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#	Paper	IF	Citations
589	Das Tumorepigenom Ivon der Genregulation Ber die Tumorklassifikation zum Therapietarget. <b>2016</b> , 28, 424-434		
588	Contrasting the effects of intra-uterine smoking and one-carbon micronutrient exposures on offspring DNA methylation. <b>2017</b> , 9, 351-367		20
587	Misclassified exposure in epigenetic mediation analyses. Does DNA methylation mediate effects of smoking on birthweight?. <b>2017</b> , 9, 253-265		26
586	Genetics and Genomics in Oncology Nursing: What Does Every Nurse Need to Know?. 2017, 52, 1-25		8
585	Epigenome-wide Association of DNA Methylation in Whole Blood With Bone Mineral Density. <b>2017</b> , 32, 1644-1650		33
584	Epigenome-wide association study of DNA methylation in panic disorder. <i>Clinical Epigenetics</i> , <b>2017</b> , 9, 6	7.7	39
583	Impact of confounding by leukocyte composition on associations of leukocyte DNA methylation with common risk factors. <b>2017</b> , 9, 659-668		10
582	Evolution with No Reason: A Neutral View on Epigenetic Changes, Genomic Variability, and Evolutionary Novelty. <b>2017</b> , 67, 469-476		10
581	Epigenome-wide analysis of DNA methylation in lung tissue shows concordance with blood studies and identifies tobacco smoke-inducible enhancers. <i>Human Molecular Genetics</i> , <b>2017</b> , 26, 3014-3027	5.6	64
580	Establishment of a Strong Link Between Smoking and Cancer Pathogenesis through DNA Methylation Analysis. <i>Scientific Reports</i> , <b>2017</b> , 7, 1811	4.9	43
579	Accuracy and utility of an epigenetic biomarker for smoking in populations with varying rates of false self-report. <b>2017</b> , 174, 641-650		28
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577	Tea and coffee consumption in relation to DNA methylation in four European cohorts. <i>Human Molecular Genetics</i> , <b>2017</b> , 26, 3221-3231	5.6	19
576	Epigenetics and allergy: from basic mechanisms to clinical applications. 2017, 9, 539-571		134
575	Smoking and chronic kidney disease: seeing the signs through the smoke?. <b>2017</b> , 32, 403-405		6
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573	Shared genetic origin of asthma, hay fever and eczema elucidates allergic disease biology. <b>2017</b> , 49, 17	752-175	<b>57</b> 256

572	Cigarette smoking significantly alters sperm DNA methylation patterns. <b>2017</b> , 5, 1089-1099	75
571	Decreased expression of cytochrome p450 1B1 in non-small cell lung cancer. <b>2017</b> , 95, 339-345	5
570	Drivers of the immunopathogenesis in systemic lupus erythematosus. <b>2017</b> , 31, 321-333	24
569	Quantitative Multiple-Reaction Monitoring Proteomic Analysis of Gland Glaubunits in C57Bl6/J Brain Synaptosomes. <b>2017</b> , 56, 5405-5416	12
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567	Asbestos-associated genome-wide DNA methylation changes in lung cancer. <b>2017</b> , 141, 2014-2029	32
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564	Cigarette Smoking, Diabetes, and Diabetes Complications: Call for Urgent Action. <b>2017</b> , 17, 78	17
563	Challenges and recommendations for epigenomics in precision health. <b>2017</b> , 35, 1128-1132	16
562	The Impact of Traditional Food and Lifestyle Behavior on Epigenetic Burden of Chronic Disease. <b>2017</b> , 1, 1700043	11
561	Smoking induces DNA methylation changes in Multiple Sclerosis patients with exposure-response relationship. <i>Scientific Reports</i> , <b>2017</b> , 7, 14589	41
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558	Smoking and Promoter-Specific Deoxyribonucleic Acid Methylation of the Atrial Natriuretic Peptide Gene: Methylation of Smokers and Non-Smokers Differs Significantly during Withdrawal. <b>2017</b> , 23, 306-311	6
557	"DNA Methylation signatures in panic disorder". <b>2017</b> , 7, 1287	30
556	An epigenome-wide association study meta-analysis of educational attainment. <b>2017</b> , 22, 1680-1690	46
555	Tobacco exposure-related alterations in DNA methylation and gene expression in human monocytes: the Multi-Ethnic Study of Atherosclerosis (MESA). <b>2017</b> , 12, 1092-1100	21

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543	Tobacco smoking and alcohol drinking at diagnosis of head and neck cancer and all-cause mortality: Results from head and neck 5000, a prospective observational cohort of people with head and neck cancer. <b>2018</b> , 143, 1114-1127	74
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541	Longitudinal analysis strategies for modelling epigenetic trajectories. <b>2018</b> , 47, 516-525	8
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539	DNA methylation as a mediator of the association between prenatal adversity and risk factors for metabolic disease in adulthood. <b>2018</b> , 4, eaao4364	143
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535	Picking the Right Fruit: Intersecting Chronic Obstructive Pulmonary Disease Genome-Wide Association Study Discoveries with Epigenetics. <i>American Journal of Respiratory and Critical Care Medicine</i> , <b>2018</b> , 197, 1237-1239	2
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526	Cell-type-specific disturbance of DNA methylation pattern: a chance to get more benefit from and to minimize cohorts for epigenome-wide association studies. <b>2018</b> , 47, 917-927	12
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444	New Biomarkers for Smoking: Epigenetic Changes. <b>2019</b> , 55, 293-294		
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420	Genomewide Study of Epigenetic Biomarkers of Opioid Dependence in European- American Women. <i>Scientific Reports</i> , <b>2019</b> , 9, 4660	9	14
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410	Mendelian Randomization and the Environmental Epigenetics of Health: a Systematic Review.  Current Environmental Health Reports, <b>2019</b> , 6, 38-51	.5	3
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407	The role of cigarette smoke-induced epigenetic alterations in inflammation. <b>2019</b> , 12, 65		47
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405	Validation and characterisation of a DNA methylation alcohol biomarker across the life course.  7: Clinical Epigenetics, <b>2019</b> , 11, 163	7	6
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403	DNA methylation aging clocks: challenges and recommendations. <b>2019</b> , 20, 249		248
402	Investigating the impact of cigarette smoking behaviours on DNA methylation patterns in adolescence. <i>Human Molecular Genetics</i> , <b>2019</b> , 28, 155-165	.6	13
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400	Tobacco Heating System 2.2 has a limited impact on DNA methylation of candidate enhancers in mouse lung compared with cigarette smoke. <b>2019</b> , 123, 501-510		8
399	Methods for Analysis of DNA Methylation. <b>2019</b> , 347-377		2
398	Epigenome-wide association study of serum cotinine in current smokers reveals novel genetically driven loci. <i>Clinical Epigenetics</i> , <b>2019</b> , 11, 1	7	40
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395	Epigenetics in eating disorders: a systematic review. <b>2019</b> , 24, 901-915		32
394	Epigenetics and the Exposome. <b>2019</b> , 127-146		3
393	Using DNA methylation to validate an electronic medical record phenotype for smoking. <b>2019</b> , 24, 1056-1	065	7

