Alicia K Smith

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6480881/publications.pdf

Version: 2024-02-01

234 papers

12,322 citations

54 h-index 100 g-index

251 all docs

251 does citations

251 times ranked

15493 citing authors

#	Article	IF	CITATIONS
1	Post-traumatic stress disorder is associated with PACAP and the PAC1 receptor. Nature, 2011, 470, 492-497.	27.8	695
2	Epigenetic Signatures of Cigarette Smoking. Circulation: Cardiovascular Genetics, 2016, 9, 436-447.	5.1	678
3	The transcriptional landscape of age in human peripheral blood. Nature Communications, 2015, 6, 8570.	12.8	533
4	Childhood maltreatment is associated with distinct genomic and epigenetic profiles in posttraumatic stress disorder. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 8302-8307.	7.1	482
5	Trauma exposure and stress-related disorders in inner city primary care patients. General Hospital Psychiatry, 2009, 31, 505-514.	2.4	401
6	International meta-analysis of PTSD genome-wide association studies identifies sex- and ancestry-specific genetic risk loci. Nature Communications, 2019, 10, 4558.	12.8	363
7	Lifetime stress accelerates epigenetic aging in an urban, African American cohort: relevance of glucocorticoid signaling. Genome Biology, 2015, 16, 266.	8.8	340
8	Differential immune system DNA methylation and cytokine regulation in postâ€traumatic stress disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2011, 156, 700-708.	1.7	294
9	DNA extracted from saliva for methylation studies of psychiatric traits: Evidence tissue specificity and relatedness to brain. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2015, 168, 36-44.	1.7	281
10	A DNA methylation biomarker of alcohol consumption. Molecular Psychiatry, 2018, 23, 422-433.	7.9	280
11	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. Genome Biology, 2016, 17, 255.	8.8	251
12	Neonatal DNA methylation profile in human twins is specified by a complex interplay between intrauterine environmental and genetic factors, subject to tissue-specific influence. Genome Research, 2012, 22, 1395-1406.	5.5	246
13	Methylation quantitative trait loci (meQTLs) are consistently detected across ancestry, developmental stage, and tissue type. BMC Genomics, 2014, 15, 145.	2.8	217
14	CpGassoc: an R function for analysis of DNA methylation microarray data. Bioinformatics, 2012, 28, 1280-1281.	4.1	207
15	Accounting for Population Stratification in DNA Methylation Studies. Genetic Epidemiology, 2014, 38, 231-241.	1.3	207
16	An epigenetic clock for gestational age at birth based on blood methylation data. Genome Biology, 2016, 17, 206.	8.8	193
17	Epigenetic upregulation of FKBP5 by aging and stress contributes to NF-κB–driven inflammation and cardiovascular risk. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 11370-11379.	7.1	193
18	Traumatic stress and accelerated DNA methylation age: A meta-analysis. Psychoneuroendocrinology, 2018, 92, 123-134.	2.7	190

