

Caroline L Relton

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

208
papers

9,959
citations

48
h-index

96
g-index

241
ext. papers

14,712
ext. citations

8.2
avg. IF

6.25
L-index

#	Paper	IF	Citations
208	The MR-Base platform supports systematic causal inference across the human phenome. <i>ELife</i> , 2018 , 7,	8.9	1190
207	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. <i>Nature</i> , 2017 , 541, 81-86	50.4	511
206	DNA Methylation in Newborns and Maternal Smoking in Pregnancy: Genome-wide Consortium Meta-analysis. <i>American Journal of Human Genetics</i> , 2016 , 98, 680-96	11	489
205	Systematic identification of genetic influences on methylation across the human life course. <i>Genome Biology</i> , 2016 , 17, 61	18.3	331
204	Multi-ancestry genome-wide association study of 21,000 cases and 95,000 controls identifies new risk loci for atopic dermatitis. <i>Nature Genetics</i> , 2015 , 47, 1449-1456	36.3	329
203	Two-step epigenetic Mendelian randomization: a strategy for establishing the causal role of epigenetic processes in pathways to disease. <i>International Journal of Epidemiology</i> , 2012 , 41, 161-76	7.8	273
202	Prenatal exposure to maternal smoking and offspring DNA methylation across the lifecourse: findings from the Avon Longitudinal Study of Parents and Children (ALSPAC). <i>Human Molecular Genetics</i> , 2015 , 24, 2201-17	5.6	256
201	DNA methylation aging clocks: challenges and recommendations. <i>Genome Biology</i> , 2019 , 20, 249	18.3	248
200	Best (but oft-forgotten) practices: the design, analysis, and interpretation of Mendelian randomization studies. <i>American Journal of Clinical Nutrition</i> , 2016 , 103, 965-78	7	245
199	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases: A Mendelian Randomization Study. <i>JAMA Oncology</i> , 2017 , 3, 636-651	13.4	236
198	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. <i>Nature Genetics</i> , 2019 , 51, 804-814	36.3	181
197	Maternal pre-pregnancy BMI and gestational weight gain, offspring DNA methylation and later offspring adiposity: findings from the Avon Longitudinal Study of Parents and Children. <i>International Journal of Epidemiology</i> , 2015 , 44, 1288-304	7.8	181
196	Differences in smoking associated DNA methylation patterns in South Asians and Europeans. <i>Clinical Epigenetics</i> , 2014 , 6, 4	7.7	176
195	Epigenetic epidemiology of common complex disease: prospects for prediction, prevention, and treatment. <i>PLoS Medicine</i> , 2010 , 7, e1000356	11.6	165
194	Data Resource Profile: Accessible Resource for Integrated Epigenomic Studies (ARIES). <i>International Journal of Epidemiology</i> , 2015 , 44, 1181-90	7.8	162
193	Guidelines for performing Mendelian randomization investigations. <i>Wellcome Open Research</i> , 2019 , 4, 186	4.8	154
192	Prenatal and early life influences on epigenetic age in children: a study of mother-offspring pairs from two cohort studies. <i>Human Molecular Genetics</i> , 2016 , 25, 191-201	5.6	153

