# Michael E Weale

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/9380379/publications.pdf

Version: 2024-02-01

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|---|---|---|---|
| 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 | A Whole-Genome Association Study of Major Determinants for Host Control of HIV-1. Science, 2007, 317, 944-947. | 12.6 | 1,136 |
| 2 | A genome-wide association study identifies new psoriasis susceptibility loci and an interaction between HLA-C and ERAP1. Nature Genetics, 2010, 42, 985-990. | 21.4 | 918 |
| 3 | Identification of 15 new psoriasis susceptibility loci highlights the role of innate immunity. Nature Genetics, 2012, 44, 1341-1348. | 21.4 | 848 |
| 4 | Common genetic variants influence human subcortical brain structures. Nature, 2015, 520, 224-229. | 27.8 | 772 |
| 5 | Natural selection on EPAS1 ( HIF2Î± ) associated with low hemoglobin concentration in Tibetan highlanders. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 11459-11464. | 7.1 | 708 |
| 6 | The ENIGMA Consortium: large-scale collaborative analyses of neuroimaging and genetic data. Brain Imaging and Behavior, 2014, 8, 153-182. | 2.1 | 696 |
| 7 | Association of Multidrug Resistance in Epilepsy with a Polymorphism in the Drug-Transporter GeneABCB1. New England Journal of Medicine, 2003, 348, 1442-1448. | 27.0 | 690 |
| 8 | Genetic variability in the regulation of gene expression in ten regions of the human brain. Nature Neuroscience, 2014, 17, 1418-1428. | 14.8 | 620 |
| 9 | Identification of common variants associated with human hippocampal and intracranial volumes. Nature Genetics, 2012, 44, 552-561. | 21.4 | 594 |
| 10 | The transcriptional landscape of age in human peripheral blood. Nature Communications, 2015, 6, 8570. | 12.8 | 533 |
| 11 | Population genetic structure of variable drug response. Nature Genetics, 2001, 29, 265-269. | 21.4 | 425 |
| 12 | Rare coding variants in the phospholipase D3 gene confer risk for Alzheimerâ€™s disease. Nature, 2014, 505, 550-554. | 27.8 | 425 |
| 13 | A Genome-Wide Investigation of SNPs and CNVs in Schizophrenia. PLoS Genetics, 2009, 5, e1000373. | 3.5 | 383 |
| 14 | Long-Range LD Can Confound Genome Scans in Admixed Populations. American Journal of Human Genetics, 2008, 83, 132-135. | 6.2 | 366 |
| 15 | Novel insights into the genetics of smoking behaviour, lung function, and chronic obstructive pulmonary disease (UK BiLEVE): a genetic association study in UK Biobank. Lancet Respiratory Medicine,the, 2015, 3, 769-781. | 10.7 | 346 |
| 16 | Genome-wide association study of obsessive-compulsive disorder. Molecular Psychiatry, 2013, 18, 788-798. | 7.9 | 312 |
| 17 | Gene expression changes with age in skin, adipose tissue, blood and brain. Genome Biology, 2013, 14, R75. | 9.6 | 263 |
| 18 | Widespread sex differences in gene expression and splicing in the adult human brain. Nature Communications, 2013, 4, 2771. | 12.8 | 255 |

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|---|---|---|---|
| 19 | An additional k-means clustering step improves the biological features of WGCNA gene co-expression networks. BMC Systems Biology, 2017, 11, 47. | 3.0 | 253 |
| 20 | Novel genetic loci associated with hippocampal volume. Nature Communications, 2017, 8, 13624. | 12.8 | 250 |
| 21 | A novel polymorphism associated with lactose tolerance in Africa: multiple causes for lactase persistence?. Human Genetics, 2007, 120, 779-788. | 3.8 | 247 |
| 22 | Genome-wide Pleiotropy Between Parkinson Disease and Autoimmune Diseases. JAMA Neurology, 2017, 74, 780. | 9.0 | 245 |