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19	Epigenomic association analysis identifies smoking-related DNA methylation sites in African Americans. Human Genetics, 2013, 132, 1027-1037.	3.8	153
20	Exposure to Violence Accelerates Epigenetic Aging in Children. Scientific Reports, 2017, 7, 8962.	3.3	131
21	Oxytocin Receptor Genetic and Epigenetic Variations: Association With Child Abuse and Adult Psychiatric Symptoms. Child Development, 2016, 87, 122-134.	3.0	127
22	The impact of maternal childhood abuse on maternal and infant HPA axis function in the postpartum period. Psychoneuroendocrinology, 2010, 35, 686-693.	2.7	125
23	The Psychiatric Genomics Consortium Posttraumatic Stress Disorder Workgroup: Posttraumatic Stress Disorder Enters the Age of Large-Scale Genomic Collaboration. Neuropsychopharmacology, 2015, 40, 2287-2297.	5.4	123
24	The neural correlates of visual imagery vividness – An fMRI study and literature review. Cortex, 2018, 105, 26-40.	2.4	104
25	The correlation of methylation levels measured using Illumina 450K and EPIC BeadChips in blood samples. Epigenomics, 2017, 9, 1363-1371.	2.1	102
26	Epigenetic and genetic variation at SKA2 predict suicidal behavior and post-traumatic stress disorder. Translational Psychiatry, 2015, 5, e627-e627.	4.8	100
27	Genetic approaches to understanding post-traumatic stress disorder. International Journal of Neuropsychopharmacology, 2014, 17, 355-370.	2.1	97
28	Neonatal DNA methylation patterns associate with gestational age. Epigenetics, 2011, 6, 1498-1504.	2.7	95
29	Differential Genetic and Epigenetic Regulation of catechol-O-methyltransferase is Associated with Impaired Fear Inhibition in Posttraumatic Stress Disorder. Frontiers in Behavioral Neuroscience, 2013, 7, 30.	2.0	93
30	Accelerated placental aging in early onset preeclampsia pregnancies identified by DNA methylation. Epigenomics, 2017, 9, 279-289.	2.1	91
31	Blood-Derived DNA Methylation Signatures of Crohn's Disease and Severity of Intestinal Inflammation. Gastroenterology, 2019, 156, 2254-2265.e3.	1.3	91
32	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	8.8	90
33	SKA2 methylation is associated with decreased prefrontal cortical thickness and greater PTSD severity among trauma-exposed veterans. Molecular Psychiatry, 2016, 21, 357-363.	7.9	86
34	Fetal DNA Methylation Associates with Early Spontaneous Preterm Birth and Gestational Age. PLoS ONE, 2013, 8, e67489.	2.5	84
35	Epigenome-wide meta-analysis of PTSD across 10 military and civilian cohorts identifies methylation changes in AHRR. Nature Communications, 2020, 11, 5965.	12.8	84
36	Polymorphisms in <i>CRHR1</i> and the serotonin transporter loci: Gene × Gene × Environi interactions on depressive symptoms. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2010, 153B, 812-824.	ment 1.7	83

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37	DICER1 and microRNA regulation in post-traumatic stress disorder with comorbid depression. Nature Communications, 2015, 6, 10106.	12.8	81
38	Comparison of different cell type correction methods for genome-scale epigenetics studies. BMC Bioinformatics, 2017, 18, 216.	2.6	80
39	Epigenetic modification of <i>OXT</i> and human sociability. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E3816-23.	7.1	79
40	The Epigenetic Clock at Birth: Associations With Maternal Antenatal Depression and Child Psychiatric Problems. Journal of the American Academy of Child and Adolescent Psychiatry, 2018, 57, 321-328.e2.	0.5	78
41	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.	2.7	77
42	Estrogen-dependent association of HDAC4 with fear in female mice and women with PTSD. Molecular Psychiatry, 2018, 23, 658-665.	7.9	77
43	Association of a polymorphism in the indoleamine- 2,3-dioxygenase gene and interferon-α-induced depression in patients with chronic hepatitis C. Molecular Psychiatry, 2012, 17, 781-789.	7.9	74
44	Posttraumatic stress disorder is a risk factor for metabolic syndrome in an impoverished urban population. General Hospital Psychiatry, 2011, 33, 135-142.	2.4	73
45	A genomeâ€wide identified risk variant for PTSD is a methylation quantitative trait locus and confers decreased cortical activation to fearful faces. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2015, 168, 327-336.	1.7	70
46	Epigenomeâ€wide association of PTSD from heterogeneous cohorts with a common multiâ€site analysis pipeline. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2017, 174, 619-630.	1.7	69
47	Glucocorticoid receptor polymorphisms and haplotypes associated with chronic fatigue syndrome. Genes, Brain and Behavior, 2007, 6, 167-176.	2.2	68
48	DNA methylation in neonates born to women receiving psychiatric care. Epigenetics, 2012, 7, 409-414.	2.7	68
49	Associations between maternal risk factors of adverse pregnancy and birth outcomes and the offspring epigenetic clock of gestational age at birth. Clinical Epigenetics, 2017, 9, 49.	4.1	68
50	Polymorphisms in genes regulating the HPA axis associated with empirically delineated classes of unexplained chronic fatigue. Pharmacogenomics, 2006, 7, 387-394.	1.3	65
51	Genetic evaluation of the serotonergic system in chronic fatigue syndrome. Psychoneuroendocrinology, 2008, 33, 188-197.	2.7	65
52	An epigenome-wide association study of posttraumatic stress disorder in US veterans implicates several new DNA methylation loci. Clinical Epigenetics, 2020, 12, 46.	4.1	64
53	Successful treatment of post-traumatic stress disorder reverses DNA methylation marks. Molecular Psychiatry, 2021, 26, 1264-1271.	7.9	64
54	Evaluating the impact of trauma and PTSD on epigenetic prediction of lifespan and neural integrity. Neuropsychopharmacology, 2020, 45, 1609-1616.	5.4	63

