

Charles E Mordaunt

List of Publications by Year in descending order

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Version: 2024-02-01

15
papers

456
citations

840585

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996849

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24
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24
docs citations

24
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540
citing authors

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