# Kathryn L Evans

List of Publications by Year
in descending order



| 83 | 5,005 | 230014 | 129628 |
|---|---|---|---|
| papers | citations | 27 h-index | 63 g-index |

| 119 | 119 | 119 | 9729 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Loss of SORCS2 is Associated with Neuronal DNA Double-Strand Breaks. Cellular and Molecular Neurobiology, 2023, 43, 237-249. | 1.7 | 4 |
| 2 | Additive Effects of Stress and Alcohol Exposure on Accelerated Epigenetic Aging in Alcohol Use Disorder. Biological Psychiatry, 2023, 93, 331-341. | 0.7 | 10 |
| 3 | Methylome-wide association study of early life stressors and adult mental health. Human Molecular Genetics, 2022, 31, 651-664. | 1.4 | 7 |
| 4 | Associations between alcohol use and accelerated biological ageing. Addiction Biology, 2022, 27, e13100. | 1.4 | 19 |
| 5 | Epigenome-wide association study of global cortical volumes in generation Scotland: Scottish family health study. Epigenetics, 2022, 17, 1143-1158. | 1.3 | 3 |
| 6 | Epigenome-wide association study of alcohol consumption in Nâ€‰=â€‰8161 individuals and relevance to alcohol use disorder pathophysiology: identification of the cystine/glutamate transporter SLC7A11 as a top target. Molecular Psychiatry, 2022, 27, 1754-1764. | 4.1 | 18 |
| 7 | Blood-based epigenome-wide analyses of cognitive abilities. Genome Biology, 2022, 23, 26. | 3.8 | 20 |
| 8 | Epigenetic scores for the circulating proteome as tools for disease prediction. ELife, 2022, 11, . | 2.8 | 37 |
| 9 | DNA methylome-wide association study of genetic risk for depression implicates antigen processing and immune responses. Genome Medicine, 2022, 14, 36. | 3.6 | 16 |
| 10 | Methylome-wide association study of antidepressant use in Generation Scotland and the Netherlands Twin Register implicates the innate immune system. Molecular Psychiatry, 2022, 27, 1647-1657. | 4.1 | 10 |
| 11 | Genomeâ€•and epigenomeâ€wide studies of plasma protein biomarkers for Alzheimer's disease implicate TBCA and TREM2 in disease risk. Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2022, 14, e12280. | 1.2 | 4 |
| 12 | Complex trait methylation scores in the prediction of major depressive disorder. EBioMedicine, 2022, 79, 104000. | 2.7 | 4 |
| 13 | Alcohol use disorder is associated with DNA methylation-based shortening of telomere length and regulated by TESPA1: implications for aging. Molecular Psychiatry, 2022, 27, 3875-3884. | 4.1 | 7 |
| 14 | An epigenetic predictor of death captures multi-modal measures of brain health. Molecular Psychiatry, 2021, 26, 3806-3816. | 4.1 | 77 |
| 15 | Birth weight associations with DNA methylation differences in an adult population. Epigenetics, 2021, 16, 783-796. | 1.3 | 18 |
| 16 | Epigenome-wide association study and multi-tissue replication of individuals with alcohol use disorder: evidence for abnormal glucocorticoid signaling pathway gene regulation. Molecular Psychiatry, 2021, 26, 2224-2237. | 4.1 | 32 |
| 17 | Epigenetic prediction of major depressive disorder. Molecular Psychiatry, 2021, 26, 5112-5123. | 4.1 | 44 |
| 18 | Structural brain correlates of serum and epigenetic markers of inflammation in major depressive disorder. Brain, Behavior, and Immunity, 2021, 92, 39-48. | 2.0 | 53 |