392	Smoking and its interaction with genetics in MS etiology. <b>2019</b> , 25, 180-186	12
391	Effects of cigarette smoke condensate on proliferation and pluripotency gene expression in mouse embryonic stem cells. <b>2019</b> , 120, 4071-4080	10
390	The emerging role of epigenetic modifiers in repair of DNA damage associated with chronic inflammatory diseases. <b>2019</b> , 780, 69-81	18
389	Smoking and blood DNA methylation: an epigenome-wide association study and assessment of reversibility. <b>2020</b> , 15, 358-368	22
388	Polychlorinated biphenyl exposure and DNA methylation in the Anniston Community Health Survey. <b>2020</b> , 15, 337-357	6
387	The influence of human leukocyte antigen-DRB1*15:01 and its interaction with smoking in MS development is dependent on DQA1*01:01 status. <b>2020</b> , 26, 1638-1646	1
386	Epigenome-wide association study of DNA methylation and microRNA expression highlights novel pathways for human complex traits. <b>2020</b> , 15, 183-198	5
385	Differential DNA methylation in bronchial biopsies between persistent asthma and asthma in remission. <b>2020</b> , 55,	14
384	Agnostic Cys34-albumin adductomics and DNA methylation: Implication of N-acetylcysteine in lung carcinogenesis years before diagnosis. <b>2020</b> , 146, 3294-3303	7
	Deplication and expansion of enigonems wide association literature in a black Courth African	
383	Replication and expansion of epigenome-wide association literature in a black South African population. <i>Clinical Epigenetics</i> , <b>2020</b> , 12, 6	9
383		9
	population. <i>Clinical Epigenetics</i> , <b>2020</b> , 12, 6  Questionnaire Design, Development, Evaluation, and Testing: Where Are We, and Where Are We	
382	population. <i>Clinical Epigenetics</i> , <b>2020</b> , 12, 6  Questionnaire Design, Development, Evaluation, and Testing: Where Are We, and Where Are We Headed?. <b>2020</b> , 1-23  Genetic and Epigenetic Analysis Revealing Variants in the NCAM1-TTC12-ANKK1-DRD2 Cluster	3
382	population. <i>Clinical Epigenetics</i> , <b>2020</b> , 12, 6  Questionnaire Design, Development, Evaluation, and Testing: Where Are We, and Where Are We Headed?. <b>2020</b> , 1-23  Genetic and Epigenetic Analysis Revealing Variants in the NCAM1-TTC12-ANKK1-DRD2 Cluster Associated Significantly With Nicotine Dependence in Chinese Han Smokers. <b>2020</b> , 22, 1301-1309  Accelerating the Search for Interventions Aimed at Expanding the Health Span in Humans: The Role	3
382 381 380	Questionnaire Design, Development, Evaluation, and Testing: Where Are We, and Where Are We Headed?. 2020, 1-23  Genetic and Epigenetic Analysis Revealing Variants in the NCAM1-TTC12-ANKK1-DRD2 Cluster Associated Significantly With Nicotine Dependence in Chinese Han Smokers. 2020, 22, 1301-1309  Accelerating the Search for Interventions Aimed at Expanding the Health Span in Humans: The Role of Epidemiology. 2020, 75, 77-86	3 8 5
382 381 380 379	Questionnaire Design, Development, Evaluation, and Testing: Where Are We, and Where Are We Headed?. 2020, 1-23  Genetic and Epigenetic Analysis Revealing Variants in the NCAM1-TTC12-ANKK1-DRD2 Cluster Associated Significantly With Nicotine Dependence in Chinese Han Smokers. 2020, 22, 1301-1309  Accelerating the Search for Interventions Aimed at Expanding the Health Span in Humans: The Role of Epidemiology. 2020, 75, 77-86  Physical Activity and Genome-wide DNA Methylation: The REgistre GlronIdel COR Study. 2020, 52, 589-597	3 8 5 5
382 381 380 379 378	Questionnaire Design, Development, Evaluation, and Testing: Where Are We, and Where Are We Headed?. 2020, 1-23  Genetic and Epigenetic Analysis Revealing Variants in the NCAM1-TTC12-ANKK1-DRD2 Cluster Associated Significantly With Nicotine Dependence in Chinese Han Smokers. 2020, 22, 1301-1309  Accelerating the Search for Interventions Aimed at Expanding the Health Span in Humans: The Role of Epidemiology. 2020, 75, 77-86  Physical Activity and Genome-wide DNA Methylation: The REgistre Gironidel COR Study. 2020, 52, 589-597  The leading role of epithelial cells in the pathogenesis of idiopathic pulmonary fibrosis. 2020, 66, 109482  Epigenetic reprogramming in periodontal disease: Dynamic crosstalk with potential impact in	<ul><li>3</li><li>8</li><li>5</li><li>5</li><li>59</li></ul>

374	The DNA methylome of human sperm is distinct from blood with little evidence for tissue-consistent obesity associations. <b>2020</b> , 16, e1009035		4
373	Changes in global DNA methylation and hydroxymethylation in oral mucosa according to tobacco smoke exposure. <b>2020</b> , 48, 300060520954677		О
372	Single-cell analyses identify dysfunctional CD16 CD8 T cells in smokers. <b>2020</b> , 1,		4
371	AHRR hypomethylation as an epigenetic marker of smoking history predicts risk of myocardial infarction in former smokers. <b>2020</b> , 312, 8-15		2
370	Patterns of Reliability: Assessing the Reproducibility and Integrity of DNA Methylation Measurement. <b>2020</b> , 1,		24
369	Epigenome-wide meta-analysis of PTSD across 10 military and civilian cohorts identifies methylation changes in AHRR. <i>Nature Communications</i> , <b>2020</b> , 11, 5965	17.4	34
368	Epigenome-wide meta-analysis of DNA methylation differences in prefrontal cortex implicates the immune processes in Alzheimer's disease. <i>Nature Communications</i> , <b>2020</b> , 11, 6114	17.4	12
367	AHRR cg05575921 methylation in relation to smoking and PM exposure among Taiwanese men and women. <i>Clinical Epigenetics</i> , <b>2020</b> , 12, 117	7.7	7
366	Epigenetic alterations in aging tooth and the reprogramming potential. <b>2020</b> , 63, 101140		4
365	Analysis of genome-wide methylation using reduced representation bisulfite sequencing (RRBS) technology. <b>2020</b> , 141-156		
364	A Mendelian randomization study of telomere length and blood-cell traits. <i>Scientific Reports</i> , <b>2020</b> , 10, 12223	4.9	1
363	Methylation vs. Protein Inflammatory Biomarkers and Their Associations With Cardiovascular Function. <b>2020</b> , 11, 1577		O
362	Epigenetic measures of ageing predict the prevalence and incidence of leading causes of death and disease burden. <i>Clinical Epigenetics</i> , <b>2020</b> , 12, 115	7.7	40
361	DNA methylation signature of passive smoke exposure is less pronounced than active smoking: The Understanding Society study. <b>2020</b> , 190, 109971		3
360	DNA methylation in human sperm: a systematic review. <b>2020</b> , 26, 841-873		15
359	Reducing Tobacco-Related Disability in Chronic Smokers. <b>2020</b> , 133, 908-915		2
358	Use of an Exposome Approach to Understand the Effects of Exposures From the Natural, Built, and Social Environments on Cardio-Vascular Disease Onset, Progression, and Outcomes. <b>2020</b> , 8, 379		12
357	An integrative machine learning approach to discovering multi-level molecular mechanisms of obesity using data from monozygotic twin pairs. <b>2020</b> , 7, 200872		0

