# M Daniele Fallin

## List of Publications by Year in Descending Order



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| 71 papers | 7,372 citations | 36 h-index | 79 g-index |
| 79 ext. papers | 8,758 ext. citations | 8.8 avg, IF | 5.36 L-index |

| # | Paper | IF | Citations |
|---|---|---|---|
| 71 | The association between maternal lipid profile after birth and offspring risk of autism spectrum disorder. *Annals of Epidemiology*, **2021**, 53, 50-55.e1 | 6.4 | 2 |
| 70 | Novel Alzheimer Disease Risk Loci and Pathways in African American Individuals Using the African Genome Resources Panel: A Meta-analysis. *JAMA Neurology*, **2021**, 78, 102-113 | 17.2 | 32 |
| 69 | Maternal Psychiatric Conditions, Treatment With Selective Serotonin Reuptake Inhibitors, and Neurodevelopmental Disorders. *Biological Psychiatry*, **2021**, 90, 253-262 | 7.9 | 4 |
| 68 | The Association Between Parental Age and Autism-Related Outcomes in Children at High Familial Risk for Autism. *Autism Research*, **2020**, 13, 998-1010 | 5.1 | 4 |
| 67 | Cord blood DNA methylome in newborns later diagnosed with autism spectrum disorder reflects early dysregulation of neurodevelopmental and X-linked genes. *Genome Medicine*, **2020**, 12, 88 | 14.4 | 17 |
| 66 | A prospective birth cohort study on cord blood folate subtypes and risk of autism spectrum disorder. *American Journal of Clinical Nutrition*, **2020**, 112, 1304-1317 | 7 | 6 |
| 65 | DNA methylation signatures as biomarkers of prior environmental exposures. *Current Epidemiology Reports*, **2019**, 6, 1-13 | 2.9 | 14 |
| 64 | Preterm birth subtypes, placental pathology findings, and risk of neurodevelopmental disabilities during childhood. *Placenta*, **2019**, 83, 17-25 | 3.4 | 14 |
| 63 | Meta-analysis of epigenome-wide association studies in neonates reveals widespread differential DNA methylation associated with birthweight. *Nature Communications*, **2019**, 10, 1893 | 17.4 | 79 |
| 62 | Epigenetic marks of prenatal air pollution exposure found in multiple tissues relevant for child health. *Environment International*, **2019**, 126, 363-376 | 12.9 | 31 |
| 61 | Variable DNA methylation in neonates mediates the association between prenatal smoking and birth weight. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2019**, 374, 20180120 | 5.8 | 28 |
| 60 | Cord and Early Childhood Plasma Adiponectin Levels and Autism Risk: A Prospective Birth Cohort Study. *Journal of Autism and Developmental Disorders*, **2019**, 49, 173-184 | 4.6 | 6 |
| 59 | Infection and Fever in Pregnancy and Autism Spectrum Disorders: Findings from the Study to Explore Early Development. *Autism Research*, **2019**, 12, 1551-1561 | 5.1 | 28 |
| 58 | Invited Commentary: Is DNA Methylation an Actionable Mediator of Prenatal Exposure Effects on Child Health?. *American Journal of Epidemiology*, **2019**, 188, 1887-1889 | 3.8 | 3 |
| 57 | Cord blood buffy coat DNA methylation is comparable to whole cord blood methylation. *Epigenetics*, **2018**, 13, 108-116 | 5.7 | 3 |
| 56 | Tau Phosphorylation is Impacted by Rare AKAP9 Mutations Associated with Alzheimer Disease in African Americans. *Journal of NeuroImmune Pharmacology*, **2018**, 13, 254-264 | 6.9 | 13 |
| 55 | Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. *International Journal of Epidemiology*, **2018**, 47, 22-23u | 7.8 | 62 |