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55	Genome-wide gene-based analysis suggests an association between Neuroligin 1 (NLGN1) and post-traumatic stress disorder. Translational Psychiatry, 2016, 6, e820-e820.	4.8	62
56	Serum Polybrominated Biphenyls (PBBs) and Polychlorinated Biphenyls (PCBs) and Thyroid Function among Michigan Adults Several Decades after the 1973–1974 PBB Contamination of Livestock Feed. Environmental Health Perspectives, 2017, 125, 097020.	6.0	62
57	Epigenetic modification of the oxytocin receptor gene: implications for autism symptom severity and brain functional connectivity. Neuropsychopharmacology, 2020, 45, 1150-1158.	5.4	62
58	Convergent Genomic Studies Identify Association of GRIK2 and NPAS2 with Chronic Fatigue Syndrome. Neuropsychobiology, 2011, 64, 183-194.	1.9	60
59	Epigenetic changes associated with inflammation in breast cancer patients treated with chemotherapy. Brain, Behavior, and Immunity, 2014, 38, 227-236.	4.1	59
60	The brainâ€derived neurotrophicâ€factor (<i>BDNF</i>) val66met polymorphism is associated with geriatric depression: A metaâ€analysis. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2012, 159B, 560-566.	1.7	57
61	Genetic regulation of OAS1 nonsense-mediated decay underlies association with COVID-19 hospitalization in patients of European and African ancestries. Nature Genetics, 2022, 54, 1103-1116.	21.4	54
62	DNA Methylation: An Epigenetic Risk Factor in Preterm Birth. Reproductive Sciences, 2012, 19, 6-13.	2.5	53
63	Genomewide <scp>DNA</scp> methylation analysis in combat veterans reveals a novel locus for <scp>PTSD</scp> . Acta Psychiatrica Scandinavica, 2017, 136, 493-505.	4.5	53
64	Fetal DNA methylation of autism spectrum disorders candidate genes: association with spontaneous preterm birth. American Journal of Obstetrics and Gynecology, 2015, 212, 533.e1-533.e9.	1.3	51
65	Maternal Antibody Response, Neutralizing Potency, and Placental Antibody Transfer After Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Infection. Obstetrics and Gynecology, 2021, 138, 189-197.	2.4	51
66	A serotonin transporter gene polymorphism predicts peripartum depressive symptoms in an at-risk psychiatric cohort. Journal of Psychiatric Research, 2010, 44, 640-646.	3.1	49
67	Oxytocin receptor DNA methylation and alterations of brain volumes in maltreated children. Neuropsychopharmacology, 2019, 44, 2045-2053.	5.4	49
68	Adverse Childhood Experiences: Implications for Offspring Telomere Length and Psychopathology. American Journal of Psychiatry, 2020, 177, 47-57.	7.2	48
69	DNA methylation provides insight into intergenerational risk for preterm birth in African Americans. Epigenetics, 2015, 10, 784-792.	2.7	47
70	Discovery and replication of a peripheral tissue DNA methylation biosignature to augment a suicide prediction model. Clinical Epigenetics, 2016, 8, 113.	4.1	47
71	Genomic Approaches to Posttraumatic Stress Disorder: The Psychiatric Genomic Consortium Initiative. Biological Psychiatry, 2018, 83, 831-839.	1.3	47
72	Prenatal antiepileptic exposure associates with neonatal DNA methylation differences. Epigenetics, 2012, 7, 458-463.	2.7	46

