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Epigenetic Signatures of Cigarette Smoking

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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
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200	Epigenome-wide meta-analysis of PTSD across 10 military and civilian cohorts identifies novel methylation loci.	3
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182	Epigenetic signatures of starting and stopping smoking.		
181	DNA methylation links prenatal smoking exposure to later life health outcomes in offspring.		0
180	Alcohol consumption is associated with widespread changes in blood DNA methylation: analysis of cross-sectional and longitudinal data.		0
179	Epigenetic regulation of PAR4-related platelet activation: mechanistic links between environmental exposure and cardiovascular disease.		1
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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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152	Cigarette Smoke and Nicotine-Containing E-cigarette Vapor Downregulate Lung WWOX Expression Which is Associated with Increased Severity of Murine ARDS.		0
151	Methylome-wide association study of antidepressant use in Generation Scotland and the Netherlands Twin Register implicates the innate immune system.		0
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.		
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133	Data Associated with Epigenetic Changes Brought by SARS-Cov-2 : Enlightment on the Treatment and Public Health Practices. **2020**,		
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131	Genome-Wide Evaluation of Transcriptomic Responses of Human Tissues to Smoke: A Systems Biology Study.. **2022**, 820, 146114		
130	AHRR (cg5575921) methylation safely improves specificity of lung cancer screening eligibility criteria: A cohort study.. **2022**,		0
129	Epigenetics of single-site and multi-site atherosclerosis in African Americans from the Genetic Epidemiology Network of Arteriopathy (GENOA).. *Clinical Epigenetics*, **2022**, 14, 10	7.7	0
128	GMQN: A Reference-Based Method for Correcting Batch Effects and Probe Bias in HumanMethylation BeadChip.. **2021**, 12, 810985		0
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**,		0
125	Epigenetics in Epidemiology. **2022**, 45-54		
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