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|---|---|---|---|
| 19 | DNA methylation signatures of aggression and closely related constructs: A meta-analysis of epigenome-wide studies across the lifespan. Molecular Psychiatry, 2021, 26, 2148-2162. | 4.1 | 21 |
| 20 | 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 |
| 21 | Epigenome-wide association study of kidney function identifies trans-ethnic and ethnic-specific loci. Genome Medicine, 2021, 13, 74. | 3.6 | 20 |
| 22 | Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321. | 9.4 | 218 |
| 23 | Genome-wide methylation data improves dissection of the effect of smoking on body mass index. PLoS Genetics, 2021, 17, e1009750. | 1.5 | 7 |
| 24 | Identification of epigenome-wide DNA methylation differences between carriers of APOE Îµ4 and APOE Îµ2 alleles. Genome Medicine, 2021, 13, 1. | 3.6 | 76 |
| 25 | Lifestyle and Genetic Factors Modify Parent-of-Origin Effects on the Human Methylome. EBioMedicine, 2021, 74, 103730. | 2.7 | 5 |
| 26 | Meta-analyses identify DNA methylation associated with kidney function and damage. Nature Communications, 2021, 12, 7174. | 5.8 | 30 |
| 27 | Epigenetic Age Acceleration and Cognitive Function in African American Adults in Midlife: The Atherosclerosis Risk in Communities Study. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2020, 75, 473-480. | 1.7 | 15 |
| 28 | An epigenome-wide association study of sex-specific chronological ageing. Genome Medicine, 2020, 12, 1. | 3.6 | 117 |
| 29 | Characterisation of an inflammation-related epigenetic score and its association with cognitive ability. Clinical Epigenetics, 2020, 12, 113. | 1.8 | 38 |
| 30 | Epigenetic measures of ageing predict the prevalence and incidence of leading causes of death and disease burden. Clinical Epigenetics, 2020, 12, 115. | 1.8 | 109 |
| 31 | Epigenomeâ€wide analyses identify DNA methylation signatures of dementia risk. Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2020, 12, e12078. | 1.2 | 8 |
| 32 | DNA methylation in APOE: The relationship with Alzheimer's and with cardiovascular health. Alzheimer's and Dementia: Translational Research and Clinical Interventions, 2020, 6, e12026. | 1.8 | 14 |
| 33 | Bayesian reassessment of the epigenetic architecture of complex traits. Nature Communications, 2020, 11, 2865. | 5.8 | 43 |
| 34 | Multi-method genome- and epigenome-wide studies of inflammatory protein levels in healthy older adults. Genome Medicine, 2020, 12, 60. | 3.6 | 30 |
| 35 | DNA methylation outlier burden, health, and ageing in Generation Scotland and the Lothian Birth Cohorts of 1921 and 1936. Clinical Epigenetics, 2020, 12, 49. | 1.8 | 17 |
| 36 | Genome and epigenome wide studies of neurological protein biomarkers in the Lothian Birth Cohort 1936. Nature Communications, 2019, 10, 3160. | 5.8 | 42 |