191	Statistical and integrative system-level analysis of DNA methylation data. <i>Nature Reviews Genetics</i> , 2018 , 19, 129-147	30.1	153
190	Hypomethylation of smoking-related genes is associated with future lung cancer in four prospective cohorts. <i>Nature Communications</i> , 2015 , 6, 10192	17.4	144
189	Guidelines for performing Mendelian randomization investigations. <i>Wellcome Open Research</i> , 2019 , 4, 186	4.8	133
188	DNA methylation mediates the effect of maternal smoking during pregnancy on birthweight of the offspring. <i>International Journal of Epidemiology</i> , 2015 , 44, 1224-37	7.8	130
187	The Role of Obesity, Type 2 Diabetes, and Metabolic Factors in Pancreatic Cancer: A Mendelian Randomization Study. <i>Journal of the National Cancer Institute</i> , 2017 , 109,	9.7	123
186	DNA methylation patterns in cord blood DNA and body size in childhood. <i>PLoS ONE</i> , 2012 , 7, e31821	3.7	118
185	Sensitive Periods for the Effect of Childhood Adversity on DNA Methylation: Results From a Prospective, Longitudinal Study. <i>Biological Psychiatry</i> , 2019 , 85, 838-849	7.9	115
184	Characterization of whole-genome autosomal differences of DNA methylation between men and women. <i>Epigenetics and Chromatin</i> , 2015 , 8, 43	5.8	111
183	The influence of erythrocyte folate and serum vitamin B12 status on birth weight. <i>British Journal of Nutrition</i> , 2005 , 93, 593-9	3.6	101
182	Approaches for drawing causal inferences from epidemiological birth cohorts: a review. <i>Early Human Development</i> , 2014 , 90, 769-80	2.2	91
181	Longitudinal analysis of DNA methylation associated with birth weight and gestational age. <i>Human Molecular Genetics</i> , 2015 , 24, 3752-63	5.6	91
180	Epigenome-wide meta-analysis of DNA methylation and childhood asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2019 , 143, 2062-2074	11.5	87
179	DNA methylation changes measured in pre-diagnostic peripheral blood samples are associated with smoking and lung cancer risk. <i>International Journal of Cancer</i> , 2017 , 140, 50-61	7.5	83
178	(cg05575921) hypomethylation marks smoking behaviour, morbidity and mortality. <i>Thorax</i> , 2017 , 72, 646-653	7.3	82
177	Meta-analysis of epigenome-wide association studies in neonates reveals widespread differential DNA methylation associated with birthweight. <i>Nature Communications</i> , 2019 , 10, 1893	17.4	79
176	Low erythrocyte folate status and polymorphic variation in folate-related genes are associated with risk of neural tube defect pregnancy. <i>Molecular Genetics and Metabolism</i> , 2004 , 81, 273-81	3.7	77
175	MR-Base: a platform for systematic causal inference across the phenome using billions of genetic associations		77
174	DNA Methylation and BMI: Investigating Identified Methylation Sites at HIF3A in a Causal Framework. <i>Diabetes</i> , 2016 , 65, 1231-44	0.9	76

173	Age-related DNA methylation changes are tissue-specific with ELOVL2 promoter methylation as exception. <i>Epigenetics and Chromatin</i> , 2018 , 11, 25	5.8	76
172	Psychosocial adversity and socioeconomic position during childhood and epigenetic age: analysis of two prospective cohort studies. <i>Human Molecular Genetics</i> , 2018 , 27, 1301-1308	5.6	75
171	Role of obesity in smoking behaviour: Mendelian randomisation study in UK Biobank. <i>BMJ, The</i> , 2018 , 361, k1767	5.9	66
170	DNA methylation as a marker for prenatal smoke exposure in adults. <i>International Journal of Epidemiology</i> , 2018 , 47, 1120-1130	7.8	64
169	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. <i>International Journal of Epidemiology</i> , 2018 , 47, 22-23u	7.8	62
168	An epigenome-wide association meta-analysis of prenatal maternal stress in neonates: A model approach for replication. <i>Epigenetics</i> , 2016 , 11, 140-9	5.7	62
167	The epigenetic clock and physical development during childhood and adolescence: longitudinal analysis from a UK birth cohort. <i>International Journal of Epidemiology</i> , 2017 , 46, 549-558	7.8	60
166	Distinct DNA methylation profiles in subtypes of orofacial cleft. <i>Clinical Epigenetics</i> , 2017 , 9, 63	7.7	58
165	Obesity, metabolic factors and risk of different histological types of lung cancer: A Mendelian randomization study. <i>PLoS ONE</i> , 2017 , 12, e0177875	3.7	56
164	DNA methylation signatures in cord blood associated with maternal gestational weight gain: results from the ALSPAC cohort. <i>BMC Research Notes</i> , 2014 , 7, 278	2.3	53
163	Alcohol intake and cardiovascular risk factors: A Mendelian randomisation study. <i>Scientific Reports</i> , 2015 , 5, 18422	4.9	52
162	Prenatal unhealthy diet, insulin-like growth factor 2 gene (IGF2) methylation, and attention deficit hyperactivity disorder symptoms in youth with early-onset conduct problems. <i>Journal of Child Psychology and Psychiatry and Allied Disciplines</i> , 2017 , 58, 19-27	7.9	51
161	The role of longitudinal cohort studies in epigenetic epidemiology: challenges and opportunities 2012 , 13, 246		50
160	Tracking the Epigenetic Clock Across the Human Life Course: A Meta-analysis of Longitudinal Cohort Data. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2019 , 74, 57-61	6.4	45
159	Mendelian Randomization Analysis Identifies CpG Sites as Putative Mediators for Genetic Influences on Cardiovascular Disease Risk. <i>American Journal of Human Genetics</i> , 2017 , 101, 590-602	11	44
158	Epigenome-wide association study of asthma and wheeze in childhood and adolescence. <i>Clinical Epigenetics</i> , 2017 , 9, 112	7.7	43
157	Maternal alcohol consumption and offspring DNA methylation: findings from six general population-based birth cohorts. <i>Epigenomics</i> , 2018 , 10, 27-42	4.4	43
156	Causal Inference in Cancer Epidemiology: What Is the Role of Mendelian Randomization?. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018 , 27, 995-1010	4	43

