

# Phillip E Melton

## List of Publications by Year in descending order

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Version: 2024-02-01

86  
papers

2,923  
citations

218381

26  
h-index

197535

49  
g-index

91  
all docs

91  
docs citations

91  
times ranked

5643  
citing authors

#	ARTICLE	IF	CITATIONS
1	Adiposity associated DNA methylation signatures in adolescents are related to leptin and perinatal factors. <i>Epigenetics</i> , 2022, 17, 819-836.	1.3	10
2	Maternal haemoglobin levels in pregnancy and child DNA methylation: a study in the pregnancy and childhood epigenetics consortium. <i>Epigenetics</i> , 2022, 17, 19-31.	1.3	3
3	A Methylome and Transcriptome Analysis of Normal Human Scar Cells Reveals a Role for FOXF2 in Scar Maintenance. <i>Journal of Investigative Dermatology</i> , 2022, 142, 1489-1498.e12.	0.3	4
4	Evaluation of epigenetic age calculators between preeclampsia and normotensive pregnancies in an Australian cohort. <i>Scientific Reports</i> , 2022, 12, 1664.	1.6	2
5	Prevalence of common sleep disorders in a middle-aged community sample. <i>Journal of Clinical Sleep Medicine</i> , 2022, 18, 1503-1514.	1.4	17
6	Variants in mitochondrial amidoxime reducing component 1 and hydroxysteroid 17 $\beta$ dehydrogenase 13 reduce severity of nonalcoholic fatty liver disease in children and suppress fibrotic pathways through distinct mechanisms. <i>Hepatology Communications</i> , 2022, 6, 1934-1948.	2.0	18
7	Association of protein function-altering variants with cardiometabolic traits: the strong heart study. <i>Scientific Reports</i> , 2022, 12, .	1.6	0
8	Comprehensive genetic analysis of the human lipidome identifies loci associated with lipid homeostasis with links to coronary artery disease. <i>Nature Communications</i> , 2022, 13, .	5.8	30
9	rs641738C>T near MBOAT7 is associated with liver fat, ALT and fibrosis in NAFLD: A meta-analysis. <i>Journal of Hepatology</i> , 2021, 74, 20-30.	1.8	77
10	Epigenome-Wide Association Study of Thyroid Function Traits Identifies Novel Associations of fT3 With <i>KLF9</i> and <i>DOT1L</i> . <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021, 106, e2191-e2202.	1.8	14
11	Late/post-term decidual basalis-derived mesenchymal stem/stromal cells show evidence of advanced ageing and downregulation of microRNA-516b-5p. <i>Placenta</i> , 2021, 109, 43-54.	0.7	1
12	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	9.4	218
13	Lipidomic signatures for APOE genotypes provides new insights about mechanisms of resilience in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2021, 17, .	0.4	0
14	Butyrate generated by gut microbiota and its therapeutic role in metabolic syndrome. <i>Pharmacological Research</i> , 2020, 160, 105174.	3.1	57
15	The LifeCycle Project-EU Child Cohort Network: a federated analysis infrastructure and harmonized data of more than 250,000 children and parents. <i>European Journal of Epidemiology</i> , 2020, 35, 709-724.	2.5	81
16	Machine Learning-Based DNA Methylation Score for Fetal Exposure to Maternal Smoking: Development and Validation in Samples Collected from Adolescents and Adults. <i>Environmental Health Perspectives</i> , 2020, 128, 97003.	2.8	22
17	Methylome-wide association study of central adiposity implicates genes involved in immune and endocrine systems. <i>Epigenomics</i> , 2020, 12, 1483-1499.	1.0	6
18	Bile acids associate with specific gut microbiota, low level alcohol consumption and liver fibrosis in patients with non-alcoholic fatty liver disease. <i>Liver International</i> , 2020, 40, 1356-1365.	1.9	42

