

Calen P Ryan

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.

152 papers	5,639 citations	42 h-index	72 g-index
156 ext. papers	7,533 ext. citations	6.7 avg, IF	6 L-index

#	Paper	IF	Citations
152	DNA methylation and healthy human aging. <i>Aging Cell</i> , 2015 , 14, 924-32	9.9	454
151	An epigenetic clock analysis of race/ethnicity, sex, and coronary heart disease. <i>Genome Biology</i> , 2016 , 17, 171	18.3	357
150	Additional annotation enhances potential for biologically-relevant analysis of the Illumina Infinium HumanMethylation450 BeadChip array. <i>Epigenetics and Chromatin</i> , 2013 , 6, 4	5.8	349
149	Factors underlying variable DNA methylation in a human community cohort. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109 Suppl 2, 17253-60	11.5	346
148	The effect of genotype and in utero environment on interindividual variation in neonate DNA methylomes. <i>Genome Research</i> , 2014 , 24, 1064-74	9.7	253
147	Reversal of epigenetic aging and immunosenescent trends in humans. <i>Aging Cell</i> , 2019 , 18, e13028	9.9	174
146	Genome-wide profiling of yeast DNA:RNA hybrid prone sites with DRIP-chip. <i>PLoS Genetics</i> , 2014 , 10, e1004288	6	153
145	Landscape of DNA methylation on the X chromosome reflects CpG density, functional chromatin state and X-chromosome inactivation. <i>Human Molecular Genetics</i> , 2015 , 24, 1528-39	5.6	151
144	Bacterial infection remodels the DNA methylation landscape of human dendritic cells. <i>Genome Research</i> , 2015 , 25, 1801-11	9.7	138
143	Greater inflammatory activity and blunted glucocorticoid signaling in monocytes of chronically stressed caregivers. <i>Brain, Behavior, and Immunity</i> , 2014 , 41, 191-9	16.6	116
142	Concordant and discordant DNA methylation signatures of aging in human blood and brain. <i>Epigenetics and Chromatin</i> , 2015 , 8, 19	5.8	99
141	DNA methylation signature of human fetal alcohol spectrum disorder. <i>Epigenetics and Chromatin</i> , 2016 , 9, 25	5.8	93
140	Inhalation of diesel exhaust and allergen alters human bronchial epithelium DNA methylation. <i>Journal of Allergy and Clinical Immunology</i> , 2017 , 139, 112-121	11.5	90
139	Development and the epigenome: the 'synapse' of gene-environment interplay. <i>Developmental Science</i> , 2015 , 18, 1-23	4.5	89
138	Leishmania donovani infection causes distinct epigenetic DNA methylation changes in host macrophages. <i>PLoS Pathogens</i> , 2014 , 10, e1004419	7.6	83
137	Social and physical environments early in development predict DNA methylation of inflammatory genes in young adulthood. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 7611-7616	11.5	79
136	Improving cell mixture deconvolution by identifying optimal DNA methylation libraries (IDOL). <i>BMC Bioinformatics</i> , 2016 , 17, 120	3.6	74

135	Developmental pathways to adiposity begin before birth and are influenced by genotype, prenatal environment and epigenome. <i>BMC Medicine</i> , 2017 , 15, 50	11.4	67
134	Short-term diesel exhaust inhalation in a controlled human crossover study is associated with changes in DNA methylation of circulating mononuclear cells in asthmatics. <i>Particle and Fibre Toxicology</i> , 2014 , 11, 71	8.4	67
133	Perinatally acquired HIV infection accelerates epigenetic aging in South African adolescents. <i>Aids</i> , 2018 , 32, 1465-1474	3.5	64
132	Epigenetics studies of fetal alcohol spectrum disorder: where are we now?. <i>Epigenomics</i> , 2017 , 9, 291-311	11.4	63
131	Epigenetic correlates of neonatal contact in humans. <i>Development and Psychopathology</i> , 2017 , 29, 1517-1538	15.38	60
130	Different measures of "genome-wide" DNA methylation exhibit unique properties in placental and somatic tissues. <i>Epigenetics</i> , 2012 , 7, 652-63	5.7	60
