

Michael S Kobor

List of Publications by Year in Descending Order

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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.

153 papers	9,115 citations	52 h-index	94 g-index
162 ext. papers	11,153 ext. citations	7.2 avg, IF	6.11 L-index

#	Paper	IF	Citations
153	An in vitro chronic damage model impairs inflammatory and regenerative responses in human colonoid monolayers.. <i>Cell Reports</i> , 2022 , 38, 110283	10.6	0
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	DNA methylation changes in cord blood and the developmental origins of health and disease - a systematic review and replication study.. <i>BMC Genomics</i> , 2022 , 23, 221	4.5	0
150	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
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, e1009350	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	Infant DNA methylation: an early indicator of intergenerational trauma?. <i>Early Human Development</i> , 2021 , 164, 105519	2.2	
142	Dichotomy in the Impact of Elevated Maternal Glucose Levels on Neonatal Epigenome. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021 ,	5.6	2
141	Machine Learning-Based Single Cell and Integrative Analysis Reveals That Baseline mDC Predisposition Correlates With Hepatitis B Vaccine Antibody Response. <i>Frontiers in Immunology</i> , 2021 , 12, 690470	8.4	0
140	DNA methylation is associated with airflow obstruction in patients living with HIV. <i>Thorax</i> , 2021 , 76, 448-455	15.5	4
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	Autosomal sex-associated co-methylated regions predict biological sex from DNA methylation. <i>Nucleic Acids Research</i> , 2021 , 49, 9097-9116	20.1	6
137	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

136	Maternal Prenatal Anxiety and the Fetal Origins of Epigenetic Aging. <i>Biological Psychiatry</i> , 2021 ,	7.9	2
135	Risky family climates presage increased cellular aging in young adulthood. <i>Psychoneuroendocrinology</i> , 2021 , 130, 105256	5	2
134	Paternal adverse childhood experiences: Associations with infant DNA methylation. <i>Developmental Psychobiology</i> , 2021 , 63, e22174	3	7
133	Society to cell: How child poverty gets Under the SkinTo influence child development and lifelong health. <i>Developmental Review</i> , 2021 , 61, 100983	7.4	2
132	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	
131	Risk-focused differences in molecular processes implicated in SARS-CoV-2 infection: corollaries in DNA methylation and gene expression.. <i>Epigenetics and Chromatin</i> , 2021 , 14, 54	5.8	3
130	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
129	Multi-Omic Approach to Identify Phenotypic Modifiers Underlying Cerebral Demyelination in X-Linked Adrenoleukodystrophy. <i>Frontiers in Cell and Developmental Biology</i> , 2020 , 8, 520	5.7	8
128	CoMeBack: DNA methylation array data analysis for co-methylated regions. <i>Bioinformatics</i> , 2020 , 36, 2675-2683	7.2	13
127	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
126	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
125	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
124	Maternal exposure to childhood traumatic events, but not multi-domain psychosocial stressors, predict placental corticotrophin releasing hormone across pregnancy. <i>Social Science and Medicine</i> , 2020 , 266, 113461	5.1	13
123	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
122	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
121	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
120	Parenting Interacts With Plasticity Genes in Predicting Behavioral Outcomes in Preschoolers. <i>Canadian Journal of Nursing Research</i> , 2020 , 52, 290-307	1.5	4
119	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

118	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
117	Social Environment and Epigenetics. <i>Current Topics in Behavioral Neurosciences</i> , 2019 , 42, 83-126	3.4	11
116	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
115	MRE11-RAD50-NBS1 promotes Fanconi Anemia R-loop suppression at transcription-replication conflicts. <i>Nature Communications</i> , 2019 , 10, 4265	17.4	32
114	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
113	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
112	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
111	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
110	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
109	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
108	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
107	Reversal of epigenetic aging and immunosenescent trends in humans. <i>Aging Cell</i> , 2019 , 18, e13028	9.9	174
106	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
105	Children's biobehavioral reactivity to challenge predicts DNA methylation in adolescence and emerging adulthood. <i>Developmental Science</i> , 2019 , 22, e12739	4.5	6
104	Budding yeast Rtt107 prevents checkpoint hyperactivation after replicative stress by limiting DNA damage. <i>DNA Repair</i> , 2019 , 74, 1-16	4.3	2
103	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
102	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
101	DNA methylome variation in a perinatal nurse-visitation program that reduces child maltreatment: a 27-year follow-up. <i>Translational Psychiatry</i> , 2018 , 8, 15	8.6	25