155	DNA methylation links prenatal smoking exposure to later life health outcomes in offspring. <i>Clinical Epigenetics</i> , 2019 , 11, 97	7.7	42
154	Adversity exposure during sensitive periods predicts accelerated epigenetic aging in children. <i>Psychoneuroendocrinology</i> , 2020 , 113, 104484	5	42
153	Mendelian randomization: applications and limitations in epigenetic studies. <i>Epigenomics</i> , 2015 , 7, 1239-43	4.1	41
152	Hypertensive Disorders of Pregnancy and DNA Methylation in Newborns. <i>Hypertension</i> , 2019 , 74, 375-388	5	40
151	Systematic Mendelian randomization framework elucidates hundreds of CpG sites which may mediate the influence of genetic variants on disease. <i>Human Molecular Genetics</i> , 2018 , 27, 3293-3304	5.6	40
150	Circulating Selenium and Prostate Cancer Risk: A Mendelian Randomization Analysis. <i>Journal of the National Cancer Institute</i> , 2018 , 110, 1035-1038	9.7	39
149	Association Between Genetically Proxied Inhibition of HMG-CoA Reductase and Epithelial Ovarian Cancer. <i>JAMA - Journal of the American Medical Association</i> , 2020 , 323, 646-655	27.4	38
148	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	14.4	37
147	Investigating causal relations between sleep traits and risk of breast cancer in women: mendelian randomisation study. <i>BMJ, The</i> , 2019 , 365, l2327	5.9	36
146	Breastfeeding effects on DNA methylation in the offspring: A systematic literature review. <i>PLoS ONE</i> , 2017 , 12, e0173070	3.7	36
145	Is high vitamin B12 status a cause of lung cancer?. <i>International Journal of Cancer</i> , 2019 , 145, 1499-1503	7.5	33
144	Newborn DNA-methylation, childhood lung function, and the risks of asthma and COPD across the life course. <i>European Respiratory Journal</i> , 2019 , 53,	13.6	32
143	The long-term impact of folic acid in pregnancy on offspring DNA methylation: follow-up of the Aberdeen Folic Acid Supplementation Trial (FAST). <i>International Journal of Epidemiology</i> , 2018 , 47, 928-937	7.8	32
142	Appraising the role of previously reported risk factors in epithelial ovarian cancer risk: A Mendelian randomization analysis. <i>PLoS Medicine</i> , 2019 , 16, e1002893	11.6	32
141	Appraising the causal relevance of DNA methylation for risk of lung cancer. <i>International Journal of Epidemiology</i> , 2019 , 48, 1493-1504	7.8	27
140	A transcriptome-wide Mendelian randomization study to uncover tissue-dependent regulatory mechanisms across the human phenome. <i>Nature Communications</i> , 2020 , 11, 185	17.4	27
139	Maternal pre-pregnancy obesity, offspring cord blood DNA methylation, and offspring cardiometabolic health in early childhood: an epigenome-wide association study. <i>Epigenetics</i> , 2019 , 14, 325-340	5.7	27
138	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021 , 53, 1311-1321	36.3	27