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356	cardio-metabolic traits. <i>Clinical Epigenetics</i> , <b>2020</b> , 12, 157	7.7	5
355	Leveraging the urban-rural divide for epigenetic research. <b>2020</b> , 12, 1071-1081		2
354	Suppresses Microbe-Induced Production of IL-1[In Human Normal and Cancerous Oral Cells through the PI3K/Akt/GSK-3[Axis. <b>2020</b> , 12,		1
353	A cell-type deconvolution meta-analysis of whole blood EWAS reveals lineage-specific smoking-associated DNA methylation changes. <i>Nature Communications</i> , <b>2020</b> , 11, 4779	17.4	14
352	AHRR methylation in heavy smokers: associations with smoking, lung cancer risk, and lung cancer mortality. <b>2020</b> , 20, 905		7
351	From tobacco smoking to cancer mutational signature: a mediation analysis strategy to explore the role of epigenetic changes. <b>2020</b> , 20, 880		6
350	DNA methylation mediates the effect of cocaine use on HIV severity. Clinical Epigenetics, <b>2020</b> , 12, 140	7.7	6
349	In utero and childhood exposure to tobacco smoke and multi-layer molecular signatures in children. <b>2020</b> , 18, 243		6
348	Epigenetic biotypes of post-traumatic stress disorder in war-zone exposed veteran and active duty males. <b>2021</b> , 26, 4300-4314		5
347	Scars of childhood socioeconomic stress: A systematic review. <b>2020</b> , 118, 397-410		2
346	Generalizability of "GWAS Hits" in Clinical Populations: Lessons from Childhood Cancer Survivors. <b>2020</b> , 107, 636-653		7
345	Profiling of Histone Modifications Reveals Epigenomic Dynamics During Abdominal Aortic Aneurysm Formation in Mouse Models. <b>2020</b> , 7, 595011		4
344	Review article: impact of cigarette smoking on intestinal inflammation-direct and indirect mechanisms. <b>2020</b> , 51, 1268-1285		15
343	Association of Neighborhood Disadvantage in Childhood With DNA Methylation in Young Adulthood. <b>2020</b> , 3, e206095		20
342	Bayesian reassessment of the epigenetic architecture of complex traits. <i>Nature Communications</i> , <b>2020</b> , 11, 2865	17.4	18
341	Epigenetic Effects on Pediatric Traumatic Brain Injury Recovery (EETR): An Observational, Prospective, Longitudinal Concurrent Cohort Study Protocol. <b>2020</b> , 11, 460		3
340	Epigenetic prediction of major depressive disorder. <b>2021</b> , 26, 5112-5123		18
339	Cadmium, Smoking, and Human Blood DNA Methylation Profiles in Adults from the Strong Heart Study. <b>2020</b> , 128, 67005		22

338	Blood-derived DNA methylation predictors of mortality discriminate tumor and healthy tissue in multiple organs. <b>2020</b> , 14, 2111-2123		4
337	Individual and joint contributions of genetic and methylation risk scores for enhancing lung cancer risk stratification: data from a population-based cohort in Germany. <i>Clinical Epigenetics</i> , <b>2020</b> , 12, 89	7.7	7
336	An epigenome-wide association study of posttraumatic stress disorder in US veterans implicates several new DNA methylation loci. <i>Clinical Epigenetics</i> , <b>2020</b> , 12, 46	7.7	31
335	DNA methylation and brain structure and function across the life course: A systematic review. <b>2020</b> , 113, 133-156		21
334	MethylNet: an automated and modular deep learning approach for DNA methylation analysis. <b>2020</b> , 21, 108		23
333	Smoking and disability progression in multiple sclerosis. <b>2020</b> , 20, 739-741		1
332	Identifying epigenetic biomarkers of established prognostic factors and survival in a clinical cohort of individuals with oropharyngeal cancer. <i>Clinical Epigenetics</i> , <b>2020</b> , 12, 95	7.7	4
331	Dysregulation of microRNA Modulatory Network in Abdominal Aortic Aneurysm. <b>2020</b> , 9,		3
330	Dioxin-like compound exposures and DNA methylation in the Anniston Community Health Survey Phase II. <b>2020</b> , 742, 140424		4
329	Multi-method genome- and epigenome-wide studies of inflammatory protein levels in healthy older adults. <b>2020</b> , 12, 60		9
328	Epigenome-wide association study of attention-deficit/hyperactivity disorder in adults. <b>2020</b> , 10, 199		4
327	Wandering along the epigenetic timeline. <i>Clinical Epigenetics</i> , <b>2020</b> , 12, 97	7.7	8
326	Smoking and Epstein-Barr virus infection in multiple sclerosis development. <i>Scientific Reports</i> , <b>2020</b> , 10, 10960	4.9	4
325	Systemic Investigation of Promoter-wide Methylome and Genome Variations in Gout. <i>International Journal of Molecular Sciences</i> , <b>2020</b> , 21,	6.3	6
324	Genetik und Epigenetik in der Psychotherapie von Depression und Angststflungen. <b>2020</b> , 30, 58-67		
323	DNA Methylation-Based Biomarkers of Environmental Exposures for Human Population Studies. <i>Current Environmental Health Reports</i> , <b>2020</b> , 7, 121-128	6.5	8
322	Platelet mitochondrial DNA methylation predicts future cardiovascular outcome in adults with overweight and obesity. <i>Clinical Epigenetics</i> , <b>2020</b> , 12, 29	7.7	18
321	Smoking, DNA Methylation, and Lung Function: a Mendelian Randomization Analysis to Investigate Causal Pathways. <b>2020</b> , 106, 315-326		12

320	Epigenetic insights into multiple sclerosis disease progression. <b>2020</b> , 288, 82-102		4
319	Timing- and Dose-Specific Associations of Prenatal Smoke Exposure With Newborn DNA Methylation. <b>2020</b> , 22, 1917-1922		3
318	Genetics and Epigenetics of Atopic Dermatitis: An Updated Systematic Review. 2020, 11,		23
317	Epigenetic prediction of complex traits and mortality in a cohort of individuals with oropharyngeal cancer. <i>Clinical Epigenetics</i> , <b>2020</b> , 12, 58	7.7	3
316	Leveraging biological and statistical covariates improves the detection power in epigenome-wide association testing. <b>2020</b> , 21, 88		4
315	Genome-wide DNA methylation differences in nucleus accumbens of smokers vs. nonsmokers. <b>2021</b> , 46, 554-560		3
314	Methylome and transcriptome signature of bronchoalveolar cells from multiple sclerosis patients in relation to smoking. <b>2021</b> , 27, 1014-1026		4
313	DNA methylation-based biomarkers of age acceleration and all-cause death, myocardial infarction, stroke, and cancer in two cohorts: The NAS, and KORA F4. <i>EBioMedicine</i> , <b>2021</b> , 63, 103151	8.8	13
312	Epigenetics and pulmonary diseases in the horizon of precision medicine: a review. <b>2021</b> , 57,		7
311	Structural brain correlates of serum and epigenetic markers of inflammation in major depressive disorder. <b>2021</b> , 92, 39-48		14
310	Telomere length mediates the association between polycyclic aromatic hydrocarbons exposure and abnormal glucose level among Chinese coke oven plant workers. <b>2021</b> , 266, 129111		3
309	Epigenome-wide association study of diet quality in the Women's Health Initiative and TwinsUK cohort. <b>2021</b> , 50, 675-684		8
308	Cigarette Smoke and Nicotine-Containing Electronic-Cigarette Vapor Downregulate Lung WWOX Expression, Which Is Associated with Increased Severity of Murine Acute Respiratory Distress Syndrome. <b>2021</b> , 64, 89-99		1
307	Lung DNA Methylation in Chronic Obstructive Pulmonary Disease: Relationship with Smoking Status and Airflow Limitation Severity. <i>American Journal of Respiratory and Critical Care Medicine</i> , <b>2021</b> , 203, 129-134	10.2	1
306	The Interplay of the Genetic Architecture, Aging, and Environmental Factors in the Pathogenesis of Idiopathic Pulmonary Fibrosis. <b>2021</b> , 64, 163-172		24
305	Epigenome-wide analysis uncovers a blood-based DNA methylation biomarker of lifetime cannabis use. <b>2021</b> , 186, 173-182		6
304	Alcohol consumption is associated with widespread changes in blood DNA methylation: Analysis of cross-sectional and longitudinal data. <b>2021</b> , 26, e12855		13
303	DNA methylation and breast cancer risk: value of twin and family studies. <b>2021</b> , 67-83		1