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73	Longitudinal epigenome-wide association studies of three male military cohorts reveal multiple CpG sites associated with post-traumatic stress disorder. Clinical Epigenetics, 2020, 12, 11.	4.1	45
74	Nocturnal sleep architecture disturbances in early methadone treatment patients. Psychiatry Research, 2010, 179, 91-95.	3. 3	41
75	Thyroid hormone levels associate with exposure to polychlorinated biphenyls and polybrominated biphenyls in adults exposed as children. Environmental Health, 2019, 18, 75.	4.0	41
76	Vaginal Microbiome Composition in Early Pregnancy and Risk of Spontaneous Preterm and Early Term Birth Among African American Women. Frontiers in Cellular and Infection Microbiology, 2021, 11, 641005.	3.9	41
77	Preterm Birth and Its Long-Term Effects: Methylation to Mechanisms. Biology, 2014, 3, 498-513.	2.8	40
78	Childhood Trauma and COMT Genotype Interact to Increase Hippocampal Activation in Resilient Individuals. Frontiers in Psychiatry, 2016, 7, 156.	2.6	40
79	Ancestry Dependent DNA Methylation and Influence of Maternal Nutrition. PLoS ONE, 2015, 10, e0118466.	2.5	40
80	DECOY: Documenting Experiences with Cigarettes and Other Tobacco in Young Adults. American Journal of Health Behavior, 2016, 40, 310-321.	1.4	39
81	Epigenetic meta-analysis across three civilian cohorts identifies <i>NRG1</i> and <i>HGS</i> as blood-based biomarkers for post-traumatic stress disorder. Epigenomics, 2018, 10, 1585-1601.	2.1	39
82	Epigenetic variability in the human oxytocin receptor (OXTR) gene: A possible pathway from early life experiences to psychopathologies. Neuroscience and Biobehavioral Reviews, 2019, 96, 127-142.	6.1	39
83	Interactions between the COMT Val108/158Met polymorphism and maternal prenatal smoking predict aggressive behavior outcomes. Biological Psychology, 2011, 87, 99-105.	2.2	38
84	MethLAB: A graphical user interface package for the analysis of array-based DNA methylation data. Epigenetics, 2012, 7, 225-229.	2.7	38
85	Exposure to polybrominated biphenyl (PBB) associates with genome-wide DNA methylation differences in peripheral blood. Epigenetics, 2019, 14, 52-66.	2.7	38
86	Dysfunction of the Hypothalamic–Pituitary–Adrenal Axis in Opioid Dependent Subjects: Effects of Acute and Protracted Abstinence. American Journal of Drug and Alcohol Abuse, 2008, 34, 760-768.	2.1	37
87	Advances in genetic studies of attention-deficit/hyperactivity disorder. Current Psychiatry Reports, 2009, 11, 143-148.	4.5	36
88	Impact of male partner characteristics and semen parameters on inÂvitro fertilization and obstetric outcomes in a frozen oocyte donor model. Fertility and Sterility, 2018, 110, 859-869.	1.0	36
89	An integrated -omics analysis of the epigenetic landscape of gene expression in human blood cells. BMC Genomics, 2018, 19, 476.	2.8	35
90	Preschool Outcomes Following Prenatal Serotonin Reuptake Inhibitor Exposure. Journal of Clinical Psychiatry, 2016, 77, e176-e182.	2.2	34

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91	Sex dependent influence of a functional polymorphism in steroid 5â€Î±â€reductase type 2 (<i>SRD5A2</i>) on postâ€traumatic stress symptoms. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2013, 162, 283-292.	1.7	32
92	Epigenetic Biomarkers of Preterm Birth and Its Risk Factors. Genes, 2016, 7, 15.	2.4	32
93	The impact of psychological distress during pregnancy on the developing fetus: biological mechanisms and the potential benefits of mindfulness interventions. Journal of Perinatal Medicine, 2017, 45, 999-1011.	1.4	32
94	Molecular genetic overlap between posttraumatic stress disorder and sleep phenotypes. Sleep, 2020, 43, .	1.1	32
95	Epigenome-wide association study and multi-tissue replication of individuals with alcohol use disorder: evidence for abnormal glucocorticoid signaling pathway gene regulation. Molecular Psychiatry, 2021, 26, 2224-2237.	7.9	32
96	Stability of the vaginal, oral, and gut microbiota across pregnancy among African American women: the effect of socioeconomic status and antibiotic exposure. Peerly, 2019, 7, e8004.	2.0	31
97	Predictors of neonatal hypothalamic–pituitary–adrenal axis activity at delivery. Clinical Endocrinology, 2011, 75, 90-95.	2.4	30
98	Neuroepigenetics of Post-Traumatic Stress Disorder. Progress in Molecular Biology and Translational Science, 2018, 158, 227-253.	1.7	30
99	Association of HLA locus alleles with posttraumatic stress disorder. Brain, Behavior, and Immunity, 2019, 81, 655-658.	4.1	30
100	Maternal exposure to childhood traumatic events, but not multi-domain psychosocial stressors, predict placental corticotrophin releasing hormone across pregnancy. Social Science and Medicine, 2020, 266, 113461.	3.8	30
101	DNA methylation analysis from saliva samples for epidemiological studies. Epigenetics, 2018, 13, 352-362.	2.7	28
102	DNA methylation signature of chronic low-grade inflammation and its role in cardio-respiratory diseases. Nature Communications, 2022, 13 , 2408.	12.8	26
103	Maternal Prenatal Psychological Distress and Preschool Cognitive Functioning: the Protective Role of Positive Parental Engagement. Journal of Abnormal Child Psychology, 2017, 45, 249-260.	3.5	25
104	Glucocorticoid-induced leucine zipper "quantifies―stressors and increases male susceptibility to PTSD. Translational Psychiatry, 2019, 9, 178.	4.8	25
105	Decidual cells from women with preeclampsia exhibit inadequate decidualization and reduced sFlt1 suppression. Pregnancy Hypertension, 2019, 15, 64-71.	1.4	25
106	Examining Reproductive Health Outcomes in Females Exposed to Polychlorinated Biphenyl and Polybrominated Biphenyl. Scientific Reports, 2020, 10, 3314.	3.3	25
107	An angiotensin-1 converting enzyme polymorphism is associated with allostatic load mediated by C-reactive protein, interleukin-6 and cortisol. Psychoneuroendocrinology, 2009, 34, 597-606.	2.7	24
108	Non-linear patterns in age-related DNA methylation may reflect CD4 ⁺ T cell differentiation. Epigenetics, 2017, 12, 492-503.	2.7	24