137	Neonatal DNA methylation and early-onset conduct problems: A genome-wide, prospective study. <i>Development and Psychopathology</i> , 2018 , 30, 383-397	4.3	26
136	Epigenetics and gestational diabetes: a review of epigenetic epidemiology studies and their use to explore epigenetic mediation and improve prediction. <i>Diabetologia</i> , 2019 , 62, 2171-2178	10.3	26
135	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. <i>Nature Genetics</i> , 2020 , 52, 1314-1332	36.3	26
134	Role of DNA Methylation in Type 2 Diabetes Etiology: Using Genotype as a Causal Anchor. <i>Diabetes</i> , 2017 , 66, 1713-1722	0.9	25
133	The effect of body mass index on smoking behaviour and nicotine metabolism: a Mendelian randomization study. <i>Human Molecular Genetics</i> , 2019 , 28, 1322-1330	5.6	25
132	Comparison of smoking-related DNA methylation between newborns from prenatal exposure and adults from personal smoking. <i>Epigenomics</i> , 2019 , 11, 1487-1500	4.4	24
131	Are objective measures of physical capability related to accelerated epigenetic age? Findings from a British birth cohort. <i>BMJ Open</i> , 2017 , 7, e016708	3	24
130	The causal relevance of body mass index in different histological types of lung cancer: A Mendelian randomization study. <i>Scientific Reports</i> , 2016 , 6, 31121	4.9	23
129	A randomized controlled trial of folic acid intervention in pregnancy highlights a putative methylation-regulated control element at ZFP57. <i>Clinical Epigenetics</i> , 2019 , 11, 31	7.7	22
128	DNA methylation as a potential mediator of environmental risks in the development of childhood acute lymphoblastic leukemia. <i>Epigenomics</i> , 2016 , 8, 519-36	4.4	21
127	Sex discordance in asthma and wheeze prevalence in two longitudinal cohorts. <i>PLoS ONE</i> , 2017 , 12, e0176293	16.293	20
126	Prioritizing putative influential genes in cardiovascular disease susceptibility by applying tissue-specific Mendelian randomization. <i>Genome Medicine</i> , 2019 , 11, 6	14.4	19
125	Inflammation-related epigenetic risk and child and adolescent mental health: A prospective study from pregnancy to middle adolescence. <i>Development and Psychopathology</i> , 2018 , 30, 1145-1156	4.3	19
124	Association of maternal prenatal smoking GFI1-locus and cardio-metabolic phenotypes in 18,212 adults. <i>EBioMedicine</i> , 2018 , 38, 206-216	8.8	19
123	Maternal smoking during pregnancy and autism: using causal inference methods in a birth cohort study. <i>Translational Psychiatry</i> , 2018 , 8, 262	8.6	19
122	Associations between high blood pressure and DNA methylation. <i>PLoS ONE</i> , 2020 , 15, e0227728	3.7	18
121	Longitudinal epigenetic predictors of amygdala:hippocampus volume ratio. <i>Journal of Child Psychology and Psychiatry and Allied Disciplines</i> , 2017 , 58, 1341-1350	7.9	17
120	Genetic and observational evidence supports a causal role of sex hormones on the development of asthma. <i>Thorax</i> , 2019 , 74, 633-642	7.3	17