| 23 | Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. Molecular Psychiatry, 2015, 20, 647-656. | 7.9 | 235 |
| 24 | Inferences from DNA data: population histories, evolutionary processes and forensic match probabilities. Journal of the Royal Statistical Society Series A: Statistics in Society, 2003, 166, 155-188. | 1.1 | 232 |
| 25 | Positive Selection on a High-Sensitivity Allele of the Human Bitter-Taste Receptor TAS2R16. Current Biology, 2005, 15, 1257-1265. | 3.9 | 224 |
| 26 | Genome-Wide Association Study of Major Recurrent Depression in the U.K. Population. American Journal of Psychiatry, 2010, 167, 949-957. | 7.2 | 221 |
| 27 | Quality control parameters on a large dataset of regionally dissected human control brains for whole genome expression studies. Journal of Neurochemistry, 2011, 119, 275-282. | 3.9 | 214 |
| 28 | Novel genetic loci underlying human intracranial volume identified through genome-wide association. Nature Neuroscience, 2016, 19, 1569-1582. | 14.8 | 213 |
| 29 | Chromosome 9p21 in sporadic amyotrophic lateral sclerosis in the UK and seven other countries: a genome-wide association study. Lancet Neurology, The, 2010, 9, 986-994. | 10.2 | 205 |
| 30 | Genetic influences on schizophrenia and subcortical brain volumes: large-scale proof of concept. Nature Neuroscience, 2016, 19, 420-431. | 14.8 | 204 |
| 31 | The C9ORF72 expansion mutation is a common cause of ALS+/â˜FTD in Europe and has a single founder. European Journal of Human Genetics, 2013, 21, 102-108. | 2.8 | 201 |
| 32 | 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. American Journal of Human Genetics, 2004, 74, 1102-1110. | 6.2 | 196 |
| 33 | MAPT expression and splicing is differentially regulated by brain region: relation to genotype and implication for tauopathies. Human Molecular Genetics, 2012, 21, 4094-4103. | 2.9 | 191 |
| 34 | Genetic analysis in UK Biobank links insulin resistance and transendothelial migration pathways to coronary artery disease. Nature Genetics, 2017, 49, 1392-1397. | 21.4 | 190 |
| 35 | Selection and Evaluation of Tagging SNPs in the Neuronal-Sodium-Channel Gene SCN1A: Implications for Linkage-Disequilibrium Gene Mapping. American Journal of Human Genetics, 2003, 73, 551-565. | 6.2 | 181 |
| 36 | Multicentre search for genetic susceptibility loci in sporadic epilepsy syndrome and seizure types: a case-control study. Lancet Neurology, The, 2007, 6, 970-980. | 10.2 | 175 |

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|---|---|---|---|
| 37 | Genetic Signatures Reveal High-Altitude Adaptation in a Set of Ethiopian Populations. Molecular Biology and Evolution, 2013, 30, 1877-1888. | 8.9 | 173 |
| 38 | Cost-effectiveness of pharmacogenetic-guided treatment: are we there yet?. Pharmacogenomics Journal, 2017, 17, 395-402. | 2.0 | 173 |
| 39 | Epilepsy, hippocampal sclerosis and febrile seizures linked by common genetic variation around SCN1A. Brain, 2013, 136, 3140-3150. | 7.6 | 168 |
| 40 | Genome scans and candidate gene approaches in the study of common diseases and variable drug responses. Trends in Genetics, 2003, 19, 615-622. | 6.7 | 151 |
| 41 | Y Chromosome Evidence for Anglo-Saxon Mass Migration. Molecular Biology and Evolution, 2002, 19, 1008-1021. | 8.9 | 148 |
| 42 | Insights into TREM2 biology by network analysis of human brain gene expression data. Neurobiology of Aging, 2013, 34, 2699-2714. | 3.1 | 145 |
| 43 | A single-nucleotide polymorphism tagging set for human drug metabolism and transport. Nature Genetics, 2005, 37, 84-89. | 21.4 | 142 |
| 44 | Phenome-wide association studies across large population cohorts support drug target validation. Nature Communications, 2018, 9, 4285. | 12.8 | 134 |