129	The biological embedding of early-life socioeconomic status and family adversity in children's genome-wide DNA methylation. <i>Epigenomics</i> , 2018 , 10, 1445-1461	4.4	60
128	RECQ-like helicases Sgs1 and BLM regulate R-loop-associated genome instability. <i>Journal of Cell Biology</i> , 2017 , 216, 3991-4005	7.3	58
127	Systematic evaluation of DNA methylation age estimation with common preprocessing methods and the Infinium MethylationEPIC BeadChip array. <i>Clinical Epigenetics</i> , 2018 , 10, 123	7.7	58
126	DNA methylation as a predictor of fetal alcohol spectrum disorder. <i>Clinical Epigenetics</i> , 2018 , 10, 5	7.7	57
125	The epigenomic landscape of African rainforest hunter-gatherers and farmers. <i>Nature Communications</i> , 2015 , 6, 10047	17.4	55
124	HIF3A association with adiposity: the story begins before birth. <i>Epigenomics</i> , 2015 , 7, 937-50	4.4	55
123	Integrated analysis of environmental and genetic influences on cord blood DNA methylation in new-borns. <i>Nature Communications</i> , 2019 , 10, 2548	17.4	54
122	The PedBE clock accurately estimates DNA methylation age in pediatric buccal cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 23329-23335	11.5	53
121	Natural variation in maternal care and cross-tissue patterns of oxytocin receptor gene methylation in rats. <i>Hormones and Behavior</i> , 2016 , 77, 42-52	3.7	52
120	Biological embedding of experience: A primer on epigenetics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 23261-23269	11.5	52
119	Early-life socioeconomic disadvantage, not current, predicts accelerated epigenetic aging of monocytes. <i>Psychoneuroendocrinology</i> , 2018 , 97, 131-134	5	51
118	Discordance of DNA methylation variance between two accessible human tissues. <i>Scientific Reports</i> , 2015 , 5, 8257	4.9	46

117	Associations between maternal risk factors of adverse pregnancy and birth outcomes and the offspring epigenetic clock of gestational age at birth. <i>Clinical Epigenetics</i> , 2017 , 9, 49	7.7	45
116	Trends in DNA Methylation with Age Replicate Across Diverse Human Populations. <i>Genetics</i> , 2017 , 206, 1659-1674	4	44
115	Systematic evaluation and validation of reference and library selection methods for deconvolution of cord blood DNA methylation data. <i>Clinical Epigenetics</i> , 2019 , 11, 125	7.7	44
114	Exploring the genetic basis of human population differences in DNA methylation and their causal impact on immune gene regulation. <i>Genome Biology</i> , 2018 , 19, 222	18.3	44
113	Exposure to childhood abuse is associated with human sperm DNA methylation. <i>Translational Psychiatry</i> , 2018 , 8, 194	8.6	44
112	Genome-wide analysis of DNA methylation in relation to socioeconomic status during development and early adulthood. <i>American Journal of Physical Anthropology</i> , 2019 , 169, 3-11	2.5	43
111	Principles and Challenges of Applying Epigenetic Epidemiology to Psychology. <i>Annual Review of Psychology</i> , 2018 , 69, 459-485	26.1	42
110	Nucleated red blood cells impact DNA methylation and expression analyses of cord blood hematopoietic cells. <i>Clinical Epigenetics</i> , 2015 , 7, 95	7.7	41
109	The Intersection of Aging Biology and the Pathobiology of Lung Diseases: A Joint NHLBI/NIA Workshop. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2017 , 72, 1492-1500	6.4	40
108	Adjusting for Cell Type Composition in DNA Methylation Data Using a Regression-Based Approach. <i>Methods in Molecular Biology</i> , 2017 , 1589, 99-106	1.4	38
107	DNA methylation profiling in human Huntington's disease brain. <i>Human Molecular Genetics</i> , 2016 , 25, 2013-2030	5.6	37