100	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
99	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
98	Principles and Challenges of Applying Epigenetic Epidemiology to Psychology. <i>Annual Review of Psychology</i> , 2018 , 69, 459-485	26.1	42
97	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
96	Reproduction predicts shorter telomeres and epigenetic age acceleration among young adult women. <i>Scientific Reports</i> , 2018 , 8, 11100	4.9	31
95	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
94	The early care environment and DNA methylome variation in childhood. <i>Development and Psychopathology</i> , 2018 , 30, 891-903	4.3	56
93	Early-life socioeconomic disadvantage, not current, predicts accelerated epigenetic aging of monocytes. <i>Psychoneuroendocrinology</i> , 2018 , 97, 131-134	5	51
92	DNA methylation as a predictor of fetal alcohol spectrum disorder. <i>Clinical Epigenetics</i> , 2018 , 10, 5	7.7	57
91	Perinatal acquired HIV infection accelerates epigenetic aging in South African adolescents. <i>Aids</i> , 2018 , 32, 1465-1474	3.5	64
90	Healthy Foundations Study: a randomised controlled trial to evaluate biological embedding of early-life experiences. <i>BMJ Open</i> , 2018 , 8, e018915	3	9
89	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
88	Exposure to childhood abuse is associated with human sperm DNA methylation. <i>Translational Psychiatry</i> , 2018 , 8, 194	8.6	44
87	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
86	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
85	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
84	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
83	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

82	Trends in DNA Methylation with Age Replicate Across Diverse Human Populations. <i>Genetics</i> , 2017 , 206, 1659-1674	4	44
81	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
80	Genome-Wide Interaction Analysis of Air Pollution Exposure and Childhood Asthma with Functional Follow-up. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2017 , 195, 1373-1383	10.2	71
79	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
78	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
77	Choice of surrogate tissue influences neonatal EWAS findings. <i>BMC Medicine</i> , 2017 , 15, 211	11.4	18
76	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
75	Worldwide patterns of human epigenetic variation. <i>Nature Ecology and Evolution</i> , 2017 , 1, 1577-1583	12.3	20
74	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
73	Epigenetic correlates of neonatal contact in humans. <i>Development and Psychopathology</i> , 2017 , 29, 1517-1538	15.3	60
72	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
71	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
70	Differential DNA methylation and lymphocyte proportions in a Costa Rican high longevity region. <i>Epigenetics and Chromatin</i> , 2017 , 10, 21	5.8	18
69	Longitudinal study of surrogate aging measures during human immunodeficiency virus seroconversion. <i>Aging</i> , 2017 , 9, 687-705	5.6	22
68	An epigenetic clock analysis of race/ethnicity, sex, and coronary heart disease. <i>Genome Biology</i> , 2016 , 17, 171	18.3	357
67	Improving cell mixture deconvolution by identifying optimal DNA methylation libraries (IDOL). <i>BMC Bioinformatics</i> , 2016 , 17, 120	3.6	74
66	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
65	DNA methylation profiling in human Huntington's disease brain. <i>Human Molecular Genetics</i> , 2016 , 25, 2013-2030	5.6	37