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| 54 | Elevated polygenic burden for autism is associated with differential DNA methylation at birth. *Genome Medicine*, **2018**, 10, 19 | 14.4 | 58 |
| 53 | Targeted Sequencing of Alzheimer Disease Genes in African Americans Implicates Novel Risk Variants. *Frontiers in Neuroscience*, **2018**, 12, 592 | 5.1 | 16 |
| 52 | The Changing Epidemiology of Autism Spectrum Disorders. *Annual Review of Public Health*, **2017**, 38, 81-102 | 20.6 | 404 |
| 51 | Maternal BMI at the start of pregnancy and offspring epigenome-wide DNA methylation: findings from the pregnancy and childhood epigenetics (PACE) consortium. *Human Molecular Genetics*, **2017**, 26, 4067-4085 | 5.6 | 151 |
| 50 | Two novel loci, COBL and SLC10A2, for Alzheimer's disease in African Americans. *Alzheimer's and Dementia*, **2017**, 13, 119-129 | 1.2 | 48 |
| 49 | Global and local ancestry in African-Americans: Implications for Alzheimer's disease risk. *Alzheimer's and Dementia*, **2016**, 12, 233-43 | 1.2 | 27 |
| 48 | "Gap hunting" to characterize clustered probe signals in Illumina methylation array data. *Epigenetics and Chromatin*, **2016**, 9, 56 | 5.8 | 34 |
| 47 | The role of epigenetics in genetic and environmental epidemiology. *Epigenomics*, **2016**, 8, 271-83 | 4.4 | 90 |
| 46 | The Association of Maternal Obesity and Diabetes With Autism and Other Developmental Disabilities. *Pediatrics*, **2016**, 137, e20152206 | 7.4 | 141 |
| 45 | Presence of an epigenetic signature of prenatal cigarette smoke exposure in childhood. *Environmental Research*, **2016**, 144, 139-148 | 7.9 | 75 |
| 44 | Epigenetic Research in Neuropsychiatric Disorders: the "Tissue Issue". *Current Behavioral Neuroscience Reports*, **2016**, 3, 264-274 | 1.7 | 70 |
| 43 | DNA Methylation in Newborns and Maternal Smoking in Pregnancy: Genome-wide Consortium Meta-analysis. *American Journal of Human Genetics*, **2016**, 98, 680-96 | 11 | 489 |
| 42 | DNA methylation of cord blood cell types: Applications for mixed cell birth studies. *Epigenetics*, **2016**, 11, 354-62 | 5.7 | 196 |
| 41 | Genome-wide association study identifies peanut allergy-specific loci and evidence of epigenetic mediation in US children. *Nature Communications*, **2015**, 6, 6304 | 17.4 | 152 |
| 40 | Prenatal mercury concentration is associated with changes in DNA methylation at TCEANC2 in newborns. *International Journal of Epidemiology*, **2015**, 44, 1249-62 | 7.8 | 48 |
| 39 | Paternal sperm DNA methylation associated with early signs of autism risk in an autism-enriched cohort. *International Journal of Epidemiology*, **2015**, 44, 1199-210 | 7.8 | 91 |
| 38 | Epigenetics at the Crossroads of Genes and the Environment. *JAMA - Journal of the American Medical Association*, **2015**, 314, 1129-30 | 27.4 | 62 |
| 37 | Association of Long Runs of Homozygosity With Alzheimer Disease Among African American Individuals. *JAMA Neurology*, **2015**, 72, 1313-23 | 17.2 | 27 |

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| 36 | New insights and updated guidelines for epigenome-wide association studies. *Neuroepigenetics*, **2015**, 1, 14-19 | | 20 |
| 35 | GeMes, clusters of DNA methylation under genetic control, can inform genetic and epigenetic analysis of disease. *American Journal of Human Genetics*, **2014**, 94, 485-95 | 11 | 76 |
| 34 | Epigenetic epidemiology: promises for public health research. *Environmental and Molecular Mutagenesis*, **2014**, 55, 171-83 | 3.2 | 82 |
| 33 | Two rare AKAP9 variants are associated with Alzheimer's disease in African Americans. *Alzheimers and Dementia*, **2014**, 10, 609-618.e11 | 1.2 | 83 |
| 32 | Genes and Environment in Autism Spectrum Disorders: An Integrated Perspective **2014**, 335-374 | | 1 |
| 31 | Evidence of gene-environment interaction for two genes on chromosome 4 and environmental tobacco smoke in controlling the risk of nonsyndromic cleft palate. *PLoS ONE*, **2014**, 9, e88088 | 3.7 | 27 |
| 30 | Epigenome-wide association data implicate DNA methylation as an intermediary of genetic risk in rheumatoid arthritis. *Nature Biotechnology*, **2013**, 31, 142-7 | 44.5 | 691 |
| 29 | Variants in the ATP-binding cassette transporter (ABCA7), apolipoprotein E ?4,and the risk of late-onset Alzheimer disease in African Americans. *JAMA - Journal of the American Medical Association*, **2013**, 309, 1483-92 | 27.4 | 275 |
| 28 | The FGF and FGFR Gene Family and Risk of Cleft Lip With or Without Cleft Palate. *Cleft Palate-Craniofacial Journal*, **2013**, 50, 96-103 | 1.9 | 29 |
| 27 | Bump hunting to identify differentially methylated regions in epigenetic epidemiology studies. *International Journal of Epidemiology*, **2012**, 41, 200-9 | 7.8 | 430 |
| 26 | Evidence of gene-environment interaction for the RUNX2 gene and environmental tobacco smoke in controlling the risk of cleft lip with/without cleft palate. *Birth Defects Research Part A: Clinical and Molecular Teratology*, **2012**, 94, 76-83 | | 23 |
| 25 | DNA methylation shows genome-wide association of NFIX, RAPGEF2 and MSRB3 with gestational age at birth. *International Journal of Epidemiology*, **2012**, 41, 188-99 | 7.8 | 60 |
| 24 | BMP4 was associated with NSCL/P in an Asian population. *PLoS ONE*, **2012**, 7, e35347 | 3.7 | 22 |
| 23 | ROR2 gene is associated with risk of non-syndromic cleft palate in an Asian population. *Chinese Medical Journal*, **2012**, 125, 476-80 | 2.9 | 4 |
| 22 | A comprehensive genetic association study of Alzheimer disease in African Americans. *Archives of Neurology*, **2011**, 68, 1569-79 | | 187 |
| 21 | Linkage and association on 8p21.2-p21.1 in schizophrenia. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2011**, 156, 188-97 | 3.5 | 23 |
| 20 | Evidence for gene-environment interaction in a genome wide study of nonsyndromic cleft palate. *Genetic Epidemiology*, **2011**, 35, 469-78 | 2.6 | 115 |
| 19 | A genome-wide association study of cleft lip with and without cleft palate identifies risk variants near MAFB and ABCA4. *Nature Genetics*, **2010**, 42, 525-9 | 36.3 | 419 |

