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Functional normalization of 450k methylation array data improves replication in large cancer studies

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595	Epigenome-Wide Association Study of Tic Disorders. 2015 , 18, 699-709		24
594	DNA Methylation Changes in the IGF1R Gene in Birth Weight Discordant Adult Monozygotic Twins. 2015 , 18, 635-46		20
593	Epigenome-Wide Association Study of Wellbeing. 2015 , 18, 710-9		10
592	Epigenome-Wide Association Study of Aggressive Behavior. 2015 , 18, 686-98		29
591	Patterns of gene expression and DNA methylation in human fetal and adult liver. 2015 , 16, 981		24
590	Reconstructing A/B compartments as revealed by Hi-C using long-range correlations in epigenetic data. <i>Genome Biology</i> , 2015 , 16, 180	18.3	132
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585	Removing unwanted variation in a differential methylation analysis of Illumina HumanMethylation450 array data. 2015 , 43, e106		58
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583	Hypomethylation of smoking-related genes is associated with future lung cancer in four prospective cohorts. <i>Nature Communications</i> , 2015 , 6, 10192	17.4	144
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145	A multi-omics approach to visualize early neuronal differentiation in 4D.		0
144	Maternal and Neonatal One-Carbon Metabolites and the Epigenome-wide Infant Response.. 2022 , 101, 108938		1
143	Placental genomics mediates genetic associations with complex health traits and disease.. <i>Nature Communications</i> , 2022 , 13, 706	17.4	0
142	DNA methylation-based age acceleration observed in IDH wild-type glioblastoma is associated with better outcome - including in elderly patients.		
141	Maternal adverse childhood experiences before pregnancy are associated with epigenetic aging changes in their children.. 2021 , 13,		6
140	Gender-affirming hormone therapy induces specific DNA methylation changes in blood.. <i>Clinical Epigenetics</i> , 2022 , 14, 24	7.7	1
139	Hypomethylation of miR-17-92 cluster in lupus T cells and no significant role for genetic factors in the lupus-associated DNA methylation signature.		0
138	Updates to data versions and analytic methods influence the reproducibility of results from epigenome-wide association studies.. 2022 , 1-16		0
137	Environmentally sensitive hotspots in the methylome of the early human embryo.. 2022 , 11,		3
136	Characterization of Early Peripheral Immune Responses in Patients with Sepsis and Septic Shock.. 2022 , 10,		0
135	Genome-wide study of DNA methylation shows alterations in metabolic, inflammatory, and cholesterol pathways in ALS.. 2022 , 14, eabj0264		4
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