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|---|---|---|---|
| 37 | Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. Genome Medicine, 2019, 11, 54. | 3.6 | 191 |
| 38 | Parent of origin genetic effects on methylation in humans are common and influence complex trait variation. Nature Communications, 2019, 10, 1383. | 5.8 | 37 |
| 39 | An epigenetic score for BMI based on DNA methylation correlates with poor physical health and major disease in the Lothian Birth Cohort. International Journal of Obesity, 2019, 43, 1795-1802. | 1.6 | 25 |
| 40 | Identification of novel differentially methylated sites with potential as clinical predictors of impaired respiratory function and COPD. EBioMedicine, 2019, 43, 576-586. | 2.7 | 21 |
| 41 | A meta-analysis of genome-wide association studies of epigenetic age acceleration. PLoS Genetics, 2019, 15, e1008104. | 1.5 | 83 |
| 42 | Assessment of dried blood spots for DNA methylation profiling. Wellcome Open Research, 2019, 4, 44. | 0.9 | 20 |
| 43 | Cohort profile for the STratifying Resilience and Depression Longitudinally (STRADL) study: A depression-focused investigation of Generation Scotland, using detailed clinical, cognitive, and neuroimaging assessments. Wellcome Open Research, 2019, 4, 185. | 0.9 | 27 |
| 44 | Altered DNA methylation associated with a translocation linked to major mental illness. NPJ Schizophrenia, 2018, 4, 5. | 2.0 | 9 |
| 45 | Identification of a novel locus on chromosome 2q13, which predisposes to clinical vertebral fractures independently of bone density. Annals of the Rheumatic Diseases, 2018, 77, 378-385. | 0.5 | 21 |
| 46 | Epigenetic signatures of starting and stopping smoking. EBioMedicine, 2018, 37, 214-220. | 2.7 | 67 |
| 47 | Epigenetic prediction of complex traits and death. Genome Biology, 2018, 19, 136. | 3.8 | 146 |
| 48 | DISC1 regulates N-methyl-D-aspartate receptor dynamics: abnormalities induced by a Disc1 mutation modelling a translocation linked to major mental illness. Translational Psychiatry, 2018, 8, 184. | 2.4 | 21 |
| 49 | GWAS on family history of Alzheimerâ€™s disease. Translational Psychiatry, 2018, 8, 99. | 2.4 | 406 |
| 50 | Investigating the relationship between DNA methylation age acceleration and risk factors for Alzheimer's disease. Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2018, 10, 429-437. | 1.2 | 93 |
| 51 | DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons. JAMA Psychiatry, 2018, 75, 949. | 6.0 | 78 |
| 52 | DNA sequence-level analyses reveal potential phenotypic modifiers in a large family with psychiatric disorders. Molecular Psychiatry, 2018, 23, 2254-2265. | 4.1 | 19 |
| 53 | Genome-wide haplotype-based association analysis of major depressive disorder in Generation Scotland and UK Biobank. Translational Psychiatry, 2017, 7, 1263. | 2.4 | 23 |
| 54 | Haplotype-based association analysis of general cognitive ability in Generation Scotland, the English Longitudinal Study of Ageing, and UK Biobank. Wellcome Open Research, 2017, 2, 61. | 0.9 | 4 |

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|---|---|---|---|
| 55 | Identification of polymorphic and off-target probe binding sites on the Illumina Infinium MethylationEPIC BeadChip. Genomics Data, 2016, 9, 22-24. | 1.3 | 264 |
| 56 | Preliminary assessment of preâ€morbid DNA methylation in individuals at high genetic risk of mood disorders. Bipolar Disorders, 2016, 18, 410-422. | 1.1 | 17 |
| 57 | DNA methylation in a Scottish family multiply affected by bipolar disorder and major depressive disorder. Clinical Epigenetics, 2016, 8, 5. | 1.8 | 23 |
| 58 | Preliminary investigation of miRNA expression in individuals at high familial risk of bipolar disorder. Journal of Psychiatric Research, 2015, 62, 48-55. | 1.5 | 38 |
| 59 | SuRFing the genomics wave: an R package for prioritising SNPs by functionality. Genome Medicine, 2014, 6, 79. | 3.6 | 15 |
| 60 | Expression of DISC1-Interactome Members Correlates with Cognitive Phenotypes Related to Schizophrenia. PLoS ONE, 2014, 9, e99892. | 1.1 | 23 |
| 61 | The DISC1 promoter: characterization and regulation by FOXP2. Human Molecular Genetics, 2012, 21, 2862-2872. | 1.4 | 39 |
| 62 | Alzheimer's disease risk factor complement receptor 1 is associated with depression. Neuroscience Letters, 2012, 510, 6-9. | 1.0 | 18 |
| 63 | Impact of a microRNA MIR137 Susceptibility Variant on Brain Function in People at High Genetic Risk of Schizophrenia or Bipolar Disorder. Neuropsychopharmacology, 2012, 37, 2720-2729. | 2.8 | 79 |
| 64 | Genetic variation in Hyperpolarization-activated cyclic nucleotide-gated channels and its relationship with neuroticism, cognition and risk of depression. Frontiers in Genetics, 2012, 3, 116. | 1.1 | 12 |
| 65 | Association analysis of Neuregulin 1 candidate regions in schizophrenia and bipolar disorder. Neuroscience Letters, 2010, 478, 9-13. | 1.0 | 41 |
| 66 | A case-control association study and family-based expression analysis of the bipolar disorder candidate gene PI4K2B. Journal of Psychiatric Research, 2009, 43, 1272-1277. | 1.5 | 10 |
| 67 | The PDE4B gene confers sex-specific protection against schizophrenia. Psychiatric Genetics, 2007, 17, 129-133. | 0.6 | 88 |
| 68 | Haplotype Analysis and a Novel Allele-Sharing Method Refines a Chromosome 4p Locus Linked to Bipolar Affective Disorder. Biological Psychiatry, 2007, 61, 797-805. | 0.7 | 23 |
| 69 | Are some genetic risk factors common to schizophrenia, bipolar disorder and depression? evidence fromDISC1, GRIK4 andNRG1. Neurotoxicity Research, 2007, 11, 73-83. | 1.3 | 91 |
| 70 | A neuregulin 1 variant associated with abnormal cortical function and psychotic symptoms. Nature Neuroscience, 2006, 9, 1477-1478. | 7.1 | 226 |
| 71 | The DNA sequence of the human X chromosome. Nature, 2005, 434, 325-337. | 13.7 | 985 |
| 72 | Speeding disease gene discovery by sequence based candidate prioritization. BMC Bioinformatics, 2005, 6, 55. | 1.2 | 208 |