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301	Twin and family epigenetic studies of type 2 diabetes. <b>2021</b> , 105-118		
300	A Systems-Based Approach to Toxicity Testing. <b>2021</b> , 189-206		
299	Proteomic Signatures of Lifestyle Risk Factors for Cardiovascular Disease: A Cross-Sectional Analysis of the Plasma Proteome in the Framingham Heart Study. <b>2021</b> , 10, e018020		3
298	Current Status and Future Perspectives of Liquid Biopsy in Small Cell Lung Cancer. 2021, 9,		1
297	Elucidation of Epigenetic Landscape in Coronary Artery Disease: A Review on Basic Concept to Personalized Medicine. <b>2021</b> , 14, 2516865720988567		2
296	DNA methylation changes specific to environmental exposures: The strengths of twin studies using cigarette smoking as an example. <b>2021</b> , 277-284		O
295	DNA methylation signatures of aggression and closely related constructs: A meta-analysis of epigenome-wide studies across the lifespan. <b>2021</b> , 26, 2148-2162		7
294	Genetics and Epigenetics of Addiction. 2021,		
293	Cigarette smoke-induced alterations in blood: A review of research on DNA methylation and gene expression. <b>2021</b> , 29, 116-135		11
292	Creating and Validating a DNA Methylation-Based Proxy for Interleukin-6. <b>2021</b> , 76, 2284-2292		1
291	Genome-wide identification of cis DNA methylation quantitative trait loci in three Southeast Asian Populations. <i>Human Molecular Genetics</i> , <b>2021</b> , 30, 603-618	5.6	1
290	Methylation scores for smoking, alcohol consumption, and body mass index and risk of seven types of cancer.		O
289	DNA methylation of blood cells is associated with prevalent type 2 diabetes in a meta-analysis of four European cohorts. <i>Clinical Epigenetics</i> , <b>2021</b> , 13, 40	7.7	8
288	Novel DNA methylation signatures of tobacco smoking with trans-ethnic effects. <i>Clinical Epigenetics</i> , <b>2021</b> , 13, 36	7.7	16
287	When things go wrong: exploring possible mechanisms driving the progressive fibrosis phenotype in interstitial lung diseases. <b>2021</b> , 58,		11
286	The Therapeutic Potential of Epigenome-Modifying Drugs in Cardiometabolic Disease. <b>2021</b> , 9, 22-36		
285	Mining the Selective Remodeling of DNA Methylation in Promoter Regions to Identify Robust Gene-Level Associations With Phenotype. <b>2021</b> , 8, 597513		2

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284	New biomarkers from multiomics approaches: improving risk prediction of atrial fibrillation. <b>2021</b> , 117, 1632-1644		1
283	Perspectives on Epigenetics Alterations Associated with Smoking and Vaping <b>2021</b> , 2, zqab022		1
282	Epigenome-wide association study of whole blood gene expression in Framingham Heart Study participants provides molecular insight into the potential role of CHRNA5 in cigarette smoking-related lung diseases. <i>Clinical Epigenetics</i> , <b>2021</b> , 13, 60	7.7	3
281	Sex-specific DNA methylation changes in Alzheimer∃ disease pathology.		
280	Assessing the co-variability of DNA methylation across peripheral cells and tissues: Implications for the interpretation of findings in epigenetic epidemiology. <b>2021</b> , 17, e1009443		11
279	Persistent Cigarette Smoking Attenuates Plaque Stabilization in Response to Lipid-Lowering Therapy: A Serial Optical Coherence Tomography Study. <b>2021</b> , 8, 616568		
278	Assessing the role of genome-wide DNA methylation between smoking and risk of lung cancer using repeated measurements: the HUNT study. <b>2021</b> , 50, 1482-1497		5
277	Smoking methylation marks for prediction of urothelial cancer risk.		
276	MethylDetectR: a software for methylation-based health profiling. <b>2020</b> , 5, 283		1
275	Grandmaternal smoking during pregnancy is associated with differential DNA methylation in their grandchildren.		1
274	Alterations in DNA methylation rates of brain-derived neurotrophic factor in patients with schizophrenia. <b>2021</b> , 35, 67-74		0
273	Epigenetic predictors of lifestyle traits applied to the blood and brain. 2021, 3, fcab082		1
272	Impact of Cigarette Smoking on the Risk of Osteoporosis in Inflammatory Bowel Diseases. <b>2021</b> , 10,		1
271	Genetic impacts on DNA methylation: research findings and future perspectives. <b>2021</b> , 22, 127		16
270	Dysregulated epigenetic modifications in psoriasis. <b>2021</b> , 30, 1156-1166		3
269	Maternal blood metal concentrations and whole blood DNA methylation during pregnancy in the Early Autism Risk Longitudinal Investigation (EARLI). <b>2021</b> , 1-16		1
268	Sex-specific DNA methylation differences in Alzheimer's disease pathology. <b>2021</b> , 9, 77		2
267	DNA methylation and gene expression integration in cardiovascular disease. <i>Clinical Epigenetics</i> , <b>2021</b> , 13, 75	7.7	6

266	Socioeconomic Disadvantage and the Pace of Biological Aging in Children. 2021, 147,		15
265	DNA methylation as the link between migration and the major noncommunicable diseases: the RODAM study. <b>2021</b> , 13, 653-666		O
264	Epigenome-wide association meta-analysis of DNA methylation with coffee and tea consumption. <i>Nature Communications</i> , <b>2021</b> , 12, 2830	17.4	9
263	DNA Methylation in Babies Born to Nonsmoking Mothers Exposed to Secondhand Smoke during Pregnancy: An Epigenome-Wide Association Study. <b>2021</b> , 129, 57010		4
262	Connecting the epigenome, metabolome and proteome for a deeper understanding of disease. <b>2021</b> , 290, 527-548		1
261	Epigenome-wide scan identifies differentially methylated regions for lung cancer using pre-diagnostic peripheral blood. <b>2021</b> , 1-13		3
260	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <b>2021</b> , 22, 194		14
259	Transgenerational inheritance: understanding the etiology of a disease. <b>2021</b> , 27, 122-132		O
258	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. <i>Nature Communications</i> , <b>2021</b> , 12, 3987	17.4	3
257	Risk Factors for New Vertebral Fracture After Percutaneous Vertebroplasty for Osteoporotic Vertebral Compression Fractures. <b>2021</b> , 16, 1193-1200		2
256	DNAm-based signatures of accelerated aging and mortality in blood are associated with low renal function. <i>Clinical Epigenetics</i> , <b>2021</b> , 13, 121	7.7	1
255	Genome and epigenome wide studies of plasma protein biomarkers for Alzheimer disease implicate TBCA and TREM2 in disease risk.		O
254	Association of mammographic density with blood DNA methylation. 2021, 1-16		1
253	Higher diet quality relates to decelerated epigenetic aging. 2021,		5
252	Lifestyle and Genetic Factors Modify Parent-of-Origin Effects on the Human Methylome.		
251	Predicting Complex Traits and Exposures From Polygenic Scores and Blood and Buccal DNA Methylation Profiles. <b>2021</b> , 12, 688464		4
250	Examining the association between adiposity and DNA methylation: A systematic review and meta-analysis. <b>2021</b> , 22, e13319		2
249	Hypermethylation of the oxytocin receptor gene (OXTR) in obsessive-compulsive disorder: further evidence for a biomarker of disease and treatment response. <b>2021</b> , 1-11		3

