

Monica Uddin

List of Publications by Year in descending order

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Version: 2024-02-01

59
papers

3,139
citations

201385

27
h-index

168136

53
g-index

61
all docs

61
docs citations

61
times ranked

4144
citing authors

#	ARTICLE	IF	CITATIONS
1	Epigenetic and immune function profiles associated with posttraumatic stress disorder. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 9470-9475.	3.3	452
2	International meta-analysis of PTSD genome-wide association studies identifies sex- and ancestry-specific genetic risk loci. Nature Communications, 2019, 10, 4558.	5.8	363
3	Early Experiences of Threat, but Not Deprivation, Are Associated With Accelerated Biological Aging in Children and Adolescents. Biological Psychiatry, 2019, 85, 268-278.	0.7	211
4	Traumatic stress and accelerated DNA methylation age: A meta-analysis. Psychoneuroendocrinology, 2018, 92, 123-134.	1.3	190
5	How does the social environment "get into the mind"? Epigenetics at the intersection of social and psychiatric epidemiology. Social Science and Medicine, 2012, 74, 67-74.	1.8	163
6	Pervasive exposure to violence and posttraumatic stress disorder in a predominantly African American Urban Community: The Detroit neighborhood health study. Journal of Traumatic Stress, 2011, 24, 747-751.	1.0	142
7	The Psychiatric Genomics Consortium Posttraumatic Stress Disorder Workgroup: Posttraumatic Stress Disorder Enters the Age of Large-Scale Genomic Collaboration. Neuropsychopharmacology, 2015, 40, 2287-2297.	2.8	123
8	Epigenome-wide meta-analysis of PTSD across 10 military and civilian cohorts identifies methylation changes in AHRH. Nature Communications, 2020, 11, 5965.	5.8	84
9	Glucocorticoid receptor DNA methylation, childhood maltreatment and major depression. Journal of Affective Disorders, 2016, 206, 181-188.	2.0	83
10	DICER1 and microRNA regulation in post-traumatic stress disorder with comorbid depression. Nature Communications, 2015, 6, 10106.	5.8	81
11	An analysis of gene expression in PTSD implicates genes involved in the glucocorticoid receptor pathway and neural responses to stress. Psychoneuroendocrinology, 2015, 57, 1-13.	1.3	77
12	Gene Expression and Methylation Signatures of <i>MAN2C1</i> are Associated with PTSD. Disease Markers, 2011, 30, 111-121.	0.6	69
13	Epigenome-wide association of PTSD from heterogeneous cohorts with a common multi-site analysis pipeline. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2017, 174, 619-630.	1.1	69
14	An epigenome-wide association study of posttraumatic stress disorder in US veterans implicates several new DNA methylation loci. Clinical Epigenetics, 2020, 12, 46.	1.8	64
15	Successful treatment of post-traumatic stress disorder reverses DNA methylation marks. Molecular Psychiatry, 2021, 26, 1264-1271.	4.1	64
16	Evaluating the impact of trauma and PTSD on epigenetic prediction of lifespan and neural integrity. Neuropsychopharmacology, 2020, 45, 1609-1616.	2.8	63
17	Gene expression and methylation signatures of <i>MAN2C1</i> are associated with PTSD. Disease Markers, 2011, 30, 111-21.	0.6	51
18	POTENTIALLY TRAUMATIC EVENTS AND THE RISK OF SIX PHYSICAL HEALTH CONDITIONS IN A POPULATION-BASED SAMPLE. Depression and Anxiety, 2013, 30, 451-460.	2.0	48

