

Calen P Ryan

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/2658272/calen-p-ryan-publications-by-year.pdf>

Version: 2024-04-10

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	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
151	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
150	Reply to: Crossing the "Birth Border" for Epigenetic Effects.. <i>Biological Psychiatry</i> , 2022 ,	7.9	
149	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
148	HIV, pathology and epigenetic age acceleration in different human tissues.. <i>GeroScience</i> , 2022 , 1	8.9	0
147	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
146	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
145	What makes a histone variant a variant: Changing H2A to become H2A.Z. <i>PLoS Genetics</i> , 2021 , 17, e1009950	15.0	1
144	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
143	Association between maternal depression during pregnancy and newborn DNA methylation. <i>Translational Psychiatry</i> , 2021 , 11, 572	8.6	2
142	Infant DNA methylation: an early indicator of intergenerational trauma?. <i>Early Human Development</i> , 2021 , 164, 105519	2.2	
141	Dichotomy in the Impact of Elevated Maternal Glucose Levels on Neonatal Epigenome. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021 ,	5.6	2
140	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
139	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
138	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
137	"Epigenetic clocks": Theory and applications in human biology. <i>American Journal of Human Biology</i> , 2021 , 33, e23488	2.7	13
136	DNA methylation differences associated with social anxiety disorder and early life adversity. <i>Translational Psychiatry</i> , 2021 , 11, 104	8.6	4

135	Internalizing symptoms associate with the pace of epigenetic aging in childhood. <i>Biological Psychology</i> , 2021 , 159, 108021	3.2	1
134	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
133	Maternal Prenatal Anxiety and the Fetal Origins of Epigenetic Aging. <i>Biological Psychiatry</i> , 2021 ,	7.9	2
132	Optimized CRISPR-mediated gene knockin reveals FOXP3-independent maintenance of human Treg identity. <i>Cell Reports</i> , 2021 , 36, 109494	10.6	4
131	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
130	Paternal adverse childhood experiences: Associations with infant DNA methylation. <i>Developmental Psychobiology</i> , 2021 , 63, e22174	3	7
129	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
128	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
127	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
126	Neural correlates of attentional control in social anxiety disorder: the impact of early-life adversity and DNA methylation.. <i>Journal of Psychiatry and Neuroscience</i> , 2021 , 46, E663-E674	4.5	
125	Human T-bet Governs Innate and Innate-like Adaptive IFN-Immunity against Mycobacteria. <i>Cell</i> , 2020 , 183, 1826-1847.e31	56.2	35
124	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
123	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
122	Amygdala 5-HTT Gene Network Moderates the Effects of Postnatal Adversity on Attention Problems: Anatomo-Functional Correlation and Epigenetic Changes. <i>Frontiers in Neuroscience</i> , 2020 , 14, 198	5.1	6
121	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
120	Genetic susceptibility to asthma increases the vulnerability to indoor air pollution. <i>European Respiratory Journal</i> , 2020 , 55,	13.6	8
119	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
118	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

117	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
116	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
115	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
114	Parity predicts biological age acceleration in post-menopausal, but not pre-menopausal, women. <i>Scientific Reports</i> , 2020 , 10, 20522	4.9	6
113	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
112	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
111	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
110	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
109	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		
108	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		
107	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		
106	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		
105	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		
104	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		
103	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
102	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
101	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
100	Social Environment and Epigenetics. <i>Current Topics in Behavioral Neurosciences</i> , 2019 , 42, 83-126	3.4	11

99	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
98	MRE11-RAD50-NBS1 promotes Fanconi Anemia R-loop suppression at transcription-replication conflicts. <i>Nature Communications</i> , 2019 , 10, 4265	17.4	32
97	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
96	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
95	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
94	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
93	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
92	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
91	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
90	Tandem repeat disorders. <i>Evolution, Medicine and Public Health</i> , 2019 , 2019, 17	3	1
89	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
88	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
87	Inflammation-related genes are associated with epigenetic aging in HIV. <i>Journal of NeuroVirology</i> , 2019 , 25, 853-865	3.9	12
86	Reversal of epigenetic aging and immunosenescent trends in humans. <i>Aging Cell</i> , 2019 , 18, e13028	9.9	174
85	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
84	5-Hydroxymethylcytosine in cord blood and associations of DNA methylation with sex in newborns. <i>Mutagenesis</i> , 2019 , 34, 315-322	2.8	0
83	Children's biobehavioral reactivity to challenge predicts DNA methylation in adolescence and emerging adulthood. <i>Developmental Science</i> , 2019 , 22, e12739	4.5	6
82	Budding yeast Rtt107 prevents checkpoint hyperactivation after replicative stress by limiting DNA damage. <i>DNA Repair</i> , 2019 , 74, 1-16	4.3	2

81	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
80	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
79	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
78	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
77	Principles and Challenges of Applying Epigenetic Epidemiology to Psychology. <i>Annual Review of Psychology</i> , 2018 , 69, 459-485	26.1	42
76	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
75	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
74	Reproduction predicts shorter telomeres and epigenetic age acceleration among young adult women. <i>Scientific Reports</i> , 2018 , 8, 11100	4.9	31
73	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
72	Early-life socioeconomic disadvantage, not current, predicts accelerated epigenetic aging of monocytes. <i>Psychoneuroendocrinology</i> , 2018 , 97, 131-134	5	51
71	DNA methylation as a predictor of fetal alcohol spectrum disorder. <i>Clinical Epigenetics</i> , 2018 , 10, 5	7.7	57
70	Perinatally acquired HIV infection accelerates epigenetic aging in South African adolescents. <i>Aids</i> , 2018 , 32, 1465-1474	3.5	64
69	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
68	Prenatal Alcohol Exposure: Profiling Developmental DNA Methylation Patterns in Central and Peripheral Tissues. <i>Frontiers in Genetics</i> , 2018 , 9, 610	4.5	17
67	Exposure to childhood abuse is associated with human sperm DNA methylation. <i>Translational Psychiatry</i> , 2018 , 8, 194	8.6	44
66	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
65	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
64	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

