Alicia K Smith

List of Publications by Year in descending order

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234 papers

12,322 citations

54 h-index 37326 100 g-index

251 all docs

251 docs citations

251 times ranked

16971 citing authors

#	Article	IF	CITATIONS
1	Placental Injury and Antibody Transfer after Coronavirus Disease 2019 in Pregnancy. Journal of Infectious Diseases, 2023, 227, 850-854.	1.9	2
2	Additive Effects of Stress and Alcohol Exposure on Accelerated Epigenetic Aging in Alcohol Use Disorder. Biological Psychiatry, 2023, 93, 331-341.	0.7	10
3	Enhancing Discovery of Genetic Variants for Posttraumatic Stress Disorder Through Integration of Quantitative Phenotypes and Trauma Exposure Information. Biological Psychiatry, 2022, 91, 626-636.	0.7	21
4	A Case–Control Study of Follicular Fluid Cytokine Profiles in Women with Diminished Ovarian Reserve. Reproductive Sciences, 2022, 29, 2515-2524.	1.1	3
5	Prenatal phthalate exposure in relation to placental corticotropin releasing hormone (pCRH) in the CANDLE cohort. Environment International, 2022, 160, 107078.	4.8	8
6	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.	4.1	21
7	Methylation quantitative trait loci are largely consistent across disease states in Crohn's disease. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	2
8	Establishment of a COVID-19 perinatal biorepository in a safety net population. Journal of the National Medical Association, 2022, , .	0.6	1
9	DNA methylation signature of chronic low-grade inflammation and its role in cardio-respiratory diseases. Nature Communications, 2022, 13, 2408.	5.8	26
10	P629. Establishing a DNA Methylation and Exposure Risk Score for PTSD Using Machine Learning. Biological Psychiatry, 2022, 91, S344.	0.7	0
11	Cell-Type Specific Methylation Analysis Reveals Multiple Loci Associated With PTSD in African Americans. Biological Psychiatry, 2022, 91, S2.	0.7	О
12	Advancing understanding of maternal age: correlating epigenetic clocks in blood and myometrium., 2022, 2, .		3
13	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.	9.4	54
14	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.	1.4	9
15	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.	4.1	32
16	PTSD is associated with increased DNA methylation across regions of HLA-DPB1 and SPATC1L. Brain, Behavior, and Immunity, 2021, 91, 429-436.	2.0	17
17	Genome-wide DNA methylation differences and polychlorinated biphenyl (PCB) exposure in a US population. Epigenetics, 2021, 16, 338-352.	1.3	12
18	Maternal prenatal depression and epigenetic age deceleration: testing potentially confounding effects of prenatal stress and SSRI use. Epigenetics, 2021, 16, 327-337.	1.3	16

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19	Epigenome-wide association study of diet quality in the Women's Health Initiative and TwinsUK cohort. International Journal of Epidemiology, 2021, 50, 675-684.	0.9	19
20	Successful treatment of post-traumatic stress disorder reverses DNA methylation marks. Molecular Psychiatry, 2021, 26, 1264-1271.	4.1	64
21	Biological and Environmental Factors Affecting Risk and Resilience among Syrian Refugee Children. Journal of Psychiatry and Brain Science, 2021, 6, .	0.3	9
22	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.	1.8	41
23	Epigenetic prediction of $17\hat{l}^2$ -estradiol and relationship to trauma-related outcomes in women. Comprehensive Psychoneuroendocrinology, 2021, 6, 100045.	0.7	2
24	Multi-Polygenic Analysis of Nicotine Dependence in Individuals of European Ancestry. Nicotine and Tobacco Research, 2021, 23, 2102-2109.	1.4	2
25	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	3.8	90
26	Transcriptome-wide association study of post-trauma symptom trajectories identified GRIN3B as a potential biomarker for PTSD development. Neuropsychopharmacology, 2021, 46, 1811-1820.	2.8	15
27	Examining Individual and Synergistic Contributions of PTSD and Genetics to Blood Pressure: A Trans-Ethnic Meta-Analysis. Frontiers in Neuroscience, 2021, 15, 678503.	1.4	10
28	Thyroid Disruptors: Extrathyroidal Sites of Chemical Action and Neurodevelopmental Outcomeâ€"An Examination Using Triclosan and Perfluorohexane Sulfonate. Toxicological Sciences, 2021, 183, 195-213.	1.4	23
29	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.	1.2	51
30	Prenatal phthalate exposure in relation to placental corticotropin releasing hormone (pCRH) concentrations in the CANDLE study. ISEE Conference Abstracts, 2021, 2021, .	0.0	0
31	A Review of Health Effects of Polybrominated Biphenyls Five Decades after Michigan Agricultural Contamination. ISEE Conference Abstracts, 2021, 2021, .	0.0	O
32	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.	0.4	18
33	When Anger Remains Unspoken: Anger and Accelerated Epigenetic Aging Among Stress-Exposed Black Americans. Psychosomatic Medicine, 2021, 83, 949-958.	1.3	8
34	Immune system regulation and role of the human leukocyte antigen in posttraumatic stress disorder. Neurobiology of Stress, $2021,15,100366.$	1.9	10
35	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.	2.4	13
36	Associations between DNA methylation and BMI vary by metabolic health status: a potential link to disparate cardiovascular outcomes. Clinical Epigenetics, 2021, 13, 230.	1.8	11