248	DNA methylation profiling in mummified human remains from the eighteenth-century. <i>Scientific Reports</i> , <b>2021</b> , 11, 15493	4.9	О
247	Genetics of substance use disorders in the era of big data. <b>2021</b> , 22, 712-729		7
246	Multi-omics insights into the biological mechanisms underlying gene-by-lifestyle interactions with smoking and alcohol consumption detected by genome-wide trans-ancestry meta-analysis.		
245	DNA methylome-wide association study of genetic risk for depression implicates antigen processing and immune responses.		
244	Epigenetic moderators of naltrexone efficacy in reducing heavy drinking in Alcohol Use Disorder: a randomized trial. <b>2021</b> ,		
243	Socially stratified epigenetic profiles are associated with cognitive functioning in children and adolescents.		Ο
242	DNA methylome and transcriptome landscapes of cancer-associated fibroblasts reveal a smoking-associated malignancy index. <b>2021</b> , 131,		4
241	Placental DNA methylation signatures of maternal smoking during pregnancy and potential impacts on fetal growth. <i>Nature Communications</i> , <b>2021</b> , 12, 5095	17.4	5
240	Importance of smoking cessation for cardiovascular risk reduction. <b>2021</b> , 42, 4154-4156		2
239	Cohort profile: Epigenetics in Pregnancy (EPIPREG) - population-based sample of European and South Asian pregnant women with epigenome-wide DNA methylation (850k) in peripheral blood leukocytes. <b>2021</b> , 16, e0256158		1
238	DNA methylation and regulation of gene expression: Guardian of our health. <b>2021</b> , 64, 1-12		9
237	Colorectal cancer risk in bowel adenomas based on lifestyle exposures, tissue preconditioning and DNA methylation.		
236	DNA methylome profiling reveals epigenetic regulation of lipoprotein-associated phospholipase A in human vulnerable atherosclerotic plaque. <i>Clinical Epigenetics</i> , <b>2021</b> , 13, 161	7.7	0
235	An Examination of Risk Factors for Tobacco and Cannabis Smoke Exposure in Adolescents Using an Epigenetic Biomarker. <b>2021</b> , 12, 688384		1
234	Hypomethylation of (cg05575921) Is Related to Smoking Status in the Mexican Mestizo Population. <b>2021</b> , 12,		
233	Epigenome-wide DNA methylation signature of benzo[a]pyrene exposure and their mediation roles in benzo[a]pyrene-associated lung cancer development. <b>2021</b> , 416, 125839		8
232	GMQN: A reference-based method for correcting batch effects as well as probes bias in HumanMethylation BeadChip.		2
231	Identical twins carry a persistent epigenetic signature of early genome programming. <i>Nature Communications</i> , <b>2021</b> , 12, 5618	17.4	6

230	Socially stratified DNA-methylation profiles are associated with disparities in child and adolescent mental health.		
229	Smoking Methylation Marks for Prediction of Urothelial Cancer Risk. <b>2021</b> , 30, 2197-2206		1
228	Epigenome-Wide DNA Methylation and Pesticide Use in the Agricultural Lung Health Study. <b>2021</b> , 129, 97008		5
227	Longitudinal change in blood DNA epigenetic signature after smoking cessation. <b>2021</b> , 1-12		O
226	Investigating the DNA methylation profile of e-cigarette use. Clinical Epigenetics, 2021, 13, 183	7.7	1
225	Genome-wide methylation data improves dissection of the effect of smoking on body mass index. <b>2021</b> , 17, e1009750		1
224	Prenatal Tobacco Exposure and the Risk of Tobacco Smoking and Dependence in Offspring: a Systematic Review and Meta-Analysis. <b>2021</b> , 227, 108993		1
223	Exposure to polycyclic aromatic hydrocarbons, DNA methylation and heart rate variability among non-current smokers. <b>2021</b> , 288, 117777		3
222	Epigenetics in COPD: An Epidemiological Point of View. <b>2022</b> , 526-532		
221	Peripheral blood DNA and RNA biomarkers of cardiovascular disease in clinical practice. <b>2021</b> , 261-281		
220	Epigenetics in systemic lupus erythematosus and the integration of molecular pathways. <b>2021</b> , 35-61		
219	Epigenome-wide change and variation in DNA methylation in childhood: trajectories from birth to late adolescence. <i>Human Molecular Genetics</i> , <b>2021</b> , 30, 119-134	5.6	15
218	Gene expression in blood reflects smoking exposure among cancer-free women in the Norwegian Women and Cancer (NOWAC) postgenome cohort. <i>Scientific Reports</i> , <b>2021</b> , 11, 680	4.9	1
217	Investigating the DNA methylation profile of e-cigarette use.		
216	Epigenetic Biomarkers of Aging. <b>2019</b> , 155-171		4
215	Epigenome-450K-wide methylation signatures of active cigarette smoking: The Young Finns Study. <b>2020</b> , 40,		5
214	DNA methylation signatures of adolescent victimization: analysis of a longitudinal monozygotic twin sample. <b>2021</b> , 16, 1169-1186		2
213	DNA methylation as a marker for prenatal smoke exposure in adults.		1

212	Systematic Mendelian randomization framework elucidates hundreds of genetic loci which may influence disease through changes in DNA methylation levels.	3
211	Mining the Selective Remodeling of DNA Methylation in Promoter Regions to Identify Robust Gene-Level Associations with Phenotype.	2
210	Integrated single cell analysis of human lung fibrosis resolves cellular origins of predictive protein signatures in body fluids.	4
209	DNA methylation covariation in human whole blood and sperm: implications for studies of intergenerational epigenetic effects.	2
208	Assessing the co-variability of DNA methylation across peripheral cells and tissues: implications for the interpretation of findings in epigenetic epidemiology.	2
207	Analysis of socioeconomic disadvantage and pace of aging measured in saliva DNA methylation of children and adolescents.	2
206	Epigenome-wide change and variation in DNA methylation from birth to late adolescence.	2
205	Genome-wide association studies identify 137 loci for DNA methylation biomarkers of ageing.	8
204	An epigenetic biomarker of aging for lifespan and healthspan.	2
203	Appraising the causal relevance of DNA methylation for risk of lung cancer.	3
202	Improved prediction of chronological age from DNA methylation limits it as a biomarker of ageing.	
		6
201	Smoking induces coordinated DNA methylation and gene expression changes in adipose tissue with consequences for metabolic health.	2
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	consequences for metabolic health.  Epigenome-wide meta-analysis of PTSD across 10 military and civilian cohorts identifies novel	2
200	consequences for metabolic health.  Epigenome-wide meta-analysis of PTSD across 10 military and civilian cohorts identifies novel methylation loci.  Epigenome-wide analysis uncovers a blood-based DNA methylation biomarker of lifetime cannabis	3
200 199	consequences for metabolic health.  Epigenome-wide meta-analysis of PTSD across 10 military and civilian cohorts identifies novel methylation loci.  Epigenome-wide analysis uncovers a blood-based DNA methylation biomarker of lifetime cannabis use.  Placental DNA methylation signatures of maternal smoking during pregnancy and potential	3
200 199 198	consequences for metabolic health.  Epigenome-wide meta-analysis of PTSD across 10 military and civilian cohorts identifies novel methylation loci.  Epigenome-wide analysis uncovers a blood-based DNA methylation biomarker of lifetime cannabis use.  Placental DNA methylation signatures of maternal smoking during pregnancy and potential impacts on fetal growth.  Single-cell analyses identify tobacco smoke exposure-associated, dysfunctional CD16+ CD8 T cells	2 3 2 3