106	Human T-bet Governs Innate and Innate-like Adaptive IFN- γ Immunity against Mycobacteria. <i>Cell</i> , 2020 , 183, 1826-1847.e31	56.2	35
105	Comparison of Methyl-capture Sequencing vs. Infinium 450K methylation array for methylome analysis in clinical samples. <i>Epigenetics</i> , 2016 , 11, 36-48	5.7	35
104	Comparison of DNA methylation measured by Illumina 450K and EPIC BeadChips in blood of newborns and 14-year-old children. <i>Epigenetics</i> , 2018 , 13, 655-664	5.7	35
103	MRE11-RAD50-NBS1 promotes Fanconi Anemia R-loop suppression at transcription-replication conflicts. <i>Nature Communications</i> , 2019 , 10, 4265	17.4	32
102	Epigenetics: A New Model for Intracellular Parasite-Host Cell Regulation. <i>Trends in Parasitology</i> , 2016 , 32, 515-521	6.4	32
101	Maternal blood contamination of collected cord blood can be identified using DNA methylation at three CpGs. <i>Clinical Epigenetics</i> , 2017 , 9, 75	7.7	31
100	Reproduction predicts shorter telomeres and epigenetic age acceleration among young adult women. <i>Scientific Reports</i> , 2018 , 8, 11100	4.9	31

99	The role of testosterone in coordinating male life history strategies: The moderating effects of the androgen receptor CAG repeat polymorphism. <i>Hormones and Behavior</i> , 2017 , 87, 164-175	3.7	31
98	Agreement in DNA methylation levels from the Illumina 450K array across batches, tissues, and time. <i>Epigenetics</i> , 2018 , 13, 19-32	5.7	28
97	Gestational intermittent hypoxia induces endothelial dysfunction, reduces perivascular adiponectin and causes epigenetic changes in adult male offspring. <i>Journal of Physiology</i> , 2019 , 597, 5349-5364	3.9	27
96	A biologically-informed polygenic score identifies endophenotypes and clinical conditions associated with the insulin receptor function on specific brain regions. <i>EBioMedicine</i> , 2019 , 42, 188-202	8.8	27
95	DNA methylation of HPA-axis genes and the onset of major depressive disorder in adolescent girls: a prospective analysis. <i>Translational Psychiatry</i> , 2019 , 9, 245	8.6	25
94	Integration of DNA methylation patterns and genetic variation in human pediatric tissues help inform EWAS design and interpretation. <i>Epigenetics and Chromatin</i> , 2019 , 12, 1	5.8	25
93	Hsp90 and Physiological Stress Are Linked to Autonomous Transposon Mobility and Heritable Genetic Change in Nematodes. <i>Genome Biology and Evolution</i> , 2016 , 8, 3794-3805	3.9	24
92	Comprehensive genomic profiling of glioblastoma tumors, BTICs, and xenografts reveals stability and adaptation to growth environments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 19098-19108	11.5	23
91	An empirically driven data reduction method on the human 450K methylation array to remove tissue specific non-variable CpGs. <i>Clinical Epigenetics</i> , 2017 , 9, 11	7.7	22
90	Maternal dysglycaemia, changes in the infant's epigenome modified with a diet and physical activity intervention in pregnancy: Secondary analysis of a randomised control trial. <i>PLoS Medicine</i> , 2020 , 17, e1003229	11.6	22
89	Cell type-specific DNA methylation in neonatal cord tissue and cord blood: a 850K-reference panel and comparison of cell types. <i>Epigenetics</i> , 2018 , 13, 941-958	5.7	22
88	Altered DNA methylation is associated with aberrant gene expression in parenchymal but not airway fibroblasts isolated from individuals with COPD. <i>Clinical Epigenetics</i> , 2018 , 10, 32	7.7	20
87	Worldwide patterns of human epigenetic variation. <i>Nature Ecology and Evolution</i> , 2017 , 1, 1577-1583	12.3	20
86	A pooling-based approach to mapping genetic variants associated with DNA methylation. <i>Genome Research</i> , 2015 , 25, 907-17	9.7	18