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109	Protocol for the Emory University African American maternal stress and infant gut microbiome cohort study. BMC Pediatrics, 2019, 19, 246.	1.7	24
110	A genome-wide association study of emotion dysregulation: Evidence for interleukin 2 receptor alpha. Journal of Psychiatric Research, 2016, 83, 195-202.	3.1	23
111	Locus-specific DNA methylation changes and phenotypic variability in children with attention-deficit hyperactivity disorder. Psychiatry Research, 2017, 256, 298-304.	3.3	23
112	Relationship between Epigenetic Maturity and Respiratory Morbidity in Preterm Infants. Journal of Pediatrics, 2018, 198, 168-173.e2.	1.8	23
113	Maternal depression and cortisol in pregnancy predict offspring emotional reactivity in the preschool period. Developmental Psychobiology, 2018, 60, 557-566.	1.6	23
114	Thyroid Disruptors: Extrathyroidal Sites of Chemical Action and Neurodevelopmental Outcome—An Examination Using Triclosan and Perfluorohexane Sulfonate. Toxicological Sciences, 2021, 183, 195-213.	3.1	23
115	Association between one-carbon metabolism indices and DNA methylation status in maternal and cord blood. Scientific Reports, 2018, 8, 16873.	3.3	21
116	Enhancing Discovery of Genetic Variants for Posttraumatic Stress Disorder Through Integration of Quantitative Phenotypes and Trauma Exposure Information. Biological Psychiatry, 2022, 91, 626-636.	1.3	21
117	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. Molecular Psychiatry, 2022, 27, 1720-1728.	7.9	21
118	Oxytocin receptor gene methylation and substance use problems among young African American men. Drug and Alcohol Dependence, 2018, 192, 309-315.	3.2	20
119	Translational studies support a role for serotonin 2B receptor (HTR2B) gene in aggression-related cannabis response. Molecular Psychiatry, 2018, 23, 2277-2286.	7.9	20
120	DNA methylation biomarkers prospectively predict both antenatal and postpartum depression. Psychiatry Research, 2020, 285, 112711.	3.3	20
121	<i>OXTR</i> methylation modulates exogenous oxytocin effects on human brain activity during social interaction. Genes, Brain and Behavior, 2020, 19, e12555.	2.2	19
122	Epigenome-wide association study of diet quality in the Women's Health Initiative and TwinsUK cohort. International Journal of Epidemiology, 2021, 50, 675-684.	1.9	19
123	Intergenerational effects of endocrine-disrupting compounds: a review of the Michigan polybrominated biphenyl registry. Epigenomics, 2018, 10, 845-858.	2.1	18
124	Association of Epigenetic Age Acceleration With Risk Factors, Survival, and Quality of Life in Patients With Head and Neck Cancer. International Journal of Radiation Oncology Biology Physics, 2021, 111, 157-167.	0.8	18
125	Oxytocin, vasopressin, and Williams syndrome: epigenetic effects on abnormal social behavior. Frontiers in Genetics, 2015, 6, 28.	2.3	17
126	Childhood Adversity, Socioeconomic Instability, Oxytocin-Receptor-Gene Methylation, and Romantic-Relationship Support Among Young African American Men. Psychological Science, 2019, 30, 1234-1244.	3.3	17

