Charles E Mordaunt

List of Publications by Year
in descending order

15	456	840585 11	996849 15
papers	citations	h-index	g-index

24	24	24	540
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Cumulative Impact of Polychlorinated Biphenyl and Large Chromosomal Duplications on DNA Methylation, Chromatin, and Expression of Autism Candidate Genes. Cell Reports, 2016, 17, 3035-3048.	2.9	69
2	Placental DNA methylation levels at CYP2E1 and IRS2 are associated with child outcome in a prospective autism study. Human Molecular Genetics, 2019, 28, 2659-2674.	1.4	57
3	Snord116-dependent diurnal rhythm of DNA methylation in mouse cortex. Nature Communications, 2018, 9, 1616.	5.8	53
4	Cord blood DNA methylome in newborns later diagnosed with autism spectrum disorder reflects early dysregulation of neurodevelopmental and X-linked genes. Genome Medicine, 2020, 12, 88.	3.6	47
5	Whole genome bisulfite sequencing of Down syndrome brain reveals regional DNA hypermethylation and novel disorder insights. Epigenetics, 2019, 14, 672-684.	1.3	39
6	Epigenomic signatures in liver and blood of Wilson disease patients include hypermethylation of liver-specific enhancers. Epigenetics and Chromatin, 2019, 12, 10.	1.8	32
7	Low-pass whole genome bisulfite sequencing of neonatal dried blood spots identifies a role for RUNX1 in Down syndrome DNA methylation profiles. Human Molecular Genetics, 2021, 29, 3465-3476.	1.4	32
8	Placental methylome reveals a 22q13.33 brain regulatory gene locus associated with autism. Genome Biology, 2022, 23, 46.	3.8	22
9	Experience-dependent neuroplasticity of the developing hypothalamus: integrative epigenomic approaches. Epigenetics, 2018, 13, 318-330.	1.3	21
10	UBE3A-mediated regulation of imprinted genes and epigenome-wide marks in human neurons. Epigenetics, 2017, 12, 982-990.	1.3	18
11	Epigenetic changes of the thioredoxin system in the tx-j mouse model and in patients with Wilson disease. Human Molecular Genetics, 2018, 27, 3854-3869.	1.4	18
12	A meta-analysis of two high-risk prospective cohort studies reveals autism-specific transcriptional changes to chromatin, autoimmune, and environmental response genes in umbilical cord blood. Molecular Autism, 2019, 10, 36.	2.6	14
13	Expression Changes in Epigenetic Gene Pathways Associated With Oneâ€Carbon Nutritional Metabolites in Maternal Blood From Pregnancies Resulting in Autism and Nonâ€Typical Neurodevelopment. Autism Research, 2021, 14, 11-28.	2.1	8
14	mtDNA depletionâ€like syndrome in Wilson disease. Liver International, 2020, 40, 2776-2787.	1.9	7
15	Comethyl: a network-based methylome approach to investigate the multivariate nature of health and disease. Briefings in Bioinformatics, 2022, 23, .	3.2	5