85	Choice of surrogate tissue influences neonatal EWAS findings. <i>BMC Medicine</i> , 2017 , 15, 211	11.4	18
84	Differential DNA methylation and lymphocyte proportions in a Costa Rican high longevity region. <i>Epigenetics and Chromatin</i> , 2017 , 10, 21	5.8	18
83	funtooNorm: an R package for normalization of DNA methylation data when there are multiple cell or tissue types. <i>Bioinformatics</i> , 2016 , 32, 593-5	7.2	17
82	Molecular pathways underpinning ethanol-induced neurodegeneration. <i>Frontiers in Genetics</i> , 2014 , 5, 203	4.5	17

81	Prenatal Alcohol Exposure: Profiling Developmental DNA Methylation Patterns in Central and Peripheral Tissues. <i>Frontiers in Genetics</i> , 2018 , 9, 610	4.5	17
80	Dynamic DNA methylation changes in the maternal oxytocin gene locus (OXT) during pregnancy predict postpartum maternal intrusiveness. <i>Psychoneuroendocrinology</i> , 2019 , 103, 156-162	5	16
79	Analysis of two birth tissues provides new insights into the epigenetic landscape of neonates born preterm. <i>Clinical Epigenetics</i> , 2019 , 11, 26	7.7	15
78	Exploring genetic influences underlying acute aerobic exercise effects on motor learning. <i>Scientific Reports</i> , 2017 , 7, 12123	4.9	15
77	Androgen receptor polyglutamine repeat number: models of selection and disease susceptibility. <i>Evolutionary Applications</i> , 2013 , 6, 180-96	4.8	14
76	The relation between DNA methylation patterns and serum cytokine levels in community-dwelling adults: a preliminary study. <i>BMC Genetics</i> , 2017 , 18, 57	2.6	14
75	H2A.Z and DNA methylation: irreconcilable differences. <i>Trends in Biochemical Sciences</i> , 2009 , 34, 158-61	10.3	14
74	"Epigenetic clocks": Theory and applications in human biology. <i>American Journal of Human Biology</i> , 2021 , 33, e23488	2.7	13
73	Inflammation-related genes are associated with epigenetic aging in HIV. <i>Journal of NeuroVirology</i> , 2019 , 25, 853-865	3.9	12
72	Social Environment and Epigenetics. <i>Current Topics in Behavioral Neurosciences</i> , 2019 , 42, 83-126	3.4	11
71	Neonatal amygdalae and hippocampi are influenced by genotype and prenatal environment, and reflected in the neonatal DNA methylome. <i>Genes, Brain and Behavior</i> , 2019 , 18, e12576	3.6	11
70	Infinium monkeys: Infinium 450K array for the Cynomolgus macaque (<i>Macaca fascicularis</i>). <i>G3: Genes, Genomes, Genetics</i> , 2014 , 4, 1227-34	3.2	11
69	DNA methylation signatures in peripheral blood mononuclear cells from a lifestyle intervention for women at midlife: a pilot randomized controlled trial. <i>Applied Physiology, Nutrition and Metabolism</i> , 2018 , 43, 233-239	3	10
68	Rtt107 BRCT domains act as a targeting module in the DNA damage response. <i>DNA Repair</i> , 2016 , 37, 22-32	4.3	10
67	PRS-on-Spark (PRSoS): a novel, efficient and flexible approach for generating polygenic risk scores. <i>BMC Bioinformatics</i> , 2018 , 19, 295	3.6	10
66	Second-to-fourth digit ratio (2D:4D) is unrelated to measures of somatic reproductive effort among young men from Cebu, the Philippines. <i>American Journal of Physical Anthropology</i> , 2017 , 163, 437-445	2.5	9
65	A Role of Oxytocin Receptor Gene Brain Tissue Expression Quantitative Trait Locus rs237895 in the Intergenerational Transmission of the Effects of Maternal Childhood Maltreatment. <i>Journal of the American Academy of Child and Adolescent Psychiatry</i> , 2019 , 58, 1207-1216	7.2	9
64	DNA methylation patterns are related to co-morbidity status and circulating C-reactive protein levels in the nursing home elderly. <i>Experimental Gerontology</i> , 2018 , 105, 47-52	4.5	9

63	DNA methylation signatures of chronic alcohol dependence in purified CD3 T-cells of patients undergoing alcohol treatment. <i>Scientific Reports</i> , 2017 , 7, 6605	4.9	9
