease-relevant information. <i>Nature Communications</i> , 2020 , 11, 1041	17.4	6
125	Dystonia genes functionally converge in specific neurons and share neurobiology with psychiatric disorders. <i>Brain</i> , 2020 , 143, 2771-2787	11.2	20
124	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
123	Transcriptomic and genetic analyses reveal potential causal drivers for intractable partial epilepsy. <i>Brain</i> , 2019 , 142, 1616-1630	11.2	28
122	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
121	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
120	The genetic determinants of renal allograft rejection. <i>American Journal of Transplantation</i> , 2018 , 18, 2100-2101	8.7	3
119	Transethnic differences in GWAS signals: A simulation study. <i>Annals of Human Genetics</i> , 2018 , 82, 280-286.2	10	
118	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
117	Phenome-wide association studies across large population cohorts support drug target validation. <i>Nature Communications</i> , 2018 , 9, 4285	17.4	76
116	Novel genetic loci associated with hippocampal volume. <i>Nature Communications</i> , 2017 , 8, 13624	17.4	173
115	Mutations in the vesicular trafficking protein annexin A11 are associated with amyotrophic lateral sclerosis. <i>Science Translational Medicine</i> , 2017 , 9,	17.5	74
114	Genome-wide Pleiotropy Between Parkinson Disease and Autoimmune Diseases. <i>JAMA Neurology</i> , 2017 , 74, 780-792	17.2	150
113	Cost-effectiveness of pharmacogenetic-guided treatment: are we there yet?. <i>Pharmacogenomics Journal</i> , 2017 , 17, 395-402	3.5	118

112	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
111	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
110	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
109	Genetic influences on schizophrenia and subcortical brain volumes: large-scale proof of concept. <i>Nature Neuroscience</i> , 2016 , 19, 420-431	25.5	163
108	Frontotemporal dementia: insights into the biological underpinnings of disease through gene co-expression network analysis. <i>Molecular Neurodegeneration</i> , 2016 , 11, 21	19	30
107	Systematic assessment of the influence of complement gene polymorphisms on kidney transplant outcome. <i>Immunobiology</i> , 2016 , 221, 528-34	3.4	10
106	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
105	Novel genetic loci underlying human intracranial volume identified through genome-wide association. <i>Nature Neuroscience</i> , 2016 , 19, 1569-1582	25.5	147
104	Common genetic variants influence human subcortical brain structures. <i>Nature</i> , 2015 , 520, 224-9	50.4	601
103	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
102	Recursive splicing in long vertebrate genes. <i>Nature</i> , 2015 , 521, 371-375	50.4	88
101	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
100	Assessing models for genetic prediction of complex traits: a comparison of visualization and quantitative methods. <i>BMC Genomics</i> , 2015 , 16, 405	4.5	
99	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , 2015 , 6, 8570	17.4	335
98	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. <i>Molecular Psychiatry</i> , 2015 , 20, 647-656	15.1	167
97	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
96	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
95	Patrick Matthew's law of natural selection. <i>Biological Journal of the Linnean Society</i> , 2015 , 115, 785-791	1.9	3

94	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
93	Rare coding variants in the phospholipase D3 gene confer risk for Alzheimer's disease. <i>Nature</i> , 2014 , 505, 550-554	50.4	345
92	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
91	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
90	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
89	Genome-wide association study identifies three novel susceptibility loci for severe Acne vulgaris. <i>Nature Communications</i> , 2014 , 5, 4020	17.4	48
88	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
87	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
86	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
85	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
84	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
83	Genome-wide association study of obsessive-compulsive disorder. <i>Molecular Psychiatry</i> , 2013 , 18, 788-98	15.1	244
82	Scientific community: Tapping into success and collaboration. <i>Nature</i> , 2013 , 498, 299	50.4	1
81	Epilepsy, hippocampal sclerosis and febrile seizures linked by common genetic variation around SCN1A. <i>Brain</i> , 2013 , 136, 3140-50	11.2	144
80	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
79	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
78	Widespread sex differences in gene expression and splicing in the adult human brain. <i>Nature Communications</i> , 2013 , 4, 2771	17.4	166
77	Gene expression changes with age in skin, adipose tissue, blood and brain. <i>Genome Biology</i> , 2013 , 14, R75	18.3	185