64	Differential DNA methylation in peripheral blood mononuclear cells in adolescents exposed to significant early but not later childhood adversity. <i>Development and Psychopathology</i> , 2016 , 28, 1385-1399	4.3	47
63	A single flexible RNAPII-CTD integrates many different transcriptional programs. <i>Transcription</i> , 2016 , 7, 50-6	4.8	3
62	Rtt107 BRCT domains act as a targeting module in the DNA damage response. <i>DNA Repair</i> , 2016 , 37, 22-32	4.3	10
61	DNA methylation signature of human fetal alcohol spectrum disorder. <i>Epigenetics and Chromatin</i> , 2016 , 9, 25	5.8	93
60	Brain-derived neurotrophic factor (BDNF) Val66Met polymorphism influences the association of the methylome with maternal anxiety and neonatal brain volumes. <i>Development and Psychopathology</i> , 2015 , 27, 137-50	4.3	57
59	The Canadian Healthy Infant Longitudinal Development (CHILD) Study: examining developmental origins of allergy and asthma. <i>Thorax</i> , 2015 , 70, 998-1000	7.3	105
58	Concordant and discordant DNA methylation signatures of aging in human blood and brain. <i>Epigenetics and Chromatin</i> , 2015 , 8, 19	5.8	99
57	Bacterial infection remodels the DNA methylation landscape of human dendritic cells. <i>Genome Research</i> , 2015 , 25, 1801-11	9.7	138
56	The epigenomic landscape of African rainforest hunter-gatherers and farmers. <i>Nature Communications</i> , 2015 , 6, 10047	17.4	55
55	Discordance of DNA methylation variance between two accessible human tissues. <i>Scientific Reports</i> , 2015 , 5, 8257	4.9	46
54	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
53	The RNAPII-CTD Maintains Genome Integrity through Inhibition of Retrotransposon Gene Expression and Transposition. <i>PLoS Genetics</i> , 2015 , 11, e1005608	6	2
52	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
51	DNA methylation and healthy human aging. <i>Aging Cell</i> , 2015 , 14, 924-32	9.9	454
50	Development and the epigenome: the 'synapse' of gene-environment interplay. <i>Developmental Science</i> , 2015 , 18, 1-23	4.5	89
49	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
48	Genome-wide profiling of yeast DNA:RNA hybrid prone sites with DRIP-chip. <i>PLoS Genetics</i> , 2014 , 10, e1004288	6	153
47	Maintenance of heterochromatin boundary and nucleosome composition at promoters by the Asf1 histone chaperone and SWR1-C chromatin remodeler in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2014 , 197, 133-45	4	5

46	DaVIE: Database for the Visualization and Integration of Epigenetic data. <i>Frontiers in Genetics</i> , 2014 , 5, 325	4.5	6
45	Leishmania donovani infection causes distinct epigenetic DNA methylation changes in host macrophages. <i>PLoS Pathogens</i> , 2014 , 10, e1004419	7.6	83
44	Molecular pathways underpinning ethanol-induced neurodegeneration. <i>Frontiers in Genetics</i> , 2014 , 5, 203	4.5	17
43	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
42	Spread of X-chromosome inactivation into autosomal sequences: role for DNA elements, chromatin features and chromosomal domains. <i>Human Molecular Genetics</i> , 2014 , 23, 1211-23	5.6	49
41	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
40	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
39	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
38	Distinct DNA methylation patterns of cognitive impairment and trisomy 21 in Down syndrome. <i>BMC Medical Genomics</i> , 2013 , 6, 58	3.7	64
37	DNA methylation, genotype and gene expression: who is driving and who is along for the ride?. <i>Genome Biology</i> , 2013 , 14, 126	18.3	44
36	Epigenetic vestiges of early developmental adversity: childhood stress exposure and DNA methylation in adolescence. <i>Child Development</i> , 2013 , 84, 58-75	4.9	319
35	High-throughput genetic and gene expression analysis of the RNAPII-CTD reveals unexpected connections to SRB10/CDK8. <i>PLoS Genetics</i> , 2013 , 9, e1003758	6	16
34	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
33	Population-specificity of human DNA methylation. <i>Genome Biology</i> , 2012 , 13, R8	18.3	203
32	R-loop-mediated genome instability in mRNA cleavage and polyadenylation mutants. <i>Genes and Development</i> , 2012 , 26, 163-75	12.6	159
31	CHROMATRA: a Galaxy tool for visualizing genome-wide chromatin signatures. <i>Bioinformatics</i> , 2012 , 28, 717-8	7.2	11
30	Dot1 and histone H3K79 methylation in natural telomeric and HM silencing. <i>Molecular Cell</i> , 2011 , 42, 118-26	17.6	83
29	The specificity and topology of chromatin interaction pathways in yeast. <i>Molecular Cell</i> , 2011 , 42, 536-49	17.6	175