| 45 | A genome-wide study of common SNPs and CNVs in cognitive performance in the CANTAB. Human Molecular Genetics, 2009, 18, 4650-4661. | 2.9 | 131 |
| 46 | Mutations in the vesicular trafficking protein annexin A11 are associated with amyotrophic lateral sclerosis. Science Translational Medicine, 2017, 9, . | 12.4 | 129 |
| 47 | Recursive splicing in long vertebrate genes. Nature, 2015, 521, 371-375. | 27.8 | 128 |
| 48 | Founding Mothers of Jewish Communities: Geographically Separated Jewish Groups Were Independently Founded by Very Few Female Ancestors. American Journal of Human Genetics, 2002, 70, 1411-1420. | 6.2 | 126 |
| 49 | A genome-wide association meta-analysis identifies a novel locus at 17q11.2 associated with sporadic amyotrophic lateral sclerosis. Human Molecular Genetics, 2014, 23, 2220-2231. | 2.9 | 123 |
| 50 | Integration of GWAS SNPs and tissue specific expression profiling reveal discrete eQTLs for human traits in blood and brain. Neurobiology of Disease, 2012, 47, 20-28. | 4.4 | 121 |
| 51 | Population genomics: Linkage disequilibrium holds the key. Current Biology, 2001, 11, R576-R579. | 3.9 | 119 |
| 52 | Cross-Disorder Genome-Wide Analyses Suggest a Complex Genetic Relationship Between Tourette's Syndrome and OCD. American Journal of Psychiatry, 2015, 172, 82-93. | 7.2 | 117 |
| 53 | Genetic intra-tumour heterogeneity in epithelial ovarian cancer and its implications for molecular diagnosis of tumours. Journal of Pathology, 2007, 211, 286-295. | 4.5 | 108 |
| 54 | Identifying Candidate Causal Variants Responsible for Altered Activity of the ABCB1 Multidrug Resistance Gene. Genome Research, 2004, 14, 1333-1344. | 5.5 | 107 |

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|---|---|---|---|
| 55 | Quality Control for Genome-Wide Association Studies. Methods in Molecular Biology, 2010, 628, 341-372. | 0.9 | 106 |
| 56 | Identification of Candidate Parkinson Disease Genes by Integrating Genome-Wide Association Study, Expression, and Epigenetic Data Sets. JAMA Neurology, 2021, 78, 464. | 9.0 | 95 |
| 57 | Multiple Origins of Ashkenazi Levites: Y Chromosome Evidence for Both Near Eastern and European Ancestries. American Journal of Human Genetics, 2003, 73, 768-779. | 6.2 | 90 |
| 58 | Multiple Rare Variants as a Cause of a Common Phenotype: Several Different Lactase Persistence Associated Alleles in a Single Ethnic Group. Journal of Molecular Evolution, 2009, 69, 579-588. | 1.8 | 89 |
| 59 | Genomics implicates adaptive and innate immunity in Alzheimer's and Parkinson's diseases. Annals of Clinical and Translational Neurology, 2016, 3, 924-933. | 3.7 | 84 |
| 60 | Integrated Polygenic Tool Substantially Enhances Coronary Artery Disease Prediction. Circulation Genomic and Precision Medicine, 2021, 14, e003304. | 3.6 | 73 |
| 61 | High-resolution Y chromosome haplotypes of Israeli and Palestinian Arabs reveal geographic substructure and substantial overlap with haplotypes of Jews. Human Genetics, 2000, 107, 630-641. | 3.8 | 69 |
| 62 | Genome-wide association study identifies three novel susceptibility loci for severe Acne vulgaris. Nature Communications, 2014, 5, 4020. | 12.8 | 68 |
| 63 | Evolution of a Length Polymorphism in the Human PER3 Gene, a Component of the Circadian System. Journal of Biological Rhythms, 2005, 20, 490-499. | 2.6 | 64 |
| 64 | Failure to replicate effect of kibra on human memory in two large cohorts of European origin. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2008, 147B, 667-668. | 1.7 | 62 |
