

Ben I Laufer

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6012286/publications.pdf>

Version: 2024-02-01

30
papers

1,097
citations

393982

19
h-index

433756

31
g-index

42
all docs

42
docs citations

42
times ranked

1371
citing authors

#	ARTICLE	IF	CITATIONS
1	Long-lasting alterations to DNA methylation and ncRNAs could underlie the effects of fetal alcohol exposure in mice. <i>DMM Disease Models and Mechanisms</i> , 2013, 6, 977-92.	1.2	113
2	Associative DNA methylation changes in children with prenatal alcohol exposure. <i>Epigenomics</i> , 2015, 7, 1259-1274.	1.0	93
3	The effects of olanzapine on genome-wide DNA methylation in the hippocampus and cerebellum. <i>Clinical Epigenetics</i> , 2014, 6, 1.	1.8	62
4	Long-term genomic and epigenomic dysregulation as a consequence of prenatal alcohol exposure: a model for fetal alcohol spectrum disorders. <i>Frontiers in Genetics</i> , 2014, 5, 161.	1.1	57
5	Snord116-dependent diurnal rhythm of DNA methylation in mouse cortex. <i>Nature Communications</i> , 2018, 9, 1616.	5.8	53
6	Long-term alterations to the brain transcriptome in a maternal voluntary consumption model of fetal alcohol spectrum disorders. <i>Brain Research</i> , 2012, 1458, 18-33.	1.1	52
7	Alteration of Gene Expression, DNA Methylation, and Histone Methylation in Free Radical Scavenging Networks in Adult Mouse Hippocampus following Fetal Alcohol Exposure. <i>PLoS ONE</i> , 2016, 11, e0154836.	1.1	51
8	Strategies for precision modulation of gene expression by epigenome editing: an overview. <i>Epigenetics and Chromatin</i> , 2015, 8, 34.	1.8	50
9	DNA methylation differences in monozygotic twin pairs discordant for schizophrenia identifies psychosis related genes and networks. <i>BMC Medical Genomics</i> , 2015, 8, 17.	0.7	47
10	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
11	Long-term alterations to DNA methylation as a biomarker of prenatal alcohol exposure: From mouse models to human children with fetal alcohol spectrum disorders. <i>Alcohol</i> , 2017, 60, 67-75.	0.8	44
12	Changes to histone modifications following prenatal alcohol exposure: An emerging picture. <i>Alcohol</i> , 2017, 60, 41-52.	0.8	41
13	Olanzapine induced DNA methylation changes support the dopamine hypothesis of psychosis. <i>Journal of Molecular Psychiatry</i> , 2013, 1, 19.	2.0	40
14	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
15	Reduced expression of brain cannabinoid receptor 1 (Cnr1) is coupled with an increased complementary micro-RNA (miR-26b) in a mouse model of fetal alcohol spectrum disorders. <i>Clinical Epigenetics</i> , 2013, 5, 14.	1.8	32
16	Molecular Changes during Neurodevelopment following Second-Trimester Binge Ethanol Exposure in a Mouse Model of Fetal Alcohol Spectrum Disorder: From Immediate Effects to Long-Term Adaptation. <i>Developmental Neuroscience</i> , 2014, 36, 29-43.	1.0	32
17	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
18	Epigenomic Convergence of Neural-Immune Risk Factors in Neurodevelopmental Disorder Cortex. <i>Cerebral Cortex</i> , 2020, 30, 640-655.	1.6	29

#	ARTICLE	IF	CITATIONS
19	Placenta and fetal brain share a neurodevelopmental disorder DNA methylation profile in a mouse model of prenatal PCB exposure. <i>Cell Reports</i> , 2022, 38, 110442.	2.9	27
20	Placental methylome reveals a 22q13.33 brain regulatory gene locus associated with autism. <i>Genome Biology</i> , 2022, 23, 46.	3.8	22
21	Experience-dependent neuroplasticity of the developing hypothalamus: integrative epigenomic approaches. <i>Epigenetics</i> , 2018, 13, 318-330.	1.3	21
22	Third Trimester-Equivalent Ethanol Exposure Is Characterized by an Acute Cellular Stress Response and an Ontogenetic Disruption of Genes Critical for Synaptic Establishment and Function in Mice. <i>Developmental Neuroscience</i> , 2014, 36, 499-519.	1.0	19
23	DNA methylation in psychosis: insights into etiology and treatment. <i>Epigenomics</i> , 2015, 7, 67-74.	1.0	17
24	Stable DNMT3L overexpression in SH-SY5Y neurons recreates a facet of the genome-wide Down syndrome DNA methylation signature. <i>Epigenetics and Chromatin</i> , 2021, 14, 13.	1.8	12
25	A Macro Role for Imprinted Clusters of MicroRNAs in the Brain. <i>MicroRNA (Sharjah, United Arab)</i> Tj ETQq1 1 0.784314 rgBT /Overloc 10	0.6	10
26	Imprinting effects of UBE3A loss on synaptic gene networks and Wnt signaling pathways. <i>Human Molecular Genetics</i> , 2019, 28, 3842-3852.	1.4	9
27	Long-term effects of wildfire smoke exposure during early life on the nasal epigenome in rhesus macaques. <i>Environment International</i> , 2022, 158, 106993.	4.8	9
28	Neurodevelopmental epigenetic etiologies: insights from studies on mouse models of fetal alcohol spectrum disorders. <i>Epigenomics</i> , 2013, 5, 465-468.	1.0	7
29	Epigenetic Impacts of Early Life Stress in Fetal Alcohol Spectrum Disorders Shape the Neurodevelopmental Continuum. <i>Frontiers in Molecular Neuroscience</i> , 2021, 14, 671891.	1.4	7
30	Fetal alcohol and the right to be born healthy. <i>Frontiers in Genetics</i> , 2014, 5, 356.	1.1	4