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191	Multiple gene-specific DNA methylation in blood leukocytes and colorectal cancer risk: a case-control study in China. <b>2017</b> , 8, 61239-61252	9
190	Environmental Epigenetic Changes, as Risk Factors for the Development of Diseases in Children: A Systematic Review. <b>2018</b> , 84, 212-224	29
189	Cigarette and Cannabis Smoking Effects on GPR15+ Helper T Cell Levels in Peripheral Blood: Relationships with Epigenetic Biomarkers. <b>2020</b> , 11,	4
188	Impact of BMI and waist circumference on epigenome-wide DNA methylation and identification of epigenetic biomarkers in blood: an EWAS in multi-ethnic Asian individuals. <i>Clinical Epigenetics</i> , <b>2021</b> , 7.7 13, 195	1
187	Cortactin Modulates Lung Endothelial Apoptosis Induced by Cigarette Smoke. <b>2021</b> , 10,	2
186	An epigenome-wide association study of educational attainment (n = 10,767).	
185	Epigenetic Changes and Epigenetic Targets in Head and Neck Cancer. <b>2018</b> , 327-352	
184	Epigenetic prediction of complex traits and death.	O
183	DNA methylation signature of smoking in lung cancer is enriched for exposure signatures in newborn and adult blood.	
182	Epigenetic signatures of starting and stopping smoking.	
181	DNA methylation links prenatal smoking exposure to later life health outcomes in offspring.	O
180	Alcohol consumption is associated with widespread changes in blood DNA methylation: analysis of cross-sectional and longitudinal data.	O
179	Epigenetic regulation of PAR4-related platelet activation: mechanistic links between environmental exposure and cardiovascular disease.	1
178	EpiSmokEr: A robust classifier to determine smoking status from DNA methylation data.	
177	Macrophage-specific NF- <b>B</b> activation dynamics can segregate inflammatory bowel disease patients.	

176	Epigenetics, the Vascular Wall, and Atherosclerosis. <b>2019</b> , 302-313	
175	Assessment of Dried Blood Spots for DNA Methylation Profiling.	
174	Smoking and blood DNA methylation: novel associations, replication of previous findings and assessment of reversibility.	
173	Identifying epigenetic biomarkers of established prognostic factors and survival in a clinical cohort of individuals with oropharyngeal cancer.	1
172	Epigenetic prediction of major depressive disorder.	1
171	Mitochondrial DNA Copy Number (mtDNA-CN) Can Influence Mortality and Cardiovascular Disease via Methylation of Nuclear DNA CpGs.	2
170	MethylNet: An Automated and Modular Deep Learning Approach for DNA Methylation Analysis.	
169	Smoking, DNA methylation and lung function: a Mendelian randomization analysis to investigate causal relationships.	
168	Genome-wide DNA methylation differences in nucleus accumbens of smokers vs. nonsmokers.	1
167	Genome-wide DNA methylation analysis of heavy cannabis exposure in a New Zealand longitudinal cohort.	
166	An integrative machine learning approach to discovering multi-level molecular mechanisms of obesity using data from monozygotic twin pairs.	
165	DNA methylation mediates the effect of cocaine use on HIV severity.	
164	A Mendelian randomization study of telomere length and blood-cell traits.	
163	Creating and validating a DNA methylation-based proxy for Interleukin-6.	2
162	DNA methylation signatures of aggression and closely related constructs: A meta-analysis of epigenome-wide studies across the lifespan.	
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159	Smoking May Affect Pulmonary Function through DNA Methylation: an Epigenome-Wide Association Study in Korean Men. <b>2020</b> , 9, 134-144	O

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157	Biomarkers and omics of health effects associated with traffic-related air pollution. <b>2020</b> , 281-309		
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153	DNA Methylation Abnormalities and Altered Whole Transcriptome Profiles after Switching from Combustible Tobacco Smoking to Heated Tobacco Products. <b>2021</b> ,		2
152	Cigarette Smoke and Nicotine-Containing E-cigarette Vapor Downregulate Lung WWOX Expression Which is Associated with Increased Severity of Murine ARDS.		О
151	Methylome-wide association study of antidepressant use in Generation Scotland and the Netherlands Twin Register implicates the innate immune system.		О
150	Genome-wide methylation data improves dissection of the effect of smoking on body mass index.		
149	Heterogeneous Mediation Analysis for Causal Inference.		
148	Epigenome-wide association studies of three social determinants of health and implications for lung functions among survivors of childhood cancer.		
147	No evidence for intervention-associated DNA methylation changes in monocytes of patients with posttraumatic stress disorder or anorexia nervosa.		
146	Epigenetic predictors of lifestyle traits applied to the blood and brain.		
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144	Smoking and Genomic Imprinting. <b>2017</b> , 114, 330-334		
143	[A Review of Epigenetic Modifications Regulate MicroRNA Expression in Lung Cancer]. <b>2020</b> , 23, 582-588		
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139	Head and Neck Cancers Are Not Alike When Tarred with the Same Brush: An Epigenetic Perspective from the Cancerization Field to Prognosis. <b>2021</b> , 13,		1
138	Genome-wide differentially methylated genes associated with posttraumatic stress disorder and longitudinal change in methylation in rape survivors. <b>2021</b> , 11, 594		Ο
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135	Epigenetic correlates of the psychological interventions outcomes: A systematic review and meta-analysis. <b>2022</b> , 7, 100310		O
134	Genetic variation influencing DNA methylation provides insights into molecular mechanisms regulating genomic function <b>2022</b> ,		6
133	Data Associated with Epigenetic Changes Brought by SARS-Cov-2: Enlightment on the Treatment and Public Health Practices. <b>2020</b> ,		
132	An integrative analysis of clinical and epigenetic biomarkers of mortality.		
131	Genome-Wide Evaluation of Transcriptomic Responses of Human Tissues to Smoke: A Systems Biology Study <b>2022</b> , 820, 146114		
130	AHRR (cg5575921) methylation safely improves specificity of lung cancer screening eligibility criteria: A cohort study <b>2022</b> ,		О
129	Epigenetics of single-site and multi-site atherosclerosis in African Americans from the Genetic Epidemiology Network of Arteriopathy (GENOA) <i>Clinical Epigenetics</i> , <b>2022</b> , 14, 10	7.7	O
128	GMQN: A Reference-Based Method for Correcting Batch Effects and Probe Bias in HumanMethylation BeadChip <b>2021</b> , 12, 810985		Ο
127	Complex Trait Methylation Risk Scores in the Prediction of Major Depressive Disorder.		
126	Epigenetic Regulation of F2RL3 Associates with Myocardial Infarction and Platelet Function 2022,		О
125	Epigenetics in Epidemiology. <b>2022</b> , 45-54		
124	Clinical Implication of Smoking-Related Aryl-Hydrocarbon Receptor Repressor (AHRR) Hypomethylation in Japanese Adults <b>2022</b> ,		2
123	Blood DNA methylation signatures are associated with social determinants of health among survivors of childhood cancer <b>2022</b> , 1-15		1

