

# Ben I Laufer

## List of Publications by Year in descending order

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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-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
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	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
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	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
6	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
7	Epigenomic Convergence of Neural-Immune Risk Factors in Neurodevelopmental Disorder Cortex. <i>Cerebral Cortex</i> , 2020, 30, 640-655.	1.6	29
8	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
9	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
10	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
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	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
14	Changes to histone modifications following prenatal alcohol exposure: An emerging picture. <i>Alcohol</i> , 2017, 60, 41-52.	0.8	41
15	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
16	DNA methylation in psychosis: insights into etiology and treatment. <i>Epigenomics</i> , 2015, 7, 67-74.	1.0	17
17	Associative DNA methylation changes in children with prenatal alcohol exposure. <i>Epigenomics</i> , 2015, 7, 1259-1274.	1.0	93
18	Strategies for precision modulation of gene expression by epigenome editing: an overview. <i>Epigenetics and Chromatin</i> , 2015, 8, 34.	1.8	50

#	ARTICLE	IF	CITATIONS
19	DNA methylation differences in monozygotic twin pairs discordant for schizophrenia identifies psychosis related genes and networks. BMC Medical Genomics, 2015, 8, 17.	0.7	47
20	Fetal alcohol and the right to be born healthy. Frontiers in Genetics, 2014, 5, 356.	1.1	4
21	Long-term genomic and epigenomic dysregulation as a consequence of prenatal alcohol exposure: a model for fetal alcohol spectrum disorders. Frontiers in Genetics, 2014, 5, 161.	1.1	57
22	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. Developmental Neuroscience, 2014, 36, 29-43.	1.0	32
23	The effects of olanzapine on genome-wide DNA methylation in the hippocampus and cerebellum. Clinical Epigenetics, 2014, 6, 1.	1.8	62
24	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. Developmental Neuroscience, 2014, 36, 499-519.	1.0	19
25	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. Clinical Epigenetics, 2013, 5, 14.	1.8	32
26	Olanzapine induced DNA methylation changes support the dopamine hypothesis of psychosis. Journal of Molecular Psychiatry, 2013, 1, 19.	2.0	40
27	Long-lasting alterations to DNA methylation and ncRNAs could underlie the effects of fetal alcohol exposure in mice. DMM Disease Models and Mechanisms, 2013, 6, 977-92.	1.2	113
28	Neurodevelopmental epigenetic etiologies: insights from studies on mouse models of fetal alcohol spectrum disorders. Epigenomics, 2013, 5, 465-468.	1.0	7
29	A Macro Role for Imprinted Clusters of MicroRNAs in the Brain. MicroRNA (Shariqah, United Arab) 11 0.784314 10	0.6	10
30	Long-term alterations to the brain transcriptome in a maternal voluntary consumption model of fetal alcohol spectrum disorders. Brain Research, 2012, 1458, 18-33.	1.1	52