28	Chromosome-wide DNA methylation analysis predicts human tissue-specific X inactivation. <i>Human Genetics</i> , 2011 , 130, 187-201	6.3	95
27	Splitting the task: Ubp8 and Ubp10 deubiquitinate different cellular pools of H2BK123. <i>Genes and Development</i> , 2011 , 25, 2242-7	12.6	80
26	Key functional regions in the histone variant H2A.Z C-terminal docking domain. <i>Molecular and Cellular Biology</i> , 2011 , 31, 3871-84	4.8	23
25	Rtt107 is required for recruitment of the SMC5/6 complex to DNA double strand breaks. <i>Journal of Biological Chemistry</i> , 2011 , 286, 26250-7	5.4	31
24	Loss of H3 K79 trimethylation leads to suppression of Rtt107-dependent DNA damage sensitivity through the translesion synthesis pathway. <i>Journal of Biological Chemistry</i> , 2010 , 285, 35113-22	5.4	27
23	Roles for H2A.Z and its acetylation in GAL1 transcription and gene induction, but not GAL1-transcriptional memory. <i>PLoS Biology</i> , 2010 , 8, e1000401	9.7	65
22	Reading chromatin: insights from yeast into YEATS domain structure and function. <i>Epigenetics</i> , 2010 , 5, 573-7	5.7	30
21	How the epigenome contributes to the development of psychiatric disorders. <i>Developmental Psychobiology</i> , 2010 , 52, 331-42	3	34
20	Asf1-like structure of the conserved Yaf9 YEATS domain and role in H2A.Z deposition and acetylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 21573-8	11.5	49
19	Linking cell cycle to histone modifications: SBF and H2B monoubiquitination machinery and cell-cycle regulation of H3K79 dimethylation. <i>Molecular Cell</i> , 2009 , 35, 626-41	17.6	144
18	Low early-life social class leaves a biological residue manifested by decreased glucocorticoid and increased proinflammatory signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 14716-21	11.5	623
17	YEATS domain proteins: a diverse family with many links to chromatin modification and transcription. <i>Biochemistry and Cell Biology</i> , 2009 , 87, 65-75	3.6	93
16	NuA4 and SWR1-C: two chromatin-modifying complexes with overlapping functions and components. <i>Biochemistry and Cell Biology</i> , 2009 , 87, 799-815	3.6	77
15	Slx4 regulates DNA damage checkpoint-dependent phosphorylation of the BRCT domain protein Rtt107/Esc4. <i>Molecular Biology of the Cell</i> , 2006 , 17, 539-48	3.5	75
14	Dephosphorylation of RNA polymerase I by Fcp1p is required for efficient rRNA synthesis. <i>Journal of Biological Chemistry</i> , 2004 , 279, 25251-9	5.4	27
13	A protein complex containing the conserved Swi2/Snf2-related ATPase Swr1p deposits histone variant H2A.Z into euchromatin. <i>PLoS Biology</i> , 2004 , 2, E131	9.7	453
12	Regulation of transcription elongation by phosphorylation. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2002 , 1577, 261-275		152
11	Opposing effects of Ctk1 kinase and Fcp1 phosphatase at Ser 2 of the RNA polymerase II C-terminal domain. <i>Genes and Development</i> , 2001 , 15, 3319-29	12.6	339

10	A motif shared by TFIIF and TFIIB mediates their interaction with the RNA polymerase II carboxy-terminal domain phosphatase Fcp1p in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 2000 , 20, 7438-49	4.8	65
9	An unusual eukaryotic protein phosphatase required for transcription by RNA polymerase II and CTD dephosphorylation in <i>S. cerevisiae</i> . <i>Molecular Cell</i> , 1999 , 4, 55-62	17.6	176
8	GAL4 is regulated by the RNA polymerase II holoenzyme-associated cyclin-dependent protein kinase SRB10/CDK8. <i>Molecular Cell</i> , 1999 , 3, 673-8	17.6	120
7	BECon: A tool for interpreting DNA methylation findings from blood in the context of brain		4
6	Exploring the Genetic Basis of Human Population Differences in DNA Methylation and their Causal Impact on Immune Gene Regulation		1
5	Differences in DNA methylation of white blood cell types at birth and in adulthood reflect postnatal immune maturation and influence accuracy of cell type prediction		3
4	Variably methylated regions in the newborn epigenome: environmental, genetic and combined influences		1
3	Factors Driving DNA Methylation Variation in Human Blood		2
2	Machine learning-based single cell and integrative analysis reveals that baseline mDC predisposition predicts protective Hepatitis B vaccine response		1
1	Optimized CRISPR-mediated gene knock-in reveals FOXP3-independent control of human Treg identity		1