| 65 | Patrick Matthew's law of natural selection. Biological Journal of the Linnean Society, 2015, 115, 785-791. | 1.6 | 62 |
| 66 | Pooled Sequencing of 531 Genes in Inflammatory Bowel Disease Identifies an Associated Rare Variant in BTNL2 and Implicates Other Immune Related Genes. PLoS Genetics, 2015, 11, e1004955. | 3.5 | 59 |
| 67 | Armenian Y chromosome haplotypes reveal strong regional structure within a single ethno-national group. Human Genetics, 2001, 109, 659-674. | 3.8 | 58 |
| 68 | Conditional analysis identifies three novel major histocompatibility complex loci associated with psoriasis. Human Molecular Genetics, 2012, 21, 5185-5192. | 2.9 | 58 |
| 69 | Little genetic differentiation as assessed by uniparental markers in the presence of substantial language variation in peoples of the Cross River region of Nigeria. BMC Evolutionary Biology, 2010, 10, 92. | 3.2 | 57 |
| 70 | Dystonia genes functionally converge in specific neurons and share neurobiology with psychiatric disorders. Brain, 2020, 143, 2771-2787. | 7.6 | 50 |
| 71 | Genetic determinants of variable metabolism have little impact on the clinical use of leading antipsychotics in the CATIE study. Genetics in Medicine, 2008, 10, 720-729. | 2.4 | 48 |
| 72 | Investigating the utility of human embryonic stem cellâ€derived neurons to model ageing and neurodegenerative disease using wholeâ€genome gene expression and splicing analysis. Journal of Neurochemistry, 2012, 122, 738-751. | 3.9 | 48 |

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| 73 | Validation of an Integrated Risk Tool, Including Polygenic Risk Score, for Atherosclerotic Cardiovascular Disease in Multiple Ethnicities and Ancestries. American Journal of Cardiology, 2021, 148, 157-164. | 1.6 | 48 |
| 74 | Long- and short-term outcomes in renal allografts with deceased donors: A large recipient and donor genome-wide association study. American Journal of Transplantation, 2018, 18, 1370-1379. | 4.7 | 47 |
| 75 | Transcriptomic and genetic analyses reveal potential causal drivers for intractable partial epilepsy. Brain, 2019, 142, 1616-1630. | 7.6 | 47 |
| 76 | A critical evaluation of genomic control methods for genetic association studies. Genetic Epidemiology, 2009, 33, 290-298. | 1.3 | 46 |
| 77 | Fine-Mapping, Gene Expression and Splicing Analysis of the Disease Associated LRRK2 Locus. PLoS ONE, 2013, 8, e70724. | 2.5 | 45 |
| 78 | Genetic evidence for a pathogenic role for the vitamin D3 metabolizing enzyme CYP24A1 in multiple sclerosis. Multiple Sclerosis and Related Disorders, 2014, 3, 211-219. | 2.0 | 44 |
| 79 | The potentially deleterious functional variant flavin-containing monooxygenase 2*1 is at high frequency throughout sub-Saharan Africa. Pharmacogenetics and Genomics, 2008, 18, 877-886. | 1.5 | 43 |
| 80 | Increased prevalence of M694V in patients with ankylosing spondylitis: Additional evidence for a link with familial mediterranean fever. Arthritis and Rheumatism, 2010, 62, 3059-3063. | 6.7 | 43 |
| 81 | The Val158Met COMT polymorphism is a modifier of the age at onset in Parkinson's disease with a sexual dimorphism. Journal of Neurology, Neurosurgery and Psychiatry, 2013, 84, 666-673. | 1.9 | 43 |
| 82 | Initial Assessment of the Pathogenic Mechanisms of the Recently Identified Alzheimer Risk Loci. Annals of Human Genetics, 2013, 77, 85-105. | 0.8 | 41 |
| 83 | Resolving the polymorphism-in-probe problem is critical for correct interpretation of expression QTL studies. Nucleic Acids Research, 2013, 41, e88-e88. | 14.5 | 39 |
| 84 | Frontotemporal dementia: insights into the biological underpinnings of disease through gene co-expression network analysis. Molecular Neurodegeneration, 2016, 11, 21. | 10.8 | 39 |
