Sarah J Marzi

List of Publications by Year in Descending Order

Source: https://exaly.com/author-pdf/4274575/sarah-j-marzi-publications-by-year.pdf

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

19	297	7	17
papers	citations	h-index	g-index
22	447 ext. citations	9.5	3.31
ext. papers		avg, IF	L-index

#	Paper	IF	Citations
19	Genetic variation at mouse and human ribosomal DNA influences associated epigenetic states <i>Genome Biology</i> , 2022 , 23, 54	18.3	3
18	The histone modification H3K4me3 is altered at the locus in Alzheimers disease brain. <i>Future Science OA</i> , 2021 , 7, FSO665	2.7	5
17	Chd8 regulates X chromosome inactivation in mouse through fine-tuning control of Xist expression. <i>Communications Biology</i> , 2021 , 4, 485	6.7	O
16	The DNA methylome of human sperm is distinct from blood with little evidence for tissue-consistent obesity associations. <i>PLoS Genetics</i> , 2020 , 16, e1009035	6	4
15	DNA methylation in human sperm: a systematic review. <i>Human Reproduction Update</i> , 2020 , 26, 841-873	15.8	15
14	The DNA methylome of human sperm is distinct from blood with little evidence for tissue-consistent obesity associations 2020 , 16, e1009035		
13	The DNA methylome of human sperm is distinct from blood with little evidence for tissue-consistent obesity associations 2020 , 16, e1009035		
12	The DNA methylome of human sperm is distinct from blood with little evidence for tissue-consistent obesity associations 2020 , 16, e1009035		
11	The DNA methylome of human sperm is distinct from blood with little evidence for tissue-consistent obesity associations 2020 , 16, e1009035		
10	Genetic risk variants for brain disorders are enriched in cortical H3K27ac domains. <i>Molecular Brain</i> , 2019 , 12, 7	4.5	11
9	Epigenetics in eating disorders: a systematic review. <i>Molecular Psychiatry</i> , 2019 , 24, 901-915	15.1	32
8	Analysis of DNA Methylation in Young People: Limited Evidence for an Association Between Victimization Stress and Epigenetic Variation in Blood. <i>American Journal of Psychiatry</i> , 2018 , 175, 517-52	2 5 1.9	83
7	Early life diet conditions the molecular response to post-weaning protein restriction in the mouse. <i>BMC Biology</i> , 2018 , 16, 51	7.3	7
6	A histone acetylome-wide association study of Alzheimers disease identifies disease-associated H3K27ac differences in the entorhinal cortex. <i>Nature Neuroscience</i> , 2018 , 21, 1618-1627	25.5	72
5	Genetic polymorphisms and their association with brain and behavioural measures in heterogeneous stock mice. <i>Scientific Reports</i> , 2017 , 7, 41204	4.9	1
4	Severe psychosocial deprivation in early childhood is associated with increased DNA methylation across a region spanning the transcription start site of CYP2E1. <i>Translational Psychiatry</i> , 2016 , 6, e830	8.6	41
3	Tissue-specific patterns of allelically-skewed DNA methylation. <i>Epigenetics</i> , 2016 , 11, 24-35	5.7	18

Iterative Fragmentation Improves the Detection of ChIP-seq Peaks for Inactive Histone Marks.

Bioinformatics and Biology Insights, **2016**, 10, 209-224

5.3 3

DNA methylation covariation in human whole blood and sperm: implications for studies of intergenerational epigenetic effects

2