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127	PTSD is associated with increased DNA methylation across regions of HLA-DPB1 and SPATC1L. Brain, Behavior, and Immunity, 2021, 91, 429-436.	4.1	17
128	<i>SLC9B1</i> methylation predicts fetal intolerance of labor. Epigenetics, 2018, 13, 33-39.	2.7	16
129	Maternal prenatal depression and epigenetic age deceleration: testing potentially confounding effects of prenatal stress and SSRI use. Epigenetics, 2021, 16, 327-337.	2.7	16
130	Dynamic Patterns of Threat-Associated Gene Expression in the Amygdala and Blood. Frontiers in Psychiatry, 2018, 9, 778.	2.6	15
131	Transcriptome-wide association study of post-trauma symptom trajectories identified GRIN3B as a potential biomarker for PTSD development. Neuropsychopharmacology, 2021, 46, 1811-1820.	5 . 4	15
132	Trauma, psychiatric disorders, and treatment history among pregnant African American women Psychological Trauma: Theory, Research, Practice, and Policy, 2020, 12, 138-146.	2.1	15
133	Maternal trauma and fear history predict <i>BDNF</i> methylation and gene expression in newborns. Peerl, 2020, 8, e8858.	2.0	15
134	Associations Between the Features of Gross Placental Morphology and Birthweight. Pediatric and Developmental Pathology, 2019, 22, 194-204.	1.0	14
135	Methylomic profiles reveal sex-specific differences in leukocyte composition associated with post-traumatic stress disorder. Brain, Behavior, and Immunity, 2019, 81, 280-291.	4.1	14
136	Exposure to polybrominated biphenyl and stochastic epigenetic mutations: application of a novel epigenetic approach to environmental exposure in the Michigan polybrominated biphenyl registry. Epigenetics, 2019, 14, 1003-1018.	2.7	14
137	Prenatal antidepressant exposures and gastrointestinal complaints in childhood: A gut–brain axis connection?. Developmental Psychobiology, 2020, 62, 816-828.	1.6	14
138	Environmental exposure to polybrominated biphenyl (PBB) associates with an increased rate of biological aging. Aging, 2019, 11, 5498-5517.	3.1	14
139	Distinctions in gene-specific changes in DNA methylation in response to folic acid supplementation between women with normal weight and obesity. Obesity Research and Clinical Practice, 2017, 11, 665-676.	1.8	13
140	Methylation differences reveal heterogeneity in preterm pathophysiology: results from bipartite network analyses. Journal of Perinatal Medicine, 2018, 46, 509-521.	1.4	13
141	Characterization of gene expression changes over healthy term pregnancies. PLoS ONE, 2018, 13, e0204228.	2.5	13
142	Sex-specific DNA methylation differences in people exposed to polybrominated biphenyl. Epigenomics, 2020, 12, 757-770.	2.1	13
143	A multi-modal MRI analysis of brain structure and function in relation to OXT methylation in maltreated children and adolescents. Translational Psychiatry, 2021, 11, 589.	4.8	13
144	Critical evaluation of copy number variant calling methods using DNA methylation. Genetic Epidemiology, 2020, 44, 148-158.	1.3	12