119	DNA Methylome Marks of Exposure to Particulate Matter at Three Time Points in Early Life. <i>Environmental Science & Technology</i> , 2018 , 52, 5427-5437	10.3	17
118	A Phenome-Wide Mendelian Randomization Study of Pancreatic Cancer Using Summary Genetic Data. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019 , 28, 2070-2078	4	17
117	Author response: The MR-Base platform supports systematic causal inference across the human phenome 2018 ,		17
116	Association between DNA methylation and ADHD symptoms from birth to school age: a prospective meta-analysis. <i>Translational Psychiatry</i> , 2020 , 10, 398	8.6	17
115	Adverse childhood experiences, DNA methylation age acceleration, and cortisol in UK children: a prospective population-based cohort study. <i>Clinical Epigenetics</i> , 2020 , 12, 55	7.7	17
114	Meffil: efficient normalisation and analysis of very large DNA methylation samples		16
113	Characterizing the Causal Pathway for Genetic Variants Associated with Neurological Phenotypes Using Human Brain-Derived Proteome Data. <i>American Journal of Human Genetics</i> , 2020 , 106, 885-892	11	15
112	Genome-wide survey of parent-of-origin effects on DNA methylation identifies candidate imprinted loci in humans. <i>Human Molecular Genetics</i> , 2018 , 27, 2927-2939	5.6	15
111	DNA methylation and body mass index from birth to adolescence: meta-analyses of epigenome-wide association studies. <i>Genome Medicine</i> , 2020 , 12, 105	14.4	15
110	Associations of maternal dietary inflammatory potential and quality with offspring birth outcomes: An individual participant data pooled analysis of 7 European cohorts in the ALPHABET consortium. <i>PLoS Medicine</i> , 2021 , 18, e1003491	11.6	15
109	Maternal dietary quality, inflammatory potential and childhood adiposity: an individual participant data pooled analysis of seven European cohorts in the ALPHABET consortium. <i>BMC Medicine</i> , 2021 , 19, 33	11.4	15
108	Epigenome-wide change and variation in DNA methylation in childhood: trajectories from birth to late adolescence. <i>Human Molecular Genetics</i> , 2021 , 30, 119-134	5.6	15
107	Identification of loci where DNA methylation potentially mediates genetic risk of type 1 diabetes. <i>Journal of Autoimmunity</i> , 2018 , 93, 66-75	15.5	14
106	Folic acid supplementation and social deprivation. <i>Public Health Nutrition</i> , 2005 , 8, 338-40	3.3	14
105	Sex-associated autosomal DNA methylation differences are wide-spread and stable throughout childhood		14
104	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021 , 22, 194	18.3	14
103	Evidence for DNA methylation mediating genetic liability to non-syndromic cleft lip/palate. <i>Epigenomics</i> , 2019 , 11, 133-145	4.4	14
102	Circulating concentrations of biomarkers and metabolites related to vitamin status, one-carbon and the kynurenine pathways in US, Nordic, Asian, and Australian populations. <i>American Journal of Clinical Nutrition</i> , 2017 , 105, 1314-1326	7	13

101	A structural equation modelling approach to explore the role of B vitamins and immune markers in lung cancer risk. <i>European Journal of Epidemiology</i> , 2013 , 28, 677-88	12.1	13
100	High COVID-19 transmission potential associated with re-opening universities can be mitigated with layered interventions		13
99	Investigating the impact of cigarette smoking behaviours on DNA methylation patterns in adolescence. <i>Human Molecular Genetics</i> , 2019 , 28, 155-165	5.6	13
98	The EWAS Catalog: a database of epigenome-wide association studies		13
97	A Methylome-Wide Association Study of Trajectories of Oppositional Defiant Behaviors and Biological Overlap With Attention Deficit Hyperactivity Disorder. <i>Child Development</i> , 2018 , 89, 1839-1855	4.9	13
96	Cleft lip/palate and educational attainment: cause, consequence or correlation? A Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2020 , 49, 1282-1293	7.8	12
95	Smoking, DNA Methylation, and Lung Function: a Mendelian Randomization Analysis to Investigate Causal Pathways. <i>American Journal of Human Genetics</i> , 2020 , 106, 315-326	11	12
94	Exploring the utility of alcohol flushing as an instrumental variable for alcohol intake in Koreans. <i>Scientific Reports</i> , 2018 , 8, 458	4.9	12
93	COVID-19 transmission in a university setting: a rapid review of modelling studies		12
92	The association of DNA methylation with body mass index: distinguishing between predictors and biomarkers. <i>Clinical Epigenetics</i> , 2020 , 12, 50	7.7	12
91	Use of Mendelian randomization for identifying risk factors for rain storms. <i>Frontiers in Genetics</i> , 2018 , 9, 525	4.5	12
90	Autosomal genetic variation is associated with DNA methylation in regions variably escaping X-chromosome inactivation. <i>Nature Communications</i> , 2018 , 9, 3738	17.4	12
89	Contacts and behaviours of university students during the COVID-19 pandemic at the start of the 2020/2021 academic year. <i>Scientific Reports</i> , 2021 , 11, 11728	4.9	11
88	Changes in DNA methylation from pre- to post-adolescence are associated with pubertal exposures. <i>Clinical Epigenetics</i> , 2019 , 11, 176	7.7	11
87	The Value of Biosamples in Smoking Cessation Trials: A Review of Genetic, Metabolomic, and Epigenetic Findings. <i>Nicotine and Tobacco Research</i> , 2018 , 20, 403-413	4.9	10
86	Deriving the Dietary Approaches to Stop Hypertension (DASH) Score in Women from Seven Pregnancy Cohorts from the European ALPHABET Consortium. <i>Nutrients</i> , 2019 , 11,	6.7	10
85	Exploring a potential mechanistic role of DNA methylation in the relationship between in utero and post-natal environmental exposures and risk of childhood acute lymphoblastic leukaemia. <i>International Journal of Cancer</i> , 2019 , 145, 2933-2943	7.5	9
84	Impaired functional vitamin B6 status is associated with increased risk of lung cancer. <i>International Journal of Cancer</i> , 2018 , 142, 2425-2434	7.5	9