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19	Epigenome-wide meta-analysis of blood DNA methylation in newborns and children identifies numerous loci related to gestational age. <i>Genome Medicine</i> , 2020, 12, 25.	3.6	81
20	Identification of Differentially Methylated CpG Sites in Fibroblasts from Keloid Scars. <i>Biomedicines</i> , 2020, 8, 181.	1.4	11
21	Heritability of 596 lipid species and genetic correlation with cardiovascular traits in the Busselton Family Heart Study. <i>Journal of Lipid Research</i> , 2020, 61, 537-545.	2.0	29
22	Machine learning and clinical epigenetics: a review of challenges for diagnosis and classification. <i>Clinical Epigenetics</i> , 2020, 12, 51.	1.8	111
23	Maternal Smoking During Pregnancy Induces Persistent Epigenetic Changes Into Adolescence, Independent of Postnatal Smoke Exposure and Is Associated With Cardiometabolic Risk. <i>Frontiers in Genetics</i> , 2019, 10, 770.	1.1	75
24	Western oropharyngeal and gut microbial profiles are associated with allergic conditions in Chinese immigrant children. <i>World Allergy Organization Journal</i> , 2019, 12, 100051.	1.6	19
25	In Epigenomic Studies, Including Cell-Type Adjustments in Regression Models Can Introduce Multicollinearity, Resulting in Apparent Reversal of Direction of Association. <i>Frontiers in Genetics</i> , 2019, 10, 816.	1.1	20
26	Epigenome-wide meta-analysis of DNA methylation and childhood asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, 2062-2074.	1.5	147
27	Epigenetic Age Acceleration in Adolescence Associates With BMI, Inflammation, and Risk Score for Middle Age Cardiovascular Disease. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2019, 104, 3012-3024.	1.8	53
28	Identification of novel sarcoma risk genes using a two-stage genome wide DNA sequencing strategy in cancer cluster families and population case and control cohorts. <i>BMC Medical Genetics</i> , 2019, 20, 69.	2.1	2
29	Analysis of the Epigenome in Multiplex Pre-eclampsia Families Identifies SORD, DGKI, and ICA1 as Novel Candidate Risk Genes. <i>Frontiers in Genetics</i> , 2019, 10, 227.	1.1	8
30	Meta-analysis of epigenome-wide association studies in neonates reveals widespread differential DNA methylation associated with birthweight. <i>Nature Communications</i> , 2019, 10, 1893.	5.8	140
31	Statins Do Not Directly Inhibit the Activity of Major Epigenetic Modifying Enzymes. <i>Cancers</i> , 2019, 11, 516.	1.7	12
32	Whole-exome sequencing in multiplex preeclampsia families identifies novel candidate susceptibility genes. <i>Journal of Hypertension</i> , 2019, 37, 997-1011.	0.3	19
33	Genetic influence on scar height and pliability after burn injury in individuals of European ancestry: A prospective cohort study. <i>Burns</i> , 2019, 45, 567-578.	1.1	5
34	Differential SLC6A4 methylation: a predictive epigenetic marker of adiposity from birth to adulthood. <i>International Journal of Obesity</i> , 2019, 43, 974-988.	1.6	19
35	Assessment of Cognition and Personality as Potential Endophenotypes in the Western Australian Family Study of Schizophrenia. <i>Schizophrenia Bulletin</i> , 2018, 44, 908-921.	2.3	12
36	Whole genome sequencing of 91 multiplex schizophrenia families reveals increased burden of rare, exonic copy number variation in schizophrenia probands and genetic heterogeneity. <i>Schizophrenia Research</i> , 2018, 197, 337-345.	1.1	16