122	Aging clocks & mortality timers, methylation, glycomic, telomeric and more. A window to measuring biological age.		1
121	The influence of biological and statistical properties of CpGs on epigenetic predictions of eighteen traits.		
120	Lifestyle and Genetic Factors Modify Parent-of-Origin Effects on the Human Methylome. <i>EBioMedicine</i> , <b>2021</b> , 74, 103730	8.8	1
119	Epigenomic biomarkers of posttraumatic stress disorder. <b>2022</b> , 163-177		
118	An exposomic framework to uncover environmental drivers of aging <b>2022</b> , 2, osac002		1
117	The Epigenetics of Psychosis: A Structured Review with Representative Loci <b>2022</b> , 10,		1
116	Cell-type heterogeneity: Why we should adjust for it in epigenome and biomarker studies <i>Clinical Epigenetics</i> , <b>2022</b> , 14, 31	7.7	2
115	Race-associated Molecular Changes in Gynecologic Malignancies. <b>2022</b> , 2, 99-109		O
114	Repeat measures of DNA methylation in an inception cohort of firefighters 2022,		О
113	DNA methylation-based predictors of health: applications and statistical considerations 2022,		3
112	Birth history is associated with whole-blood and T-cell methylation patterns in relapse onset multiple sclerosis.		
111	Grandmaternal smoking during pregnancy is associated with differential DNA methylation in peripheral blood of their grandchildren <b>2022</b> ,		О
110	DNA methylation changes in cord blood and the developmental origins of health and disease - a systematic review and replication study <b>2022</b> , 23, 221		О
109	Epigenome-wide association study and epigenetic age acceleration associated with cigarette smoking among Costa Rican adults <i>Scientific Reports</i> , <b>2022</b> , 12, 4277	4.9	1
108	COPD is Associated with Epigenome-wide Differential Methylation in BAL Lung Cells 2022,		О
107	Early life affects late-life health through determining DNA methylation across the lifespan: A twin study <i>EBioMedicine</i> , <b>2022</b> , 77, 103927	8.8	1
106	Evaluation of nanopore sequencing for epigenetic epidemiology: a comparison with DNA methylation microarrays.		
105	Blood-derived DNA methylation clusters associate with adverse social exposures and endophenotypes of stress-related psychiatric illness in a trauma-exposed cohort of women.		

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104	DNA methylome-wide association study of genetic risk for depression implicates antigen processing and immune responses <b>2022</b> , 14, 36		1
103	High-Dimensional DNA Methylation Mediates the Effect of Smoking on Crohn's Disease <b>2022</b> , 13, 83188	35	O
102	DNA methylation in peripheral tissues and left-handedness <i>Scientific Reports</i> , <b>2022</b> , 12, 5606	<b>4</b> .9	О
101	Epigenetic Signatures of Smoking in Five Brain Regions <b>2022</b> , 12,		Ο
100	A comparison of feature selection methodologies and learning algorithms in the development of a DNA methylation-based telomere length estimator.		О
99	Lifetime marijuana use and epigenetic age acceleration: A 17-year prospective examination <b>2022</b> , 233, 109363		O
98	Epigenome-Wide Association Study of Prostate Cancer in African Americans Identifies DNA Methylation Biomarkers for Aggressive Disease <b>2021</b> , 11,		1
97	Methylome-wide association study of antidepressant use in Generation Scotland and the Netherlands Twin Register implicates the innate immune system. <b>2021</b> ,		1
96	Influence of Environmental Factors on the Epigenome. <b>2022</b> , 277-322		
95	Cell-Type Heterogeneity in DNA Methylation Studies: Statistical Methods and Guidelines. 2022, 67-96		
94	Epigenetic Epidemiology of Cancer. <b>2022</b> , 325-342		
93	The potential of DNA methylation as a biomarker for obesity and smoking 2022,		2
92	Cross-tissue meta-analysis of blood and brain epigenome-wide association studies in Alzheimer disease.		Ο
91	Expression quantitative trait methylation analysis elucidates gene regulatory effects of DNA methylation: The Framingham Heart Study.		
90	Impact of Electronic Cigarette Vaping on Cerebral Ischemia: What We Know So Far 2022, 1		Ο
89	Detecting Blood Methylation Signatures in Response to Childhood Cancer Radiotherapy via Machine Learning Methods <i>Biology</i> , <b>2022</b> , 11,	<b>1</b> .9	
88	Characterisation of ethnic differences in DNA methylation between UK resident South Asians and Europeans.		0
87	Image_1.TIF. <b>2020</b> ,		

86	lmage_2.TIF. <b>2020</b> ,		
85	Image_3.TIF. <b>2020</b> ,		
84	Image_4.TIF. <b>2020</b> ,		
83	Image_5.TIF. <b>2020</b> ,		
82	Image_6.TIF. <b>2020</b> ,		
81	Image_7.TIF. <b>2020</b> ,		
80	Image_8.TIF. <b>2020</b> ,		
79	Data_Sheet_1.PDF. <b>2019</b> ,		
78	Data_Sheet_1.xlsx. <b>2018</b> ,		
77	Data_Sheet_1.docx. <b>2020</b> ,		
76	Lifestyle, behaviour, and environmental modification for the management of patients with inflammatory bowel diseases: an International Organization for Study of Inflammatory Bowel Diseases consensus <i>The Lancet Gastroenterology and Hepatology</i> , <b>2022</b> ,	18.8	1
75	Role of Long Noncoding RNAs in Smoking-Induced Lung Cancer: An In Silico Study <i>Computational and Mathematical Methods in Medicine</i> , <b>2022</b> , 2022, 7169353	2.8	
74	Cortactin in Lung Cell Function and Disease International Journal of Molecular Sciences, 2022, 23,	6.3	1
73	Effects of stressful life-events on DNA methylation in panic disorder and major depressive disorder <i>Clinical Epigenetics</i> , <b>2022</b> , 14, 55	7.7	О
72	Age-Related DNA Methylation in Normal Kidney Tissue Identifies Epigenetic Cancer Risk Susceptibility Loci in the ANKRD34B and ZIC1 Genes. <i>International Journal of Molecular Sciences</i> , <b>2022</b> , 23, 5327	6.3	О
71	Pulmonary Function and Blood DNA Methylation: A Multi-Ancestry Epigenome-Wide Association Meta-Analysis <i>American Journal of Respiratory and Critical Care Medicine</i> , <b>2022</b> ,	10.2	0
70	Complex trait methylation scores in the prediction of major depressive disorder <i>EBioMedicine</i> , <b>2022</b> , 79, 104000	8.8	О
69	DNA methylation signature of chronic low-grade inflammation and its role in cardio-respiratory diseases <i>Nature Communications</i> , <b>2022</b> , 13, 2408	17.4	1

68	Evaluation of nanopore sequencing for epigenetic epidemiology: a comparison with DNA methylation microarrays <i>Human Molecular Genetics</i> , <b>2022</b> ,	5.6	1
67	Cigarette Smoke Regulates the Expression of EYA4 via Alternation of DNA Methylation Status. <i>BioMed Research International</i> , <b>2022</b> , 2022, 1-7	3	
66	Dysmaturational Longitudinal Epigenetic Aging During Transition To Psychosis. <i>Schizophrenia Bulletin Open</i> ,	2.2	0
65	Epigenetic mechanisms of lung carcinogenesis involve differentially methylated CpG sites beyond those associated with smoking. <i>European Journal of Epidemiology</i> ,	12.1	О
64	Predicting risk of lung function impairment and all-cause mortality using a DNA methylation-based classifier of tobacco smoke exposure. <i>Respiratory Medicine</i> , <b>2022</b> , 106896	4.6	О
63	Epigenome-wide association study analysis of calorie restriction in humans, CALERIED rial analysis.		
62	Prenatal Maternal Smoke, DNA Methylation, and Multi-omics of Tissues and Child Health. <i>Current Environmental Health Reports</i> ,	6.5	1
61	Heterogeneous Mediation Analysis on Epigenomic PTSD and Traumatic Stress in a Predominantly African American Cohort. <i>Journal of the American Statistical Association</i> , 1-36	2.8	О
60	Association between DNA methylation variability and self-reported exposure to heavy metals. <i>Scientific Reports</i> , <b>2022</b> , 12,	4.9	О
59	Uncertainty quantification of reference based cellular deconvolution algorithms.		
58	Mortality and morbidity risk prediction for older former smokers based on a score of smoking history: evidence from UK Biobank and ESTHER cohorts. <i>Age and Ageing</i> , <b>2022</b> , 51,	3	О
57	Impact of the Exposome on the Epigenome in Inflammatory Bowel Disease Patients and Animal Models. <i>International Journal of Molecular Sciences</i> , <b>2022</b> , 23, 7611	6.3	2
56	Methylation in the Promoter Region of the Dopamine Transporter DAT1 Gene in People Addicted to Nicotine. <i>International Journal of Environmental Research and Public Health</i> , <b>2022</b> , 19, 8602	4.6	2
55	Sex-specific and generational effects of alcohol and tobacco use on epigenetic age acceleration in the Michigan longitudinal study. <b>2022</b> , 4, 100077		1
54	Toxicoepigenetics and Environmental Health: Challenges and Opportunities. <b>2022</b> , 35, 1293-1311		Ο
53	Epigenome-wide association study analysis of calorie restriction in humans, CALERIE TM Trial analysis.		1
52	Genome-wide DNA methylation profiles in smoking discordant and concordant monozygotic twin pairs.		