62	Conditional genetic interactions of RTT107, SLX4, and HRQ1 reveal dynamic networks upon DNA damage in <i>S. cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2014 , 4, 1059-69	3.2	9
61	Multi-Omic Data Integration Allows Baseline Immune Signatures to Predict Hepatitis B Vaccine Response in a Small Cohort. <i>Frontiers in Immunology</i> , 2020 , 11, 578801	8.4	9
60	Androgen receptor polyglutamine repeat length (AR-CAGn) modulates the effect of testosterone on androgen-associated somatic traits in Filipino young adult men. <i>American Journal of Physical Anthropology</i> , 2017 , 163, 317-327	2.5	8
59	Neonatal Alcohol Exposure in Mice Induces Select Differentiation- and Apoptosis-Related Chromatin Changes Both Independent of and Dependent on Sex. <i>Frontiers in Genetics</i> , 2020 , 11, 35	4.5	8
58	Genetic susceptibility to asthma increases the vulnerability to indoor air pollution. <i>European Respiratory Journal</i> , 2020 , 55,	13.6	8
57	Systems Biology Methods Applied to Blood and Tissue for a Comprehensive Analysis of Immune Response to Hepatitis B Vaccine in Adults. <i>Frontiers in Immunology</i> , 2020 , 11, 580373	8.4	8
56	Germline epigenetic inheritance: Challenges and opportunities for linking human paternal experience with offspring biology and health. <i>Evolutionary Anthropology</i> , 2020 , 29, 180-200	4.7	7
55	Epigenetic aging in children from a small-scale farming society in The Congo Basin: Associations with child growth and family conflict. <i>Developmental Psychobiology</i> , 2020 , 62, 138-153	3	7
54	Paternal adverse childhood experiences: Associations with infant DNA methylation. <i>Developmental Psychobiology</i> , 2021 , 63, e22174	3	7
53	Prenatal exposure to traffic-related air pollution, the gestational epigenetic clock, and risk of early-life allergic sensitization. <i>Journal of Allergy and Clinical Immunology</i> , 2019 , 144, 1729-1731.e5	11.5	6
52	Evolutionary life history theory as an organising framework for cohort studies: insights from the Cebu Longitudinal Health and Nutrition Survey. <i>Annals of Human Biology</i> , 2020 , 47, 94-105	1.7	6
51	Amygdala 5-HTT Gene Network Moderates the Effects of Postnatal Adversity on Attention Problems: Anatomic-Functional Correlation and Epigenetic Changes. <i>Frontiers in Neuroscience</i> , 2020 , 14, 198	5.1	6
50	DaVIE: Database for the Visualization and Integration of Epigenetic data. <i>Frontiers in Genetics</i> , 2014 , 5, 325	4.5	6
49	Parity predicts biological age acceleration in post-menopausal, but not pre-menopausal, women. <i>Scientific Reports</i> , 2020 , 10, 20522	4.9	6
48	Children's biobehavioral reactivity to challenge predicts DNA methylation in adolescence and emerging adulthood. <i>Developmental Science</i> , 2019 , 22, e12739	4.5	6
47	Occurrence of Accelerated Epigenetic Aging and Methylation Disruptions in Human Immunodeficiency Virus Infection Before Antiretroviral Therapy. <i>Journal of Infectious Diseases</i> , 2021 , 223, 1681-1689	7	6
46	Androgen receptor CAG repeat polymorphism and hypothalamic-pituitary-gonadal function in Filipino young adult males. <i>American Journal of Human Biology</i> , 2017 , 29, e22897	2.7	5

45	Regulation of Skn7-dependent, oxidative stress-induced genes by the RNA polymerase II-CTD phosphatase, Fcp1, and Mediator kinase subunit, Cdk8, in yeast. <i>Journal of Biological Chemistry</i> , 2019 , 294, 16080-16094	5.4	4
44	ISDN2014_0418: DNA methylation changes in fetal alcohol spectrum disorder. <i>International Journal of Developmental Neuroscience</i> , 2015 , 47, 126-126	2.7	4
43	Variability in DNA methylation at the serotonin transporter gene promoter: epigenetic mechanism or cell-type artifact?. <i>Molecular Psychiatry</i> , 2020 , 25, 1906-1909	15.1	4
