Phillip E Melton

List of Publications by Year
in descending order

86	2,923	218677	197818
papers	citations	26 h-index	49 g-index

91	91	91	5643
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	21.4	218
2	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.	2.9	211
3	Epigenome-wide meta-analysis of DNA methylation and childhood asthma. Journal of Allergy and Clinical Immunology, 2019, 143, 2062-2074.	2.9	147
4	Meta-analysis of epigenome-wide association studies in neonates reveals widespread differential DNA methylation associated with birthweight. Nature Communications, 2019, 10, 1893.	12.8	140
5	Epigenetic effects of metformin: From molecular mechanisms to clinical implications. Diabetes, Obesity and Metabolism, 2018, 20, 1553-1562.	4.4	138
6	Machine learning and clinical epigenetics: a review of challenges for diagnosis and classification. Clinical Epigenetics, 2020, 12, 51.	4.1	111
7	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. International Journal of Epidemiology, 2018, 47, 22-23u.	1.9	105
8	Meta-analysis of human methylation data for evidence of sex-specific autosomal patterns. BMC Genomics, 2014, 15, 981.	2.8	94
9	A Genome-Wide Integrative Genomic Study Localizes Genetic Factors Influencing Antibodies against Epstein-Barr Virus Nuclear Antigen 1 (EBNA-1). PLoS Genetics, 2013, 9, e1003147.	3.5	92
10	The LifeCycle Project-EU Child Cohort Network: a federated analysis infrastructure and harmonized data of more than 250,000 children and parents. European Journal of Epidemiology, 2020, 35, 709-724.	5.7	81
11	Epigenome-wide meta-analysis of blood DNA methylation in newborns and children identifies numerous loci related to gestational age. Genome Medicine, 2020, 12, 25.	8.2	81
12	Large scale mitochondrial sequencing in Mexican Americans suggests a reappraisal of Native American origins. BMC Evolutionary Biology, 2011, 11, 293.	3.2	77
13	rs641738C>T near MBOAT7 is associated with liver fat, ALT and fibrosis in NAFLD: A meta-analysis. Journal of Hepatology, 2021, 74, 20-30.	3.7	77
14	Maternal Smoking During Pregnancy Induces Persistent Epigenetic Changes Into Adolescence, Independent of Postnatal Smoke Exposure and Is Associated With Cardiometabolic Risk. Frontiers in Genetics, 2019, 10, 770.	2.3	75
15	Biological relationship between central and South American Chibchan speaking populations: Evidence from mtDNA. American Journal of Physical Anthropology, 2007, 133, 753-770.	2.1	66
16	ANRIL Promoter DNA Methylation: A Perinatal Marker for Later Adiposity. EBioMedicine, 2017, 19, 60-72.	6.1	65
17	Genome-Wide Transcriptome Directed Pathway Analysis of Maternal Pre-Eclampsia Susceptibility Genes. PLoS ONE, 2015, 10, e0128230.	2.5	61
18	Butyrate generated by gut microbiota and its therapeutic role in metabolic syndrome. Pharmacological Research, 2020, 160, 105174.	7.1	57

#	Article	IF	Citations
19	Genetic dissection of the pre-eclampsia susceptibility locus on chromosome 2q22 reveals shared novel risk factors for cardiovascular disease. Molecular Human Reproduction, 2013, 19, 423-437.	2.8	54
20	Epigenetic Age Acceleration in Adolescence Associates With BMI, Inflammation, and Risk Score for Middle Age Cardiovascular Disease. Journal of Clinical Endocrinology and Metabolism, 2019, 104, 3012-3024.	3.6	53
21	Transcriptome analysis of human ageing in male skin shows mid-life period of variability and central role of NF-Î¹B. Scientific Reports, 2016, 6, 26846.	3.3	52
22	A genome-wide association study for malignant mesothelioma risk. Lung Cancer, 2013, 82, 1-8.	2.0	45
23	Genome-Wide Association Study of Autistic-Like Traits in a General Population Study of Young Adults. Frontiers in Human Neuroscience, 2013, 7, 658.	2.0	43
24	Association of maternal prenatal smoking GFI1-locus and cardio-metabolic phenotypes in 18,212 adults. EBioMedicine, 2018, 38, 206-216.	6.1	43
25	Bile acids associate with specific gut microbiota, lowâ€level alcohol consumption and liver fibrosis in patients with nonâ€alcoholic fatty liver disease. Liver International, 2020, 40, 1356-1365.	3.9	42
26	Genetic structure of native circumpolar populations based on autosomal, mitochondrial, and Y chromosome DNA markers. American Journal of Physical Anthropology, 2010, 143, 62-74.	2.1	36
27	Comprehensive genetic analysis of the human lipidome identifies loci associated with lipid homeostasis with links to coronary artery disease. Nature Communications, 2022, 13, .	12.8	30
28	Heritability of 596 lipid species and genetic correlation with cardiovascular traits in the Busselton Family Heart Study. Journal of Lipid Research, 2020, 61, 537-545.	4.2	29
29	Absence of germline mutations in BAP1 in sporadic cases of malignant mesothelioma. Gene, 2015, 563, 103-105.	2.2	27
30	Bivariate genetic association of KIAA1797 with heart rate in American Indians: the Strong Heart Family Study. Human Molecular Genetics, 2010, 19, 3662-3671.	2.9	25
31	Patterns of DNA Methylation across the Leptin Core Promoter in Four Diverse Asian and North American Populations. Human Biology, 2016, 88, 121.	0.2	25
32	Genetic Architecture of Carotid Artery Intima-Media Thickness in Mexican Americans. Circulation: Cardiovascular Genetics, 2013, 6, 211-221.	5.1	24
33	Evidence of Heterogeneity by Race/Ethnicity in Genetic Determinants of QT Interval. Epidemiology, 2014, 25, 790-798.	2.7	22
34	Machine Learning-Based DNA Methylation Score for Fetal Exposure to Maternal Smoking: Development and Validation in Samples Collected from Adolescents and Adults. Environmental Health Perspectives, 2020, 128, 97003.	6.0	22
35	Refined phenotyping identifies links between preeclampsia and related diseases in a Norwegian preeclampsia family cohort. Journal of Hypertension, 2015, 33, 2294-2302.	0.5	21
36	In Epigenomic Studies, Including Cell-Type Adjustments in Regression Models Can Introduce Multicollinearity, Resulting in Apparent Reversal of Direction of Association. Frontiers in Genetics, 2019, 10, 816.	2.3	20

