

Juan Castillo-Fernandez

List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

1,101
citations

516215

16
h-index

525886

27
g-index

29
all docs

29
docs citations

29
times ranked

2295
citing authors

#	ARTICLE	IF	CITATIONS
1	Pulmonary Function and Blood DNA Methylation: A Multiancestry Epigenome-Wide Association Meta-analysis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2022, 206, 321-336.	2.5	15
2	Epigenetic changes induced by in utero dietary challenge result in phenotypic variability in successive generations of mice. <i>Nature Communications</i> , 2022, 13, 2464.	5.8	13
3	Epigenome-Wide Association Study of Thyroid Function Traits Identifies Novel Associations of fT3 With <i>KLF9</i> and <i>DOT1L</i> . <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021, 106, e2191-e2202.	1.8	14
4	Life course socioeconomic position and DNA methylation age acceleration in mid-life. <i>Journal of Epidemiology and Community Health</i> , 2021, 75, 1084-1090.	2.0	17
5	Revisiting the Impact of Local Leptin Signaling in Folliculogenesis and Oocyte Maturation in Obese Mothers. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4270.	1.8	11
6	Epigenome-wide association meta-analysis of DNA methylation with coffee and tea consumption. <i>Nature Communications</i> , 2021, 12, 2830.	5.8	35
7	Childhood growth and development and DNA methylation age in mid-life. <i>Clinical Epigenetics</i> , 2021, 13, 155.	1.8	5
8	Identical twins carry a persistent epigenetic signature of early genome programming. <i>Nature Communications</i> , 2021, 12, 5618.	5.8	26
9	Estrogen and COVID-19 symptoms: Associations in women from the COVID Symptom Study. <i>PLoS ONE</i> , 2021, 16, e0257051.	1.1	68
10	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	9.4	218
11	Leptin Signaling in the Ovary of Diet-Induced Obese Mice Regulates Activation of NOD-Like Receptor Protein 3 Inflammasome. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 738731.	1.8	4
12	DNA methylation age and physical and cognitive ageing. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2020, 75, 504-511.	1.7	35
13	Landscape of Genome-Wide DNA Methylation of Colorectal Cancer Metastasis. <i>Cancers</i> , 2020, 12, 2710.	1.7	18
14	Increased transcriptome variation and localised DNA methylation changes in oocytes from aged mice revealed by parallel single-cell analysis. <i>Aging Cell</i> , 2020, 19, e13278.	3.0	27
15	Blood DNA methylation sites predict death risk in a longitudinal study of 12, 300 individuals. <i>Aging</i> , 2020, 12, 14092-14124.	1.4	15
16	Leptin Resistance in the Ovary of Obese Mice is Associated with Profound Changes in the Transcriptome of Cumulus Cells. <i>Cellular Physiology and Biochemistry</i> , 2020, 54, 417-437.	1.1	11
17	Dissecting the role of the gut microbiota and diet on visceral fat mass accumulation. <i>Scientific Reports</i> , 2019, 9, 9758.	1.6	41
18	Association of dietary folate and vitamin B-12 intake with genome-wide DNA methylation in blood: a large-scale epigenome-wide association analysis in 5841 individuals. <i>American Journal of Clinical Nutrition</i> , 2019, 110, 437-450.	2.2	46

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19	Epigenetic findings in periodontitis in UK twins: a cross-sectional study. <i>Clinical Epigenetics</i> , 2019, 11, 27.	1.8	37
20	Genome-wide methylation analysis identifies ELOVL5 as an epigenetic biomarker for the risk of type 2 diabetes mellitus. <i>Scientific Reports</i> , 2018, 8, 14862.	1.6	22
21	Smoking induces coordinated DNA methylation and gene expression changes in adipose tissue with consequences for metabolic health. <i>Clinical Epigenetics</i> , 2018, 10, 126.	1.8	110
22	Associations between body size, nutrition and socioeconomic position in early life and the epigenome: A systematic review. <i>PLoS ONE</i> , 2018, 13, e0201672.	1.1	11
23	DNA methylation changes at infertility genes in newborn twins conceived by in vitro fertilisation. <i>Genome Medicine</i> , 2017, 9, 28.	3.6	47
24	A computational toxicogenomics approach identifies a list of highly hepatotoxic compounds from a large microarray database. <i>PLoS ONE</i> , 2017, 12, e0176284.	1.1	32
25	Genetic and environmental impacts on DNA methylation levels in twins. <i>Epigenomics</i> , 2016, 8, 105-117.	1.0	31
26	Down-Regulation of TLR and JAK/STAT Pathway Genes Is Associated with Diffuse Cutaneous Leishmaniasis: A Gene Expression Analysis in NK Cells from Patients Infected with <i>Leishmania mexicana</i> . <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004570.	1.3	33
27	Epigenetics of discordant monozygotic twins: implications for disease. <i>Genome Medicine</i> , 2014, 6, 60.	3.6	157