63	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
62	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
61	Epigenetics studies of fetal alcohol spectrum disorder: where are we now?. <i>Epigenomics</i> , 2017 , 9, 291-314	11.4	63
60	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, 1492-1506	6.4	40
59	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
58	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
57	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
56	Trends in DNA Methylation with Age Replicate Across Diverse Human Populations. <i>Genetics</i> , 2017 , 206, 1659-1674	4	44
55	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
54	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
53	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
52	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
51	Choice of surrogate tissue influences neonatal EWAS findings. <i>BMC Medicine</i> , 2017 , 15, 211	11.4	18
50	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
49	Exploring genetic influences underlying acute aerobic exercise effects on motor learning. <i>Scientific Reports</i> , 2017 , 7, 12123	4.9	15
48	Worldwide patterns of human epigenetic variation. <i>Nature Ecology and Evolution</i> , 2017 , 1, 1577-1583	12.3	20
47	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
46	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

45	Epigenetic correlates of neonatal contact in humans. <i>Development and Psychopathology</i> , 2017 , 29, 1517-1538	15.38	60
44	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
43	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
42	Differential DNA methylation and lymphocyte proportions in a Costa Rican high longevity region. <i>Epigenetics and Chromatin</i> , 2017 , 10, 21	5.8	18
41	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
40	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
39	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
38	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
37	An epigenetic clock analysis of race/ethnicity, sex, and coronary heart disease. <i>Genome Biology</i> , 2016 , 17, 171	18.3	357
36	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
35	Improving cell mixture deconvolution by identifying optimal DNA methylation libraries (IDOL). <i>BMC Bioinformatics</i> , 2016 , 17, 120	3.6	74
34	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
33	DNA methylation profiling in human Huntington's disease brain. <i>Human Molecular Genetics</i> , 2016 , 25, 2013-2030	5.6	37
32	A single flexible RNAPII-CTD integrates many different transcriptional programs. <i>Transcription</i> , 2016 , 7, 50-6	4.8	3
31	Rtt107 BRCT domains act as a targeting module in the DNA damage response. <i>DNA Repair</i> , 2016 , 37, 22-32	4.3	10
30	Epigenetics: A New Model for Intracellular Parasite-Host Cell Regulation. <i>Trends in Parasitology</i> , 2016 , 32, 515-521	6.4	32
29	DNA methylation signature of human fetal alcohol spectrum disorder. <i>Epigenetics and Chromatin</i> , 2016 , 9, 25	5.8	93
28	A pooling-based approach to mapping genetic variants associated with DNA methylation. <i>Genome Research</i> , 2015 , 25, 907-17	9.7	18

27	Concordant and discordant DNA methylation signatures of aging in human blood and brain. <i>Epigenetics and Chromatin</i> , 2015 , 8, 19	5.8	99
26	Bacterial infection remodels the DNA methylation landscape of human dendritic cells. <i>Genome Research</i> , 2015 , 25, 1801-11	9.7	138
25	The epigenomic landscape of African rainforest hunter-gatherers and farmers. <i>Nature Communications</i> , 2015 , 6, 10047	17.4	55
24	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	
23	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
22	ISDN2014_0418: DNA methylation changes in fetal alcohol spectrum disorder. <i>International Journal of Developmental Neuroscience</i> , 2015 , 47, 126-126	2.7	4
21	Discordance of DNA methylation variance between two accessible human tissues. <i>Scientific Reports</i> , 2015 , 5, 8257	4.9	46
20	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
19	The RNAPII-CTD Maintains Genome Integrity through Inhibition of Retrotransposon Gene Expression and Transposition. <i>PLoS Genetics</i> , 2015 , 11, e1005608	6	2
18	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
17	HIF3A association with adiposity: the story begins before birth. <i>Epigenomics</i> , 2015 , 7, 937-50	4.4	55
16	DNA methylation and healthy human aging. <i>Aging Cell</i> , 2015 , 14, 924-32	9.9	454
15	Development and the epigenome: the 'synapse' of gene-environment interplay. <i>Developmental Science</i> , 2015 , 18, 1-23	4.5	89
14	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
13	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
12	Genome-wide profiling of yeast DNA:RNA hybrid prone sites with DRIP-chip. <i>PLoS Genetics</i> , 2014 , 10, e1004288	6	153
11	DaVIE: Database for the Visualization and Integration of Epigenetic data. <i>Frontiers in Genetics</i> , 2014 , 5, 325	4.5	6
10	Leishmania donovani infection causes distinct epigenetic DNA methylation changes in host macrophages. <i>PLoS Pathogens</i> , 2014 , 10, e1004419	7.6	83

9	Molecular pathways underpinning ethanol-induced neurodegeneration. <i>Frontiers in Genetics</i> , 2014 , 5, 203	4.5	17
8	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
7	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
6	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
5	Androgen receptor polyglutamine repeat number: models of selection and disease susceptibility. <i>Evolutionary Applications</i> , 2013 , 6, 180-96	4.8	14
4	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
3	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
2	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
1	H2A.Z and DNA methylation: irreconcilable differences. <i>Trends in Biochemical Sciences</i> , 2009 , 34, 158-61	10.3	14