| 85 | Alternative ion channel splicing in mesial temporal lobe epilepsy and Alzheimer's disease. Genome Biology, 2007, 8, R32. | 9.6 | 38 |
| 86 | Common genetic variants in complement genes other than CFH, CD46 and the CFHRs are not associated with aHUS. Molecular Immunology, 2012, 49, 640-648. | 2.2 | 37 |
| 87 | The influence of density on frequencyâ€“dependent selection by wild birds feeding on artificial prey. Proceedings of the Royal Society B: Biological Sciences, 1998, 265, 1031-1035. | 2.6 | 35 |
| 88 | Assessment of common variability and expression quantitative trait loci for genome-wide associations for progressive supranuclear palsy. Neurobiology of Aging, 2014, 35, 1514.e1-1514.e12. | 3.1 | 33 |
| 89 | Large-scale pathways-based association study in amyotrophic lateral sclerosis. Brain, 2007, 130, 2292-2301. | 7.6 | 32 |
| 90 | No major role of common SV2A variation for predisposition or levetiracetam response in epilepsy. Epilepsy Research, 2009, 83, 44-51. | 1.6 | 32 |

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|---|---|---|---|
| 91 | Genetic enhancement of cognition in a kindred with cone-rod dystrophy due to RIMS1 mutation. Journal of Medical Genetics, 2007, 44, 373-380. | 3.2 | 29 |
| 92 | A Bayesian Method to Incorporate Hundreds of Functional Characteristics with Association Evidence to Improve Variant Prioritization. PLoS ONE, 2014, 9, e98122. | 2.5 | 29 |
| 93 | Rare Deep-Rooting Y Chromosome Lineages in Humans: Lessons for Phylogeography. Genetics, 2003, 165, 229-234. | 2.9 | 29 |
| 94 | Using Functional Annotation for the Empirical Determination of Bayes Factors for Genome-Wide Association Study Analysis. PLoS ONE, 2011, 6, e14808. | 2.5 | 26 |
| 95 | Reply to 'Haplotype block structure of the cytochrome P450 CYP2C gene cluster on chromosome 10'. Nature Genetics, 2005, 37, 916-916. | 21.4 | 25 |
| 96 | Promoter polymorphisms and allelic imbalance in ABCB1 expression. Pharmacogenetics and Genomics, 2007, 17, 951-959. | 1.5 | 23 |
| 97 | Genes predict village of origin in rural Europe. European Journal of Human Genetics, 2010, 18, 1269-1270. | 2.8 | 22 |
| 98 | Regulatory sites for splicing in human basal ganglia are enriched for disease-relevant information. Nature Communications, 2020, 11, 1041. | 12.8 | 22 |
| 99 | Transethnic differences in GWAS signals: A simulation study. Annals of Human Genetics, 2018, 82, 280-286. | 0.8 | 21 |
| 100 | Anti-apostatic selection by wild birds on quasi-natural morphs of the land snailCepaea hortensis: a generalised linear mixed models approach. Oikos, 2005, 108, 335-343. | 2.7 | 19 |
| 101 | The Genetic Legacy of Zoroastrianism in Iran and India: Insights into Population Structure, Gene Flow, and Selection. American Journal of Human Genetics, 2017, 101, 353-368. | 6.2 | 19 |
| 102 | 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. European Journal of Human Genetics, 2008, 16, 124-134. | 2.8 | 17 |
| 103 | Gene Variants at Loci Related to Blood Pressure Account for Variation in Response to Antihypertensive Drugs Between Black and White Individuals. Hypertension, 2019, 74, 614-622. | 2.7 | 14 |
| 104 | The impact of donor and recipient common clinical and genetic variation on estimated glomerular filtration rate in a European renal transplant population. American Journal of Transplantation, 2019, 19, 2262-2273. | 4.7 | 13 |
| 105 | Characterizing the Relation Between Expression QTLs and Complex Traits: Exploring the Role of Tissue Specificity. Behavior Genetics, 2018, 48, 374-385. | 2.1 | 12 |