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37	Longitudinal analytical approaches to genetic data. BMC Genetics, 2016, 17, 4.	2.7	19
38	Western oropharyngeal and gut microbial profiles are associated with allergic conditions in Chinese immigrant children. World Allergy Organization Journal, 2019, 12, 100051.	3.5	19
39	Whole-exome sequencing in multiplex preeclampsia families identifies novel candidate susceptibility genes. Journal of Hypertension, 2019, 37, 997-1011.	0.5	19
40	Differential SLC6A4 methylation: a predictive epigenetic marker of adiposity from birth to adulthood. International Journal of Obesity, 2019, 43, 974-988.	3.4	19
41	Exome array analysis suggests an increased variant burden in families with schizophrenia. Schizophrenia Research, 2017, 185, 9-16.	2.0	18
42	Variants in mitochondrial amidoxime reducing component 1 and hydroxysteroid 17â€beta dehydrogenase 13 reduce severity of nonalcoholic fatty liver disease in children and suppress fibrotic pathways through distinct mechanisms. Hepatology Communications, 2022, 6, 1934-1948.	4.3	18
43	Prevalence of common sleep disorders in a middle-aged community sample. Journal of Clinical Sleep Medicine, 2022, 18, 1503-1514.	2.6	17
44	Microevolution, migration, and the population structure of five Amerindian populations from Nicaragua and Costa Rica. American Journal of Human Biology, 2013, 25, 480-490.	1.6	16
45	Paternal Genetic Structure in Contemporary Mennonite Communities from the American Midwest. Human Biology, 2016, 88, 95.	0.2	16
46	Whole genome sequencing of 91 multiplex schizophrenia families reveals increased burden of rare, exonic copy number variation in schizophrenia probands and genetic heterogeneity. Schizophrenia Research, 2018, 197, 337-345.	2.0	16
47	The antihypertensive MTHFR gene polymorphism rs17367504-G is a possible novel protective locus for preeclampsia. Journal of Hypertension, 2017, 35, 132-139.	0.5	15
48	Preeclampsia and cardiovascular disease share genetic risk factors on chromosome 2q22. Pregnancy Hypertension, 2014, 4, 178-185.	1.4	14
49	Epigenome-Wide Association Study of Thyroid Function Traits Identifies Novel Associations of fT3 With KLF9 and DOT1L. Journal of Clinical Endocrinology and Metabolism, 2021, 106, e2191-e2202.	3.6	14
50	Longitudinal Data Analysis for Genetic Studies in the Wholeâ€Genome Sequencing Era. Genetic Epidemiology, 2014, 38, S74-80.	1.3	12
51	Genetic Analysis Workshop 18: Methods and strategies for analyzing human sequence and phenotype data in members of extended pedigrees. BMC Proceedings, 2014, 8, S1.	1.6	12
52	Assessment of Cognition and Personality as Potential Endophenotypes in the Western Australian Family Study of Schizophrenia. Schizophrenia Bulletin, 2018, 44, 908-921.	4.3	12
53	Statins Do Not Directly Inhibit the Activity of Major Epigenetic Modifying Enzymes. Cancers, 2019, 11, 516.	3.7	12
54	Identification of Differentially Methylated CpG Sites in Fibroblasts from Keloid Scars. Biomedicines, 2020, 8, 181.	3.2	11