76	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
75	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
74	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
73	Fine-mapping, gene expression and splicing analysis of the disease associated LRRK2 locus. <i>PLoS ONE</i> , 2013 , 8, e70724	3.7	40
72	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
71	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
70	Identification of common variants associated with human hippocampal and intracranial volumes. <i>Nature Genetics</i> , 2012 , 44, 552-61	36.3	498
69	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
68	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
67	Identification of 15 new psoriasis susceptibility loci highlights the role of innate immunity. <i>Nature Genetics</i> , 2012 , 44, 1341-8	36.3	681
66	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
65	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
64	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
63	Conditional analysis identifies three novel major histocompatibility complex loci associated with psoriasis. <i>Human Molecular Genetics</i> , 2012 , 21, 5185-92	5.6	39
62	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
61	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
60	Genetic and isotopic analysis and the UK Border Agency. <i>Significance</i> , 2010 , 7, 58-61	0.5	2
59	Genes predict village of origin in rural Europe. <i>European Journal of Human Genetics</i> , 2010 , 18, 1269-70	5.3	19

58	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
57	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
56	Delta-centralization fails to control for population stratification in genetic association studies. <i>Human Heredity</i> , 2010 , 69, 285-94	1.1	4
55	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
54	Quality control for genome-wide association studies. <i>Methods in Molecular Biology</i> , 2010 , 628, 341-72	1.4	83
53	Chromosome 9p21 in sporadic amyotrophic lateral sclerosis in the UK and seven other countries: a genome-wide association study. <i>Lancet Neurology</i> , 2010 , 9, 986-94	24.1	171
52	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
51	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
50	A genome-wide investigation of SNPs and CNVs in schizophrenia. <i>PLoS Genetics</i> , 2009 , 5, e1000373	6	357
49	A critical evaluation of genomic control methods for genetic association studies. <i>Genetic Epidemiology</i> , 2009 , 33, 290-8	2.6	40
48	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
47	No major role of common SV2A variation for predisposition or levetiracetam response in epilepsy. <i>Epilepsy Research</i> , 2009 , 83, 44-51	3	27
46	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
45	Genomics software: The view from 10,000 feet. <i>Human Genomics</i> , 2009 , 4, 56-8	6.8	
44	Concepts of Population Genomics 2009 , 22-32		
43	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
42	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
41	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

40	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
39	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
38	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
37	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
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	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
34	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
33	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
32	Large-scale pathways-based association study in amyotrophic lateral sclerosis. <i>Brain</i> , 2007 , 130, 2292-301	11.2	29
31	Promoter polymorphisms and allelic imbalance in ABCB1 expression. <i>Pharmacogenetics and Genomics</i> , 2007 , 17, 951-9	1.9	22
30	Alternative ion channel splicing in mesial temporal lobe epilepsy and Alzheimer's disease. <i>Genome Biology</i> , 2007 , 8, R32	18.3	28
29	A whole-genome association study of major determinants for host control of HIV-1. <i>Science</i> , 2007 , 317, 944-7	33.3	999
28	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
27	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
26	A single-nucleotide polymorphism tagging set for human drug metabolism and transport. <i>Nature Genetics</i> , 2005 , 37, 84-9	36.3	134
25	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
24	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
23	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

22	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
21	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
20	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
19	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
18	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
17	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
16	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
15	High-throughput analysis of informative CYP2D6 compound haplotypes. <i>Genomics</i> , 2003 , 81, 166-74	4.3	9
14	Rare deep-rooting Y chromosome lineages in humans: lessons for phylogeography. <i>Genetics</i> , 2003 , 165, 229-34	4	25
13	Y chromosome evidence for Anglo-Saxon mass migration. <i>Molecular Biology and Evolution</i> , 2002 , 19, 1008-21	3.1	119
12	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
11	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
10	Population genetic structure of variable drug response. <i>Nature Genetics</i> , 2001 , 29, 265-9	36.3	344
9	Population genomics: linkage disequilibrium holds the key. <i>Current Biology</i> , 2001 , 11, R576-9	6.3	98
8	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
7	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
6	Density- and frequency-dependent predation of artificial bird nests. <i>Biological Journal of the Linnean Society</i> , 1997 , 62, 195-208	1.9	4
5	Darwinism not tautological. <i>Nature</i> , 1991 , 351, 600-600	50.4	

4	Regulatory sites for known and novel splicing in human basal ganglia are enriched for disease-relevant information	1
3	The genetic legacy of Zoroastrianism in Iran and India: Insights into population structure, gene flow and selection	1
2	Transcriptomic analysis of dystonia-associated genes reveals functional convergence within specific cell types and shared neurobiology with psychiatric disorders	1
1	Genomics implicates adaptive and innate immunity in Alzheimer’s and Parkinson’s	1