83	DNA Methylation Signatures of Breastfeeding in Buccal Cells Collected in Mid-Childhood. <i>Nutrients</i> , 2019 , 11,	6.7	9
82	Associations of sex hormone-binding globulin and testosterone with genome-wide DNA methylation. <i>BMC Genetics</i> , 2018 , 19, 113	2.6	9
81	DNA methylation derived systemic inflammation indices are associated with head and neck cancer development and survival. <i>Oral Oncology</i> , 2018 , 85, 87-94	4.4	9
80	Leveraging brain cortex-derived molecular data to elucidate epigenetic and transcriptomic drivers of complex traits and disease. <i>Translational Psychiatry</i> , 2019 , 9, 105	8.6	8
79	Longitudinal analysis strategies for modelling epigenetic trajectories. <i>International Journal of Epidemiology</i> , 2018 , 47, 516-525	7.8	8
78	An integrative approach to detect epigenetic mechanisms that putatively mediate the influence of lifestyle exposures on disease susceptibility. <i>International Journal of Epidemiology</i> , 2019 , 48, 887-898	7.8	8
77	Epigenomics of being bullied: changes in DNA methylation following bullying exposure. <i>Epigenetics</i> , 2020 , 15, 750-764	5.7	8
76	Genome-wide association studies identify 137 loci for DNA methylation biomarkers of ageing		8
75	Differential methylation of the type 2 diabetes susceptibility locus KCNQ1 is associated with insulin sensitivity and is predicted by CpG site specific genetic variation. <i>Diabetes Research and Clinical Practice</i> , 2019 , 148, 189-199	7.4	8
74	Changes of DNA methylation are associated with changes in lung function during adolescence. <i>Respiratory Research</i> , 2020 , 21, 80	7.3	8
73	DNA methylation of blood cells is associated with prevalent type 2 diabetes in a meta-analysis of four European cohorts. <i>Clinical Epigenetics</i> , 2021 , 13, 40	7.7	8
72	Assessing the Role of DNA Methylation-Derived Neutrophil-to-Lymphocyte Ratio in Rheumatoid Arthritis. <i>Journal of Immunology Research</i> , 2018 , 2018, 2624981	4.5	8
71	Using Openly Accessible Resources to Strengthen Causal Inference in Epigenetic Epidemiology of Neurodevelopment and Mental Health. <i>Genes</i> , 2019 , 10,	4.2	7
70	Epigenome-wide association study of asthma and wheeze characterizes loci within. <i>Allergy, Asthma and Clinical Immunology</i> , 2019 , 15, 43	3.2	7
69	Genomic and phenomic insights from an atlas of genetic effects on DNA methylation		7
68	Collapsed methylation quantitative trait loci analysis for low frequency and rare variants. <i>Human Molecular Genetics</i> , 2016 , 25, 4339-4349	5.6	7
67	Association between Breastfeeding and DNA Methylation over the Life Course: Findings from the Avon Longitudinal Study of Parents and Children (ALSPAC). <i>Nutrients</i> , 2020 , 12,	6.7	6
66	Maternal anxiety during pregnancy and newborn epigenome-wide DNA methylation. <i>Molecular Psychiatry</i> , 2021 , 26, 1832-1845	15.1	6