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55	Pleiotropy of cardiometabolic syndrome with obesity-related anthropometric traits determined using empirically derived kinships from the Busselton Health Study. Human Genetics, 2018, 137, 45-53.	3.8	10
56	Adiposity associated DNA methylation signatures in adolescents are related to leptin and perinatal factors. Epigenetics, 2022, 17, 819-836.	2.7	10
57	Retinal genes are differentially expressed in areas of primary versus secondary degeneration following partial optic nerve injury. PLoS ONE, 2018, 13, e0192348.	2.5	10
58	Biological aging and Cox hazard analysis of mortality trends in a Mennonite community from south-central Kansas. American Journal of Human Biology, 2006, 18, 387-401.	1.6	8
59	Mitochondrial DNA Diversity in Mennonite Communities from the Midwestern United States. Human Biology, 2010, 82, 267-289.	0.2	8
60	Analysis of the Epigenome in Multiplex Pre-eclampsia Families Identifies SORD, DGKI, and ICA1 as Novel Candidate Risk Genes. Frontiers in Genetics, 2019, 10, 227.	2.3	8
61	Genetic Analysis Workshop 19: methods and strategies for analyzing human sequence and gene expression data in extended families and unrelated individuals. BMC Proceedings, 2016, 10, 67-70.	1.6	7
62	Molecular Markers in Anthropological Genetic Studies. , 2006, , 141-186.		7
63	Genetic influences on serum bilirubin in American Indians: The strong heart family study. American Journal of Human Biology, 2011, 23, 118-125.	1.6	6
64	Methylome-wide association study of central adiposity implicates genes involved in immune and endocrine systems. Epigenomics, 2020, 12, 1483-1499.	2.1	6
65	Comparative analysis of mitochondrial DNA of Yakuts and other Asian populations. Russian Journal of Genetics, 2006, 42, 1439-1446.	0.6	5
66	Epigenetics, heritability and longitudinal analysis. BMC Genetics, 2018, 19, 77.	2.7	5
67	Genetic influence on scar height and pliability after burn injury in individuals of European ancestry: A prospective cohort study. Burns, 2019, 45, 567-578.	1.9	5
68	Joint analyses of disease and correlated quantitative phenotypes using nextâ€generation sequencing data. Genetic Epidemiology, 2011, 35, S67-73.	1.3	4
69	A Methylome and Transcriptome Analysis of Normal Human Scar Cells Reveals a Role for FOXF2 in Scar Maintenance. Journal of Investigative Dermatology, 2022, 142, 1489-1498.e12.	0.7	4
70	Effect of Recent Historical Events on Migration and Isonymic Stratification among the Rama Amerindians from Nicaragua. Human Biology, 2014, 86, 37-50.	0.2	3
71	Bivariate association analysis of longitudinal phenotypes in families. BMC Proceedings, 2014, 8, S90.	1.6	3
72	Maternal haemoglobin levels in pregnancy and child DNA methylation: a study in the pregnancy and childhood epigenetics consortium. Epigenetics, 2022, 17, 19-31.	2.7	3

#	Article	IF	Citations
73	Genetic signal maximization using environmental regression. BMC Proceedings, 2011, 5, S72.	1.6	2
74	Mennonite migrations: genetic and demographic consequences. , 0, , 299-316.		2
75	[81-OR]. Pregnancy Hypertension, 2015, 5, 43-44.	1.4	2
76	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. BMC Medical Genetics, 2019, 20, 69.	2.1	2
77	Evaluation of epigenetic age calculators between preeclampsia and normotensive pregnancies in an Australian cohort. Scientific Reports, 2022, 12, 1664.	3.3	2
78	Effect of Recent Historical Events on Migration and Isonymic Stratification among the Rama Amerindians from Nicaragua. Human Biology, 2014, 86, 37.	0.2	1
79	Late/post-term decidual basalis-derived mesenchymal stem/stromal cells show evidence of advanced ageing and downregulation of microRNA-516b-5p. Placenta, 2021, 109, 43-54.	1.5	1
80	OP004. A SNP associated with susceptibility to preeclampsia near the inhibin, beta B gene, is also associated with cardiovascular disease risk traits. Pregnancy Hypertension, 2013, 3, 63.	1.4	0
81	O4. Genome wide sequencing approaches to identify missing heritability of preeclampsia. Pregnancy Hypertension, 2015, 5, 209-210.	1.4	0
82	[278-POS]. Pregnancy Hypertension, 2015, 5, 138-139.	1.4	0
83	Constrained multivariate association with longitudinal phenotypes. BMC Proceedings, 2016, 10, 329-332.	1.6	0
84	Association Between Polygenic Risk Score for Schizophrenia and Neurocognitive Measures in the Western Australian Family Study of Schizophrenia (Wafss). European Neuropsychopharmacology, 2017, 27, S505-S506.	0.7	0
85	Lipidomic signatures for APOE genotypes provides new insights about mechanisms of resilience in Alzheimerâ€™s disease. Alzheimer's and Dementia, 2021, 17, .	0.8	0
86	Association of protein function-altering variants with cardiometabolic traits: the strong heart study. Scientific Reports, 2022, 12, .	3.3	0