42	Methylation of cysteinyl leukotriene receptor 1 genes associates with lung function in asthmatics exposed to traffic-related air pollution. <i>Epigenetics</i> , 2021 , 16, 177-185	5.7	4
41	DNA methylation differences associated with social anxiety disorder and early life adversity. <i>Translational Psychiatry</i> , 2021 , 11, 104	8.6	4
40	Optimized CRISPR-mediated gene knockin reveals FOXP3-independent maintenance of human Treg identity. <i>Cell Reports</i> , 2021 , 36, 109494	10.6	4
39	Airway epithelial cell isolation techniques affect DNA methylation profiles with consequences for analysis of asthma related perturbations to DNA methylation. <i>Scientific Reports</i> , 2019 , 9, 14409	4.9	3
38	A single flexible RNAPII-CTD integrates many different transcriptional programs. <i>Transcription</i> , 2016 , 7, 50-6	4.8	3
37	Associations of peripheral blood DNA methylation and estimated monocyte proportion differences during infancy with toddler attachment style. <i>Attachment and Human Development</i> , 2021 , 1-30	2.8	3
36	Prenatal alcohol exposure alters gene expression in the rat brain: Experimental design and bioinformatic analysis of microarray data. <i>Data in Brief</i> , 2015 , 4, 239-52	1.2	2
35	Epigenetic analysis of human postmortem brain tissue. <i>Handbook of Clinical Neurology / Edited By P J Vinken and G W Bruyn</i> , 2018 , 150, 237-261	3	2
34	The RNAPII-CTD Maintains Genome Integrity through Inhibition of Retrotransposon Gene Expression and Transposition. <i>PLoS Genetics</i> , 2015 , 11, e1005608	6	2
33	Association between maternal depression during pregnancy and newborn DNA methylation. <i>Translational Psychiatry</i> , 2021 , 11, 572	8.6	2
32	Dichotomy in the Impact of Elevated Maternal Glucose Levels on Neonatal Epigenome. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021 ,	5.6	2
31	TWIST1 DNA methylation is a cell marker of airway and parenchymal lung fibroblasts that are differentially methylated in asthma. <i>Clinical Epigenetics</i> , 2020 , 12, 145	7.7	2
30	Budding yeast Rtt107 prevents checkpoint hyperactivation after replicative stress by limiting DNA damage. <i>DNA Repair</i> , 2019 , 74, 1-16	4.3	2
29	Maternal Prenatal Anxiety and the Fetal Origins of Epigenetic Aging. <i>Biological Psychiatry</i> , 2021 ,	7.9	2
28	Epigenetic age is associated with baseline and 3-year change in frailty in the Canadian Longitudinal Study on Aging. <i>Clinical Epigenetics</i> , 2021 , 13, 163	7.7	2

27	Society to cell: How child poverty gets Under the Skin to influence child development and lifelong health. <i>Developmental Review</i> , 2021 , 61, 100983	7.4	2
26	Association between the FTO rs9939609 single nucleotide polymorphism and dietary adherence during a 2-year caloric restriction intervention: Exploratory analyses from CALERIE phase 2. <i>Experimental Gerontology</i> , 2021 , 155, 111555	4.5	2
25	Tandem repeat disorders. <i>Evolution, Medicine and Public Health</i> , 2019 , 2019, 17	3	1
24	Is early postnatal growth velocity, a proxy of minipubertal androgen action, related to adult second-to-fourth digit (2D:4D) ratios in men? A test in Cebu, Philippines. <i>American Journal of Human Biology</i> , 2017 , 29, e23047	2.7	1
23	What makes a histone variant a variant: Changing H2A to become H2A.Z. <i>PLoS Genetics</i> , 2021 , 17, e1009950	3.5	1
22	Newborn Differential DNA Methylation and Subcortical Brain Volumes as Early Signs of Severe Neurodevelopmental Delay in a South African Birth Cohort Study.. <i>World Journal of Biological Psychiatry</i> , 2021 , 1-31	3.8	1