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37	Epigenetic effects of metformin: From molecular mechanisms to clinical implications. <i>Diabetes, Obesity and Metabolism</i> , 2018, 20, 1553-1562.	2.2	138
38	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. <i>International Journal of Epidemiology</i> , 2018, 47, 22-23u.	0.9	105
39	Pleiotropy of cardiometabolic syndrome with obesity-related anthropometric traits determined using empirically derived kinships from the Busselton Health Study. <i>Human Genetics</i> , 2018, 137, 45-53.	1.8	10
40	Association of maternal prenatal smoking GF11-locus and cardio-metabolic phenotypes in 18,212 adults. <i>EBioMedicine</i> , 2018, 38, 206-216.	2.7	43
41	Epigenetics, heritability and longitudinal analysis. <i>BMC Genetics</i> , 2018, 19, 77.	2.7	5
42	Retinal genes are differentially expressed in areas of primary versus secondary degeneration following partial optic nerve injury. <i>PLoS ONE</i> , 2018, 13, e0192348.	1.1	10
43	ANRIL Promoter DNA Methylation: A Perinatal Marker for Later Adiposity. <i>EBioMedicine</i> , 2017, 19, 60-72.	2.7	65
44	Exome array analysis suggests an increased variant burden in families with schizophrenia. <i>Schizophrenia Research</i> , 2017, 185, 9-16.	1.1	18
45	Association Between Polygenic Risk Score for Schizophrenia and Neurocognitive Measures in the Western Australian Family Study of Schizophrenia (Wafss). <i>European Neuropsychopharmacology</i> , 2017, 27, S505-S506.	0.3	0
46	Maternal BMI at the start of pregnancy and offspring epigenome-wide DNA methylation: findings from the pregnancy and childhood epigenetics (PACE) consortium. <i>Human Molecular Genetics</i> , 2017, 26, 4067-4085.	1.4	211
47	The antihypertensive MTHFR gene polymorphism rs17367504-G is a possible novel protective locus for preeclampsia. <i>Journal of Hypertension</i> , 2017, 35, 132-139.	0.3	15
48	Paternal Genetic Structure in Contemporary Mennonite Communities from the American Midwest. <i>Human Biology</i> , 2016, 88, 95.	0.4	16
49	Patterns of DNA Methylation across the Leptin Core Promoter in Four Diverse Asian and North American Populations. <i>Human Biology</i> , 2016, 88, 121.	0.4	25
50	Transcriptome analysis of human ageing in male skin shows mid-life period of variability and central role of NF- $\kappa$ B. <i>Scientific Reports</i> , 2016, 6, 26846.	1.6	52
51	Genetic Analysis Workshop 19: methods and strategies for analyzing human sequence and gene expression data in extended families and unrelated individuals. <i>BMC Proceedings</i> , 2016, 10, 67-70.	1.8	7
52	Constrained multivariate association with longitudinal phenotypes. <i>BMC Proceedings</i> , 2016, 10, 329-332.	1.8	0
53	Longitudinal analytical approaches to genetic data. <i>BMC Genetics</i> , 2016, 17, 4.	2.7	19
54	Refined phenotyping identifies links between preeclampsia and related diseases in a Norwegian preeclampsia family cohort. <i>Journal of Hypertension</i> , 2015, 33, 2294-2302.	0.3	21