| 106 | Analysis of European case-control studies suggests that common inherited variation in mitochondrial DNA is not involved in susceptibility to amyotrophic lateral sclerosis. Amyotrophic Lateral Sclerosis and Other Motor Neuron Disorders, 2012, 13, 341-346. | 2.1 | 11 |
| 107 | Systematic assessment of the influence of complement gene polymorphisms on kidney transplant outcome. Immunobiology, 2016, 221, 528-534. | 1.9 | 10 |
| 108 | High-throughput analysis of informative CYP2D6 compound haplotypes. Genomics, 2003, 81, 166-174. | 2.9 | 9 |

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| 109 | Density- and frequency-dependent predation of artificial bird nests. Biological Journal of the Linnean Society, 1997, 62, 195-208. | 1.6 | 8 |
| 110 | Sexâ€Specific Genetic Data Support One of Two Alternative Versions of the Foundation of the Ruling Dynasty of the Nsoâ€² in Cameroon. Current Anthropology, 2008, 49, 707-714. | 1.6 | 8 |
| 111 | Genome-Scale Methods Converge on Key Mitochondrial Genes for the Survival of Human Cardiomyocytes in Hypoxia. Circulation: Cardiovascular Genetics, 2014, 7, 407-415. | 5.1 | 7 |
| 112 | Smoking Gun or Circumstantial Evidence? Comparison of Statistical Learning Methods using Functional Annotations for Prioritizing Risk Variants. Scientific Reports, 2015, 5, 13373. | 3.3 | 7 |
| 113 | Network-Informed Gene Ranking Tackles Genetic Heterogeneity in Exome-Sequencing Studies of Monogenic Disease. Human Mutation, 2015, 36, 1135-1144. | 2.5 | 7 |
| 114 | An assessment of the Irish population for large-scale genetic mapping studies involving epilepsy and other complex diseases. European Journal of Human Genetics, 2008, 16, 176-183. | 2.8 | 5 |
| 115 | Delta-Centralization Fails to Control for Population Stratification in Genetic Association Studies. Human Heredity, 2010, 69, 285-294. | 0.8 | 5 |
| 116 | Inferring separate parental admixture components in unknown DNA samples using autosomal SNPs. European Journal of Human Genetics, 2012, 20, 1283-1289. | 2.8 | 5 |
| 117 | Population genetic approaches to neurological disease: Parkinson's disease as an example. Philosophical Transactions of the Royal Society B: Biological Sciences, 2005, 360, 1573-1578. | 4.0 | 4 |
| 118 | Quality control parameters on a large dataset of regionally dissected human control brains for whole genome expression studies. Journal of Neurochemistry, 2012, 120, 473-473. | 3.9 | 4 |
| 119 | The genetic determinants of renal allograft rejection. American Journal of Transplantation, 2018, 18, 2100-2101. | 4.7 | 4 |
| 120 | Genetic and isotopic analysis and the UK Border Agency. Significance, 2010, 7, 58-61. | 0.4 | 2 |
| 121 | Darwinism not tautological. Nature, 1991, 351, 600-600. | 27.8 | 1 |
| 122 | Tapping into success and collaboration. Nature, 2013, 498, 299-299. | 27.8 | 1 |
| 123 | Concepts of Population Genomics. , 2009, , 22-32. | | 0 |
| 124 | Genomics software: The view from 10,000 feet. Human Genomics, 2009, 4, 56-8. | 2.9 | 0 |
| 125 | Endless possibility. New Scientist, 2010, 208, 27. | 0.0 | 0 |
| 126 | Assessing models for genetic prediction of complex traits: a comparison of visualization and quantitative methods. BMC Genomics, 2015, 16, 405. | 2.8 | 0 |

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|---|---|---|---|
| 127 | 693. Identification, Regulation and Characterisation of Transcribed Intergenic Regions in Human Substantia Nigra and Putamen. Biological Psychiatry, 2017, 81, S281. | 1.3 | 0 |
| 128 | Abstract 021: ARHGEF26 is a Novel Genetic Risk Factor for Vascular Inflammation and Coronary Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2018, 38, . | 2.4 | 0 |