21	Maternal antenatal depression and child mental health: Moderation by genomic risk for attention-deficit/hyperactivity disorder. <i>Development and Psychopathology</i> , 2020 , 32, 1810-1821	4.3	1
20	Maternal psychosocial risk factors and child gestational epigenetic age in a South African birth cohort study. <i>Translational Psychiatry</i> , 2021 , 11, 358	8.6	1
19	Internalizing symptoms associate with the pace of epigenetic aging in childhood. <i>Biological Psychology</i> , 2021 , 159, 108021	3.2	1
18	Epigenome-wide association study and epigenetic age acceleration associated with cigarette smoking among Costa Rican adults.. <i>Scientific Reports</i> , 2022 , 12, 4277	4.9	1
17	In-utero exposure to indoor air pollution or tobacco smoke and cognitive development in a South African birth cohort study.. <i>Science of the Total Environment</i> , 2022 , 155394	10.2	1
16	5-Hydroxymethylcytosine in cord blood and associations of DNA methylation with sex in newborns. <i>Mutagenesis</i> , 2019 , 34, 315-322	2.8	0
15	Immune cell type and DNA methylation vary with reproductive status in women: possible pathways for costs of reproduction.. <i>Evolution, Medicine and Public Health</i> , 2022 , 10, 47-58	3	0
14	Prefrontal cortex VAMP1 gene network moderates the effect of the early environment on cognitive flexibility in children. <i>Neurobiology of Learning and Memory</i> , 2021 , 185, 107509	3.1	0
13	Prenatal exposure to phthalates and peripheral blood and buccal epithelial DNA methylation in infants: An epigenome-wide association study.. <i>Environment International</i> , 2022 , 163, 107183	12.9	0
12	HIV, pathology and epigenetic age acceleration in different human tissues.. <i>GeroScience</i> , 2022 , 1	8.9	0
11	Birth weight and maternal energy status during pregnancy as predictors of epigenetic age acceleration in young adults from metropolitan Cebu, Philippines.. <i>Epigenetics</i> , 2022 , 1-11	5.7	0
10	ISDN2014_0378: Prenatal alcohol exposure alters the developmental methylation profile of the rat hypothalamus. <i>International Journal of Developmental Neuroscience</i> , 2015 , 47, 109-109	2.7	

- 9 Infant DNA methylation: an early indicator of intergenerational trauma?. *Early Human Development*, **2021**, 164, 105519 2.2
- 8 Reply to: Crossing the "Birth Border" for Epigenetic Effects.. *Biological Psychiatry*, **2022**, 7.9
- 7 Neural correlates of attentional control in social anxiety disorder: the impact of early-life adversity and DNA methylation.. *Journal of Psychiatry and Neuroscience*, **2021**, 46, E663-E674 4.5
- 6 Maternal dysglycaemia, changes in the infant's epigenome modified with a diet and physical activity intervention in pregnancy: Secondary analysis of a randomised control trial **2020**, 17, e1003229
- 5 Maternal dysglycaemia, changes in the infant's epigenome modified with a diet and physical activity intervention in pregnancy: Secondary analysis of a randomised control trial **2020**, 17, e1003229
- 4 Maternal dysglycaemia, changes in the infant's epigenome modified with a diet and physical activity intervention in pregnancy: Secondary analysis of a randomised control trial **2020**, 17, e1003229
- 3 Maternal dysglycaemia, changes in the infant's epigenome modified with a diet and physical activity intervention in pregnancy: Secondary analysis of a randomised control trial **2020**, 17, e1003229
- 2 Maternal dysglycaemia, changes in the infant's epigenome modified with a diet and physical activity intervention in pregnancy: Secondary analysis of a randomised control trial **2020**, 17, e1003229
- 1 Maternal dysglycaemia, changes in the infant's epigenome modified with a diet and physical activity intervention in pregnancy: Secondary analysis of a randomised control trial **2020**, 17, e1003229