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| 18 | Personalized epigenomic signatures that are stable over time and covary with body mass index. *Science Translational Medicine*, **2010**, 2, 49ra67 | 17.5 | 254 |
| 17 | Meta-analysis confirms CR1, CLU, and PICALM as alzheimer disease risk loci and reveals interactions with APOE genotypes. *Archives of Neurology*, **2010**, 67, 1473-84 | | 330 |
| 16 | Methods: genetic epidemiology. *Clinics in Laboratory Medicine*, **2010**, 30, 795-814 | 2.1 | |
| 15 | Methods: genetic epidemiology. *Psychiatric Clinics of North America*, **2010**, 33, 15-34 | 3.1 | |
| 14 | Detection of SNP-SNP interactions in trios of parents with schizophrenic children. *Genetic Epidemiology*, **2010**, 34, 396-406 | 2.6 | 18 |
| 13 | Fine mapping on chromosome 10q22-q23 implicates Neuregulin 3 in schizophrenia. *American Journal of Human Genetics*, **2009**, 84, 21-34 | 11 | 78 |
| 12 | Genetic epidemiology in aging research. *Journals of Gerontology - Series A Biological Sciences and Medical Sciences*, **2009**, 64, 47-60 | 6.4 | 17 |
| 11 | Intra-individual change over time in DNA methylation with familial clustering. *JAMA - Journal of the American Medical Association*, **2008**, 299, 2877-83 | 27.4 | 533 |
| 10 | Association between IRF6 and nonsyndromic cleft lip with or without cleft palate in four populations. *Genetics in Medicine*, **2007**, 9, 219-27 | 8.1 | 86 |
| 9 | Stage II follow-up on a linkage scan for bipolar disorder in the Ashkenazim provides suggestive evidence for chromosome 12p and the GRIN2B gene. *Genetics in Medicine*, **2007**, 9, 745-51 | 8.1 | 28 |
| 8 | Bipolar I disorder and schizophrenia: a 440-single-nucleotide polymorphism screen of 64 candidate genes among Ashkenazi Jewish case-parent trios. *American Journal of Human Genetics*, **2005**, 77, 918-36 | 11 | 323 |
| 7 | Comparison of type I error for multiple test corrections in large single-nucleotide polymorphism studies using principal components versus haplotype blocking algorithms. *BMC Genetics*, **2005**, 6 Suppl 1, S78 | 2.6 | 60 |
| 6 | An integrated epigenetic and genetic approach to common human disease. *Trends in Genetics*, **2004** , 20, 350-8 | 8.5 | 367 |
| 5 | Genomewide linkage scan for bipolar-disorder susceptibility loci among Ashkenazi Jewish families. *American Journal of Human Genetics*, **2004**, 75, 204-19 | 11 | 83 |
| 4 | Genomewide linkage scan for schizophrenia susceptibility loci among Ashkenazi Jewish families shows evidence of linkage on chromosome 10q22. *American Journal of Human Genetics*, **2003**, 73, 601-11 | 11 | 94 |
| 3 | Maternal BMI at the start of pregnancy and offspring epigenome-wide DNA methylation: Findings from the Pregnancy and Childhood Epigenetics (PACE) consortium | | 1 |
| 2 | Cord blood DNA methylome in newborns later diagnosed with autism spectrum disorder reflects early dysregulation of neurodevelopmental and X-linked genes | | 1 |
| 1 | Placenta DNA methylation at ZNF300 is associated with fetal sex and placental morphology | | 2 |