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19	Genomic Approaches to Posttraumatic Stress Disorder: The Psychiatric Genomic Consortium Initiative. <i>Biological Psychiatry</i> , 2018, 83, 831-839.	0.7	47
20	Herpesviruses, inflammatory markers and incident depression in a longitudinal study of Detroit residents. <i>Psychoneuroendocrinology</i> , 2014, 50, 139-148.	1.3	45
21	Longitudinal epigenome-wide association studies of three male military cohorts reveal multiple CpG sites associated with post-traumatic stress disorder. <i>Clinical Epigenetics</i> , 2020, 12, 11.	1.8	45
22	An in-depth look into PTSD-depression comorbidity: A longitudinal study of chronically-exposed Detroit residents. <i>Journal of Affective Disorders</i> , 2017, 208, 653-661.	2.0	44
23	FKBP5 DNA methylation does not mediate the association between childhood maltreatment and depression symptom severity in the Detroit Neighborhood Health Study. <i>Journal of Psychiatric Research</i> , 2018, 96, 39-48.	1.5	44
24	PTSD is associated with an increase in aged T cell phenotypes in adults living in Detroit. <i>Psychoneuroendocrinology</i> , 2016, 67, 133-141.	1.3	39
25	Epigenetic meta-analysis across three civilian cohorts identifies <i>NRG1</i> and <i>HGS</i> as blood-based biomarkers for post-traumatic stress disorder. <i>Epigenomics</i> , 2018, 10, 1585-1601.	1.0	39
26	Gender differences in the genetic and environmental determinants of adolescent depression. <i>Depression and Anxiety</i> , 2010, 27, 658-666.	2.0	34
27	Neuroepigenetics of Post-Traumatic Stress Disorder. <i>Progress in Molecular Biology and Translational Science</i> , 2018, 158, 227-253.	0.9	30
28	RORA and posttraumatic stress trajectories: main effects and interactions with childhood physical abuse history. <i>Brain and Behavior</i> , 2015, 5, e00323.	1.0	29
29	Epigenetic predictors of all-cause mortality are associated with objective measures of neighborhood disadvantage in an urban population. <i>Clinical Epigenetics</i> , 2020, 12, 44.	1.8	28
30	Enhancing Discovery of Genetic Variants for Posttraumatic Stress Disorder Through Integration of Quantitative Phenotypes and Trauma Exposure Information. <i>Biological Psychiatry</i> , 2022, 91, 626-636.	0.7	21
31	Epigenome-wide meta-analysis of PTSD symptom severity in three military cohorts implicates DNA methylation changes in genes involved in immune system and oxidative stress. <i>Molecular Psychiatry</i> , 2022, 27, 1720-1728.	4.1	21
32	Increased H3K4me3 methylation and decreased miR-7113-5p expression lead to enhanced Wnt/ β 2-catenin signaling in immune cells from PTSD patients leading to inflammatory phenotype. <i>Molecular Medicine</i> , 2020, 26, 110.	1.9	20
33	Neighborhood environment, social cohesion, and epigenetic aging. <i>Aging</i> , 2021, 13, 7883-7899.	1.4	19
34	Rapid Fractionation and Isolation of Whole Blood Components in Samples Obtained from a Community-based Setting. <i>Journal of Visualized Experiments</i> , 2015, , .	0.2	17
35	Racial differences in IGF1 methylation and birth weight. <i>Clinical Epigenetics</i> , 2015, 7, 47.	1.8	17
36	Topical Review: The Emerging Field of Epigenetics: Informing Models of Pediatric Trauma and Physical Health. <i>Journal of Pediatric Psychology</i> , 2016, 41, 55-64.	1.1	17