65	Residential exposure to radon and DNA methylation across the lifecourse: an exploratory study in the ALSPAC birth cohort. <i>Wellcome Open Research</i> , 2019 , 4, 3	4.8	5
64	Epigenome-wide association study of seizures in childhood and adolescence. <i>Clinical Epigenetics</i> , 2020 , 12, 8	7.7	5
63	Assessing the role of genome-wide DNA methylation between smoking and risk of lung cancer using repeated measurements: the HUNT study. <i>International Journal of Epidemiology</i> , 2021 , 50, 1482-1497	7.8	5
62	DNA Methylation and Type 2 Diabetes: the Use of Mendelian Randomization to Assess Causality. <i>Current Genetic Medicine Reports</i> , 2019 , 7, 191-207	2.2	5
61	DNA methylation at birth is associated with lung function development until age 26 years. <i>European Respiratory Journal</i> , 2021 , 57,	13.6	5
60	Dietary Quality and Dietary Inflammatory Potential During Pregnancy and Offspring Emotional and Behavioral Symptoms in Childhood: An Individual Participant Data Meta-analysis of Four European Cohorts. <i>Biological Psychiatry</i> , 2021 , 89, 550-559	7.9	5
59	Identifying epigenetic biomarkers of established prognostic factors and survival in a clinical cohort of individuals with oropharyngeal cancer. <i>Clinical Epigenetics</i> , 2020 , 12, 95	7.7	4
58	Migration and DNA methylation: a comparison of methylation patterns in type 2 diabetes susceptibility genes between indians and europeans. <i>Journal of Diabetes Research & Clinical Metabolism</i> , 2013 , 2, 6	0	4
57	Residential exposure to radon and DNA methylation across the lifecourse: an exploratory study in the ALSPAC birth cohort. <i>Wellcome Open Research</i> , 2019 , 4, 3	4.8	4
56	Investigating the added value of biomarkers compared with self-reported smoking in predicting future e-cigarette use: Evidence from a longitudinal UK cohort study		4
55	Pre-adolescence DNA methylation is associated with lung function trajectories from pre-adolescence to adulthood. <i>Clinical Epigenetics</i> , 2021 , 13, 5	7.7	4
54	Multi-omics analyses of cognitive traits and psychiatric disorders highlights brain-dependent mechanisms. <i>Human Molecular Genetics</i> , 2021 ,	5.6	4
53	Impact of sex hormone-binding globulin on the human phenome. <i>Human Molecular Genetics</i> , 2020 , 29, 1824-1832	5.6	3
52	Birth weight and early socio-economic disadvantage as predictors of sex hormones and sex hormone binding globulin in men at age 49-51 years. <i>American Journal of Human Biology</i> , 2011 , 23, 185-92.7		3
51	The EWAS Catalog: a database of epigenome-wide association studies.. <i>Wellcome Open Research</i> , 2022 , 7, 41	4.8	3
50	Epigenetic modelling of former, current and never smokers. <i>Clinical Epigenetics</i> , 2021 , 13, 206	7.7	3
49	Contacts and behaviours of university students during the COVID-19 pandemic at the start of the 2020/21 academic year		3
48	Systematic evaluation of the causal relationship between DNA methylation and C-reactive protein		3

47	DNA methylation signature of passive smoke exposure is less pronounced than active smoking: The Understanding Society study. <i>Environmental Research</i> , 2020 , 190, 109971	7.9	3
46	"Environmental risk factors associated with juvenile idiopathic arthritis associated uveitis: a systematic review of the literature". <i>Journal of Ophthalmic Inflammation and Infection</i> , 2021 , 11, 15	2.3	3
45	Epigenetic prediction of complex traits and mortality in a cohort of individuals with oropharyngeal cancer. <i>Clinical Epigenetics</i> , 2020 , 12, 58	7.7	3
44	Maternal diet in pregnancy and child's respiratory outcomes: an individual participant data meta-analysis of 18 000 children. <i>European Respiratory Journal</i> , 2021 ,	13.6	3
43	Epigenetic profiling of social communication trajectories and co-occurring mental health problems: a prospective, methylome-wide association study. <i>Development and Psychopathology</i> , 2021 , 1-10	4.3	3
42	DNA methylation-based predictors of health: applications and statistical considerations.. <i>Nature Reviews Genetics</i> , 2022 ,	30.1	3
41	Causal relationships between lipid and glycemic levels in an Indian population: A bidirectional Mendelian randomization approach. <i>PLoS ONE</i> , 2020 , 15, e0228269	3.7	2
40	Meta-analysis of epigenome-wide associations between DNA methylation at birth and childhood cognitive skills.. <i>Molecular Psychiatry</i> , 2022 ,	15.1	2
39	A Combined Proteomics and Mendelian Randomization Approach to Investigate the Effects of Aspirin-Targeted Proteins on Colorectal Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021 , 30, 564-575	4	2
38	Paternal body mass index and offspring DNA methylation: findings from the PACE consortium		2
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