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55	O4. Genome wide sequencing approaches to identify missing heritability of preeclampsia. <i>Pregnancy Hypertension</i> , 2015, 5, 209-210.	0.6	0
56	Genome-Wide Transcriptome Directed Pathway Analysis of Maternal Pre-Eclampsia Susceptibility Genes. <i>PLoS ONE</i> , 2015, 10, e0128230.	1.1	61
57	[81-OR]. <i>Pregnancy Hypertension</i> , 2015, 5, 43-44.	0.6	2
58	[278-POS]. <i>Pregnancy Hypertension</i> , 2015, 5, 138-139.	0.6	0
59	Absence of germline mutations in BAP1 in sporadic cases of malignant mesothelioma. <i>Gene</i> , 2015, 563, 103-105.	1.0	27
60	Longitudinal Data Analysis for Genetic Studies in the Whole-Genome Sequencing Era. <i>Genetic Epidemiology</i> , 2014, 38, S74-80.	0.6	12
61	Meta-analysis of human methylation data for evidence of sex-specific autosomal patterns. <i>BMC Genomics</i> , 2014, 15, 981.	1.2	94
62	Evidence of Heterogeneity by Race/Ethnicity in Genetic Determinants of QT Interval. <i>Epidemiology</i> , 2014, 25, 790-798.	1.2	22
63	Effect of Recent Historical Events on Migration and Isonymic Stratification among the Rama Amerindians from Nicaragua. <i>Human Biology</i> , 2014, 86, 37-50.	0.4	3
64	Genetic Analysis Workshop 18: Methods and strategies for analyzing human sequence and phenotype data in members of extended pedigrees. <i>BMC Proceedings</i> , 2014, 8, S1.	1.8	12
65	Bivariate association analysis of longitudinal phenotypes in families. <i>BMC Proceedings</i> , 2014, 8, S90.	1.8	3
66	Preeclampsia and cardiovascular disease share genetic risk factors on chromosome 2q22. <i>Pregnancy Hypertension</i> , 2014, 4, 178-185.	0.6	14
67	Effect of Recent Historical Events on Migration and Isonymic Stratification among the Rama Amerindians from Nicaragua. <i>Human Biology</i> , 2014, 86, 37.	0.4	1
68	A genome-wide association study for malignant mesothelioma risk. <i>Lung Cancer</i> , 2013, 82, 1-8.	0.9	45
69	OP004. A SNP associated with susceptibility to preeclampsia near the inhibin, beta B gene, is also associated with cardiovascular disease risk traits. <i>Pregnancy Hypertension</i> , 2013, 3, 63.	0.6	0
70	Microevolution, migration, and the population structure of five Amerindian populations from Nicaragua and Costa Rica. <i>American Journal of Human Biology</i> , 2013, 25, 480-490.	0.8	16
71	A Genome-Wide Integrative Genomic Study Localizes Genetic Factors Influencing Antibodies against Epstein-Barr Virus Nuclear Antigen 1 (EBNA-1). <i>PLoS Genetics</i> , 2013, 9, e1003147.	1.5	92
72	Genetic Architecture of Carotid Artery Intima-Media Thickness in Mexican Americans. <i>Circulation: Cardiovascular Genetics</i> , 2013, 6, 211-221.	5.1	24

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73	Genetic dissection of the pre-eclampsia susceptibility locus on chromosome 2q22 reveals shared novel risk factors for cardiovascular disease. <i>Molecular Human Reproduction</i> , 2013, 19, 423-437.	1.3	54
74	Genome-Wide Association Study of Autistic-Like Traits in a General Population Study of Young Adults. <i>Frontiers in Human Neuroscience</i> , 2013, 7, 658.	1.0	43
75	Large scale mitochondrial sequencing in Mexican Americans suggests a reappraisal of Native American origins. <i>BMC Evolutionary Biology</i> , 2011, 11, 293.	3.2	77
76	Genetic signal maximization using environmental regression. <i>BMC Proceedings</i> , 2011, 5, S72.	1.8	2
77	Genetic influences on serum bilirubin in American Indians: The strong heart family study. <i>American Journal of Human Biology</i> , 2011, 23, 118-125.	0.8	6
78	Joint analyses of disease and correlated quantitative phenotypes using next-generation sequencing data. <i>Genetic Epidemiology</i> , 2011, 35, S67-73.	0.6	4
79	Genetic structure of native circumpolar populations based on autosomal, mitochondrial, and Y chromosome DNA markers. <i>American Journal of Physical Anthropology</i> , 2010, 143, 62-74.	2.1	36
80	Bivariate genetic association of KIAA1797 with heart rate in American Indians: the Strong Heart Family Study. <i>Human Molecular Genetics</i> , 2010, 19, 3662-3671.	1.4	25
81	Mitochondrial DNA Diversity in Mennonite Communities from the Midwestern United States. <i>Human Biology</i> , 2010, 82, 267-289.	0.4	8
82	Biological relationship between central and South American Chibchan speaking populations: Evidence from mtDNA. <i>American Journal of Physical Anthropology</i> , 2007, 133, 753-770.	2.1	66
83	Comparative analysis of mitochondrial DNA of Yakuts and other Asian populations. <i>Russian Journal of Genetics</i> , 2006, 42, 1439-1446.	0.2	5
84	Biological aging and Cox hazard analysis of mortality trends in a Mennonite community from south-central Kansas. <i>American Journal of Human Biology</i> , 2006, 18, 387-401.	0.8	8
85	Molecular Markers in Anthropological Genetic Studies. , 2006, , 141-186.		7
86	Mennonite migrations: genetic and demographic consequences. , 0, , 299-316.		2