50	Contribution of the Environment, Epigenetic Mechanisms and Non-Coding RNAs in Psoriasis. <b>2022</b> , 10, 1934	1
49	A bibliometric analysis of DNA methylation in cardiovascular diseases from 2001 to 2021. <b>2022</b> , 101, e30029	
48	How does age determine the development of human immune-mediated arthritis?. 2022, 18, 501-512	1
47	Schizophrenia-associated differential DNA methylation in brain is distributed across the genome and annotated to MAD1L1, a locus at which DNA methylation and transcription phenotypes share genetic variation with schizophrenia risk. <b>2022</b> , 12,	O
46	DNA methylation analysis for smoking status prediction in the Chinese population based on the methylation-sensitive single-nucleotide primer extension method. <b>2022</b> , 339, 111412	1
45	Epigenetics. <b>2022</b> , 585-616	O
44	Derivation and validation of an epigenetic frailty risk score in population-based cohorts of older adults. <b>2022</b> , 13,	0
43	Translation of a tissue epigenetic signature to circulating free DNA suggests BCAT1 as a potential noninvasive diagnostic biomarker for lung cancer. <b>2022</b> , 14,	O
42	Brain-Derived Neurotrophic Factor (BDNF) Epigenomic Modifications and Brain-Related Phenotypes in Humans: A Systematic Review.	О
41	A Brief Landscape of Epigenetic Mechanisms in Dental Pathologies. <b>2022</b> , 56, 475-480	o
40	Blood transcriptomic biomarkers of alcohol consumption and cardiovascular disease risk factors: the Framingham Heart Study.	О
39	Methylation-based markers of aging and lifestyle-related factors and risk of breast cancer: a pooled analysis of four prospective studies. <b>2022</b> , 24,	O
38	Influence of smoking on disease activity and quality of life in patients with rheumatoid arthritis: results from a Swedish case-control study with longitudinal follow-up.	0
37	Longitudinal Association of DNA Methylation with Type 2 Diabetes and Glycemic Traits: A 5-year Cross-Lagged Twin Study.	1
36	Overexpression of Cancer- and Neurotransmitter-Associated Genes in the Nucleus Accumbens of Smokers.	0
35	Osteoporosis and Alveolar Bone Health in Periodontitis Niche: A Predisposing Factors-Centered Review. <b>2022</b> , 11, 3380	O
34	Developmental origins of psycho-cardiometabolic multimorbidity in adolescence and their underlying pathways through methylation markers: A two cohorts study.	О
33	Characterisation of ethnic differences in DNA methylation between UK-resident South Asians and Europeans. <b>2022</b> , 14,	1

32	The Interplay of Epigenetic, Genetic, and Traditional Risk Factors on Blood Pressure: Findings from the Health and Retirement Study. <b>2022</b> , 13, 1959	O
31	No evidence for intervention-associated DNA methylation changes in monocytes of patients with posttraumatic stress disorder. <b>2022</b> , 12,	O
30	The impact of low input DNA on the reliability of DNA methylation as measured by the Illumina Infinium MethylationEPIC BeadChip. 1-11	1
29	Implications of the changing epidemiology of inflammatory bowel disease in a changing world.	2
28	Chronische Immunaktivierung. <b>2022</b> , 141-243	О
27	Epigenomic Links Between Social Determinants of Health and Symptoms: A Scoping Review. 109980042211	473
26	Uncertainty quantification of reference-based cellular deconvolution algorithms. 1-15	О
25	Socially Stratified Epigenetic Profiles Are Associated With Cognitive Functioning in Children and Adolescents. 095679762211227	O
24	Multi-omics insights into the biological mechanisms underlying statistical gene-by-lifestyle interactions with smoking and alcohol consumption. 13,	1
23	Fathers[preconception smoking and offspring DNA methylation: A two generation study.	O
22	ROS induced the Rab26 promoter hypermethylation to promote cigarette smoking-induced airway epithelial inflammation of COPD through activation of MAPK signaling. <b>2023</b> , 195, 359-370	0
21	Whole-blood methylation signatures are associated with and accurately classify multiple sclerosis disease severity. <b>2022</b> , 14,	O
20	Trans-ancestry epigenome-wide association meta-analysis of DNA methylation with lifetime cannabis use.	О
19	Measuring the long arm of childhood in real-time: Epigenetic predictors of BMI and social determinants of health across childhood and adolescence.	O
18	Traffic-Related Air Pollution and Ground-Level Ozone Associated Global DNA Hypomethylation and Bulky DNA Adduct Formation. <b>2023</b> , 24, 2041	О
17	Chronic Immune System Activation. <b>2023</b> , 135-231	O
16	DNA methylation analysis identifies novel genetic loci associated with circulating fibrinogen levels in blood. <b>2023</b> ,	Ο
15	Opioid medication use and blood DNA methylation: epigenome-wide association meta-analysis.	O

14	Methylation scores for smoking, alcohol consumption, and body mass index and risk of seven types of cancer.	Ο
13	Epigenetic biomarkers for smoking cessation. <b>2023</b> , 6, 100079	О
12	Present and future challenges for the investigation of transgenerational epigenetic inheritance. <b>2023</b> , 172, 107776	0
11	Molecular mechanisms of environmental exposures and human disease. <b>2023</b> , 24, 332-344	O
10	Brain-derived neurotrophic factor (BDNF) epigenomic modifications and brain-related phenotypes in humans: A systematic review. <b>2023</b> , 147, 105078	O
9	Parity is associated with long-term differences in DNA methylation at genes related to neural plasticity in multiple sclerosis. <b>2023</b> , 15,	O
8	Epigenome-wide association study using peripheral blood leukocytes identifies genomic regions associated with periodontal disease and edentulism in the Atherosclerosis Risk in Communities Study.	O
7	An overview of DNA methylation-derived trait score methods and applications. <b>2023</b> , 24,	О
6	DNA-Methylation Signatures of Tobacco Smoking in a High Cardiovascular Risk Population: Modulation by the Mediterranean Diet. <b>2023</b> , 20, 3635	0
5	SERPINA1 and More? A Putative Genetic Contributor to Pulmonary Dysfunction in Alpha-1 Antitrypsin Deficiency. <b>2023</b> , 12, 1708	О
4	Refining epigenetic prediction of chronological and biological age. <b>2023</b> , 15,	1
3	Probabilistic inference of epigenetic age acceleration from cellular dynamics.	О
2	By what molecular mechanisms do social determinants impact cardiometabolic risk?. 2023, 137, 469-494	0
1	Association of frequent hypermethylation with high grade histological subtype in lung adenocarcinoma.	O