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|---|---|---|---|
| 73 | SNP genotyping on pooled DNAs: comparison of genotyping technologies and a semi automated method for data storage and analysis. Nucleic Acids Research, 2002, 30, 74e-74. | 6.5 | 114 |
| 74 | Computational Comparison of Human Genomic Sequence Assemblies for a Region of Chromosome 4. Genome Research, 2002, 12, 424-429. | 2.4 | 12 |
| 75 | A 6.9-Mb High-Resolution BAC/PAC Contig of Human 4p15.3â€“p16.1, a Candidate Region for Bipolar Affective Disorder. Genomics, 2001, 71, 315-323. | 1.3 | 12 |
| 76 | Nuts and bolts of psychiatric genetics: building on the Human Genome Project. Trends in Genetics, 2001, 17, 35-40. | 2.9 | 36 |
| 77 | Comparing Human Genome Mapping Data. Science, 2001, 293, 2394b-2395. | 6.0 | 1 |
| 78 | Clues to the causes of neurodegeneration. Trends in Molecular Medicine, 2000, 6, 219. | 2.6 | 0 |
| 79 | Novel transcribed sequences neighbouring a translocation breakpoint associated with schizophrenia. , 1997, 74, 82-90. | | 12 |
| 80 | A Contiguous Clone Map over 3 Mb on the Long Arm of Chromosome 11 across a Balanced Translocation Associated with Schizophrenia. Genomics, 1995, 28, 420-428. | 1.3 | 8 |
| 81 | Placement and Refined Mapping of Established and New Markers on Human Chromosome 11q Using a Small Panel of Somatic Cell Hybrids. European Journal of Human Genetics, 1995, 3, 42-48. | 1.4 | 1 |
| 82 | Human olfactory marker protein maps close to tyrosinase and is a candidate gene for Usher syndrome type I. Human Molecular Genetics, 1993, 2, 115-118. | 1.4 | 23 |
| 83 | Cohort profile for the STratifying Resilience and Depression Longitudinally (STRADL) study: A depression-focused investigation of Generation Scotland, using detailed clinical, cognitive, and neuroimaging assessments. Wellcome Open Research, 0, 4, 185. | 0.9 | 12 |