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	Adiposity associated DNA methylation signatures in adolescents are related to leptin and perinatal factors. Epigenetics, 2022, 17, 819-836.	2.7	10
2	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
3	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
4	Evaluation of epigenetic age calculators between preeclampsia and normotensive pregnancies in an Australian cohort. Scientific Reports, 2022, 12, 1664.	3.3	2
5	Prevalence of common sleep disorders in a middle-aged community sample. Journal of Clinical Sleep Medicine, 2022, 18, 1503-1514.	2.6	17
6	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
7	Association of protein function-altering variants with cardiometabolic traits: the strong heart study. Scientific Reports, 2022, 12, .	3.3	0
8	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
9	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
10	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
11	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
12	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	21.4	218
13	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
14	Butyrate generated by gut microbiota and its therapeutic role in metabolic syndrome. Pharmacological Research, 2020, 160, 105174.	7.1	57
15	The LifeCycle Project-EU Child Cohort Network: a federated analysis infrastructure and harmonized data of more than 250,000 children and parents. European Journal of Epidemiology, 2020, 35, 709-724.	5.7	81
16	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
17	Methylome-wide association study of central adiposity implicates genes involved in immune and endocrine systems. Epigenomics, 2020, 12, 1483-1499.	2.1	6
18	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

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19	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
20	Identification of Differentially Methylated CpG Sites in Fibroblasts from Keloid Scars. Biomedicines, 2020, 8, 181.	3.2	11
21	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
22	Machine learning and clinical epigenetics: a review of challenges for diagnosis and classification. Clinical Epigenetics, 2020, 12, 51.	4.1	111
23	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
24	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
25	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
26	Epigenome-wide meta-analysis of DNA methylation and childhood asthma. Journal of Allergy and Clinical Immunology, 2019, 143, 2062-2074.	2.9	147
27	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
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. BMC Medical Genetics, 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. Frontiers in Genetics, 2019, 10, 227.	2.3	8
30	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
31	Statins Do Not Directly Inhibit the Activity of Major Epigenetic Modifying Enzymes. Cancers, 2019, 11, 516.	3.7	12
32	Whole-exome sequencing in multiplex preeclampsia families identifies novel candidate susceptibility genes. Journal of Hypertension, 2019, 37, 997-1011.	0.5	19
33	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
34	Differential SLC6A4 methylation: a predictive epigenetic marker of adiposity from birth to adulthood. International Journal of Obesity, 2019, 43, 974-988.	3.4	19
35	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
36	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

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37	Epigenetic effects of metformin: From molecular mechanisms to clinical implications. Diabetes, Obesity and Metabolism, 2018, 20, 1553-1562.	4.4	138
38	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. International Journal of Epidemiology, 2018, 47, 22-23u.	1.9	105
39	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
40	Association of maternal prenatal smoking GFI1-locus and cardio-metabolic phenotypes in 18,212 adults. EBioMedicine, 2018, 38, 206-216.	6.1	43
41	Epigenetics, heritability and longitudinal analysis. BMC Genetics, 2018, 19, 77.	2.7	5
42	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
43	ANRIL Promoter DNA Methylation: A Perinatal Marker for Later Adiposity. EBioMedicine, 2017, 19, 60-72.	6.1	65
44	Exome array analysis suggests an increased variant burden in families with schizophrenia. Schizophrenia Research, 2017, 185, 9-16.	2.0	18
45	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
46	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
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	Paternal Genetic Structure in Contemporary Mennonite Communities from the American Midwest. Human Biology, 2016, 88, 95.	0.2	16
49	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
50	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
51	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
52	Constrained multivariate association with longitudinal phenotypes. BMC Proceedings, 2016, 10, 329-332.	1.6	0
53	Longitudinal analytical approaches to genetic data. BMC Genetics, 2016, 17, 4.	2.7	19
54	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

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55	O4. Genome wide sequencing approaches to identify missing heritability of preeclampsia. Pregnancy Hypertension, 2015, 5, 209-210.	1.4	0
56	Genome-Wide Transcriptome Directed Pathway Analysis of Maternal Pre-Eclampsia Susceptibility Genes. PLoS ONE, 2015, 10, e0128230.	2.5	61
57	[81-OR]. Pregnancy Hypertension, 2015, 5, 43-44.	1.4	2
58	[278-POS]. Pregnancy Hypertension, 2015, 5, 138-139.	1.4	0
59	Absence of germline mutations in BAP1 in sporadic cases of malignant mesothelioma. Gene, 2015, 563, 103-105.	2.2	27
60	Longitudinal Data Analysis for Genetic Studies in the Wholeâ€Genome Sequencing Era. Genetic Epidemiology, 2014, 38, S74-80.	1.3	12
61	Meta-analysis of human methylation data for evidence of sex-specific autosomal patterns. BMC Genomics, 2014, 15, 981.	2.8	94
62	Evidence of Heterogeneity by Race/Ethnicity in Genetic Determinants of QT Interval. Epidemiology, 2014, 25, 790-798.	2.7	22
63	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
64	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
65	Bivariate association analysis of longitudinal phenotypes in families. BMC Proceedings, 2014, 8, S90.	1.6	3
66	Preeclampsia and cardiovascular disease share genetic risk factors on chromosome 2q22. Pregnancy Hypertension, 2014, 4, 178-185.	1.4	14
67	Effect of Recent Historical Events on Migration and Isonymic Stratification among the Rama Amerindians from Nicaragua. Human Biology, 2014, 86, 37.	0.2	1
68	A genome-wide association study for malignant mesothelioma risk. Lung Cancer, 2013, 82, 1-8.	2.0	45
69	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
70	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
71	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
72	Genetic Architecture of Carotid Artery Intima-Media Thickness in Mexican Americans. Circulation: Cardiovascular Genetics, 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. Molecular Human Reproduction, 2013, 19, 423-437.	2.8	54
74	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
75	Large scale mitochondrial sequencing in Mexican Americans suggests a reappraisal of Native American origins. BMC Evolutionary Biology, 2011, 11, 293.	3.2	77
76	Genetic signal maximization using environmental regression. BMC Proceedings, 2011, 5, S72.	1.6	2
77	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
78	Joint analyses of disease and correlated quantitative phenotypes using nextâ€generation sequencing data. Genetic Epidemiology, 2011, 35, S67-73.	1.3	4
79	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
80	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
81	Mitochondrial DNA Diversity in Mennonite Communities from the Midwestern United States. Human Biology, 2010, 82, 267-289.	0.2	8
82	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
83	Comparative analysis of mitochondrial DNA of Yakuts and other Asian populations. Russian Journal of Genetics, 2006, 42, 1439-1446.	0.6	5
84	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
85	Molecular Markers in Anthropological Genetic Studies. , 2006, , 141-186.		7
86	Mennonite migrations: genetic and demographic consequences. , 0, , 299-316.		2