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145	Genome-wide DNA methylation differences and polychlorinated biphenyl (PCB) exposure in a US population. Epigenetics, 2021, 16, 338-352.	2.7	12
146	Resilience and biomarkers of health risk in Black smokers and nonsmokers Health Psychology, 2017, 36, 1047-1058.	1.6	12
147	Insights into genetic susceptibility in the etiology of spontaneous preterm birth. The Application of Clinical Genetics, 2015, 8, 283.	3.0	11
148	Biomarker Development for Brain-Based Disorders: Recent Progress in Psychiatry. Journal of Neurology and Psychology, 2013, 01, 7.	0.3	11
149	Associations between DNA methylation and BMI vary by metabolic health status: a potential link to disparate cardiovascular outcomes. Clinical Epigenetics, 2021, 13, 230.	4.1	11
150	Maternal Trauma Exposure and Childhood Anxiety Outcomes: Examining Psychosocial Mechanisms of Risk. Journal of Abnormal Child Psychology, 2019, 47, 645-657.	3.5	10
151	Examining Individual and Synergistic Contributions of PTSD and Genetics to Blood Pressure: A Trans-Ethnic Meta-Analysis. Frontiers in Neuroscience, 2021, 15, 678503.	2.8	10
152	Immune system regulation and role of the human leukocyte antigen in posttraumatic stress disorder. Neurobiology of Stress, 2021, 15, 100366.	4.0	10
153	Additive Effects of Stress and Alcohol Exposure on Accelerated Epigenetic Aging in Alcohol Use Disorder. Biological Psychiatry, 2023, 93, 331-341.	1.3	10
154	Problematic alcohol use associates with sodium channel and clathrin linker 1 (⟨i⟩SCLT1⟨ i⟩) in traumaâ€exposed populations. Addiction Biology, 2018, 23, 1145-1159.	2.6	9
155	Associations Between Features of Placental Morphology and Birth Weight in Dichorionic Twins. American Journal of Epidemiology, 2019, 188, 518-526.	3.4	9
156	School-age social behavior and pragmatic language ability in children with prenatal serotonin reuptake inhibitor exposure. Development and Psychopathology, 2020, 32, 21-30.	2.3	9
157	Pathways linking adverse environments to emerging adults' substance abuse and depressive symptoms: A prospective analysis of rural African American men. Development and Psychopathology, 2021, 33, 1496-1506.	2.3	9
158	Biological and Environmental Factors Affecting Risk and Resilience among Syrian Refugee Children. Journal of Psychiatry and Brain Science, 2021, 6, .	0.5	9
159	Gestational age predicted by DNA methylation: potential clinical and research utility. Epigenomics, 2017, 9, 101-104.	2.1	8
160	Kernel machine methods for integrative analysis of genomeâ€wide methylation and genotyping studies. Genetic Epidemiology, 2018, 42, 156-167.	1.3	8
161	When Anger Remains Unspoken: Anger and Accelerated Epigenetic Aging Among Stress-Exposed Black Americans. Psychosomatic Medicine, 2021, 83, 949-958.	2.0	8
162	Prenatal phthalate exposure in relation to placental corticotropin releasing hormone (pCRH) in the CANDLE cohort. Environment International, 2022, 160, 107078.	10.0	8

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163	A Gene-Based Analysis of Acoustic Startle Latency. Frontiers in Psychiatry, 2017, 8, 117.	2.6	7
164	Role of autobiographical memory in patient response to cognitive behavioural therapies for depression: protocol of an individual patient data meta-analysis. BMJ Open, 2019, 9, e031110.	1.9	7
165	CLINICAL STUDY: Alterations in pituitaryâ€thyroid axis function among opioidâ€dependent subjects after acute and protracted abstinence. Addiction Biology, 2009, 14, 310-314.	2.6	6
166	Down-regulation of PRKCB1 expression in Han Chinese patients with subsyndromal symptomatic depression. Journal of Psychiatric Research, 2015, 69, 1-6.	3.1	6
167	Association analysis between mitogen-activated protein/extracellular signal-regulated kinase (MEK) gene polymorphisms and depressive disorder in the Han Chinese population. Journal of Affective Disorders, 2017, 222, 120-125.	4.1	6
168	Evaluation of a Support Group for Parents of Children Hospitalized for Cancer and Hematopoietic Stem Cell Transplantation. Social Work With Groups, 2018, 41, 276-290.	0.5	6
169	Epigenetic Modification of <i>OXTR</i> is Associated with Openness to Experience. Personality Neuroscience, 2018, 1, e7.	1.6	6
170	Correction for multiple testing in candidate-gene methylation studies. Epigenomics, 2019, 11, 1089-1105.	2.1	6
171	Methylation of OXT and OXTR genes, central oxytocin, and social behavior in female macaques. Hormones and Behavior, 2020, 126, 104856.	2.1	5
172	DNA Methylation Changes in Whole Blood and CD16+ Neutrophils in Response to Chronic Folic Acid Supplementation in Women of Childbearing Age. International Journal for Vitamin and Nutrition Research, 2017, 87, 271-278.	1.5	5
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