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37	<i>FKBP5</i> : A Key Mediator of How Vertebrates Flexibly Cope with Adversity. <i>BioScience</i> , 2020, 70, 1127-1138.	2.2	16
38	The impact of psychopathology, social adversity and stress-relevant DNA methylation on prospective risk for post-traumatic stress: A machine learning approach. <i>Journal of Affective Disorders</i> , 2021, 282, 894-905.	2.0	16
39	Epigenetic profiles associated with major depression in the human brain. <i>Psychiatry Research</i> , 2018, 260, 439-442.	1.7	15
40	Methylomic profiles reveal sex-specific differences in leukocyte composition associated with post-traumatic stress disorder. <i>Brain, Behavior, and Immunity</i> , 2019, 81, 280-291.	2.0	14
41	Inhibition of DNA Methylation With Zebularine Alters Lipopolysaccharide-Induced Sickness Behavior and Neuroinflammation in Mice. <i>Frontiers in Neuroscience</i> , 2018, 12, 636.	1.4	13
42	Burden of post-traumatic stress disorder in postgenocide Rwandan population following exposure to 1994 genocide against the Tutsi: A meta-analysis. <i>Journal of Affective Disorders</i> , 2020, 275, 7-13.	2.0	13
43	Adolescent depression linked to socioeconomic status? Molecular approaches for revealing premorbid risk factors. <i>BioEssays</i> , 2017, 39, 1600194.	1.2	12
44	Building Conditions, 5-HTTLPR Genotype, and Depressive Symptoms in Adolescent Males and Females. <i>Journal of Adolescent Health</i> , 2011, 49, 379-385.	1.2	11
45	Sex-specific and shared expression profiles of vulnerability and resilience to trauma in brain and blood. <i>Biology of Sex Differences</i> , 2020, 11, 13.	1.8	11
46	The association between residential proximity to brownfield sites and high-traffic areas and measures of immunity. <i>Journal of Exposure Science and Environmental Epidemiology</i> , 2020, 30, 824-834.	1.8	9
47	Traumatic Stress Epigenetics. <i>Current Behavioral Neuroscience Reports</i> , 2018, 5, 81-93.	0.6	8
48	Epigenetics of early-life adversity in youth: cross-sectional and longitudinal associations. <i>Clinical Epigenetics</i> , 2022, 14, 48.	1.8	8
49	Leukocyte methylomic imprints of exposure to the genocide against the Tutsi in Rwanda: a pilot epigenome-wide analysis. <i>Epigenomics</i> , 2022, 14, 11-25.	1.0	7
50	Population Distributions of Thymic Function in Adults: Variation by Sociodemographic Characteristics and Health Status. <i>Biodemography and Social Biology</i> , 2016, 62, 208-221.	0.4	6
51	Dysregulated TP53 Among PTSD Patients Leads to Downregulation of miRNA let-7a and Promotes an Inflammatory Th17 Phenotype. <i>Frontiers in Immunology</i> , 2021, 12, 815840.	2.2	6
52	Transgenerational effects of the genocide against the Tutsi in Rwanda: A post-traumatic stress disorder symptom domain analysis. <i>AAS Open Research</i> , 0, 1, 10.	1.5	5
53	Transgenerational effects of the genocide against the Tutsi in Rwanda: A post-traumatic stress disorder symptom domain analysis. <i>AAS Open Research</i> , 0, 1, 10.	1.5	5
54	Long non-coding RNA LINC00926 regulates WNT10B signaling pathway thereby altering inflammatory gene expression in PTSD. <i>Translational Psychiatry</i> , 2022, 12, 200.	2.4	4

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55	Heterogeneous Mediation Analysis on Epigenomic PTSD and Traumatic Stress in a Predominantly African American Cohort. <i>Journal of the American Statistical Association</i> , 2022, 117, 1669-1683.	1.8	4
56	DNA methylation of Nuclear Factor of Activated T Cells 1 mediates the prospective relation between exposure to different traumatic event types and post-traumatic stress disorder. <i>Psychiatry Research</i> , 2022, 311, 114510.	1.7	2
57	Mental health delivery and neurogenetics discovery in Africa. <i>Lancet Psychiatry</i> , 2020, 7, 473-474.	3.7	1
58	Associations between childhood family emotional health, fronto-limbic grey matter volume, and saliva 5mC in young adulthood. <i>Clinical Epigenetics</i> , 2021, 13, 68.	1.8	0
59	RANDOMIZE: A Web Server for Data Randomization. , 2020, 1, 31-37.		0