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37	<i>OXTR</i> methylation modulates exogenous oxytocin effects on human brain activity during social interaction. Genes, Brain and Behavior, 2020, 19, e12555.	1.1	19
38	School-age social behavior and pragmatic language ability in children with prenatal serotonin reuptake inhibitor exposure. Development and Psychopathology, 2020, 32, 21-30.	1.4	9
39	Adverse Childhood Experiences: Implications for Offspring Telomere Length and Psychopathology. American Journal of Psychiatry, 2020, 177, 47-57.	4.0	48
40	Current progress and future direction in the genetics of PTSD: Focus on the development and contributions of the PGC-PTSD working group., 2020,, 285-296.		0
41	Molecular genetic overlap between posttraumatic stress disorder and sleep phenotypes. Sleep, 2020, 43, .	0.6	32
42	Critical evaluation of copy number variant calling methods using DNA methylation. Genetic Epidemiology, 2020, 44, 148-158.	0.6	12
43	DNA methylation biomarkers prospectively predict both antenatal and postpartum depression. Psychiatry Research, 2020, 285, 112711.	1.7	20
44	CYTOKINE CONTENT OF FOLLICULAR FLUID IN WOMEN WITH POLYCYSTIC OVARIAN SYNDROME (PCOS). Fertility and Sterility, 2020, 114, e398-e399.	0.5	0
45	HLA Allelic Variations as Modifiers of Longitudinal Changes in DNA Methylation Related to PTSD; an Opportunity for Precision Medicine?. Biological Psychiatry, 2020, 87, S57.	0.7	0
46	Epigenome-Wide Association Study and Multi-Tissue Replication of Individuals With Alcohol Use Disorder: Evidence for Abnormal Glucocorticoid Signaling Pathway Gene Regulation. Biological Psychiatry, 2020, 87, S113.	0.7	3
47	Epigenome-wide meta-analysis of PTSD across 10 military and civilian cohorts identifies methylation changes in AHRR. Nature Communications, 2020, 11, 5965.	5.8	84
48	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.	1.8	30
49	DIFFERENCES IN FOLLICULAR FLUID CYTOKINE PROFILE IN WOMEN WITH DIMINISHED OVARIAN RESERVE. Fertility and Sterility, 2020, 114, e452.	0.5	1
50	Maternal Prenatal Depression and Decelerated Epigenetic Gestational Aging: Competing Roles of SSRIs and Prenatal Stress. Biological Psychiatry, 2020, 87, S195-S196.	0.7	0
51	GWAS-Implicated Genes Inform Cross-Tissue Studies of DNA Methylation. Biological Psychiatry, 2020, 87, S53.	0.7	0
52	614 RECTAL TISSUE DNA METHYLATION IN ULCERATIVE COLITIS SHOWS DISEASE-SPECIFIC ASSOCIATIONS: INSIGHTS FROM LONGITUDINAL ANALYSIS OF PROTECT STUDY PARTICIPANTS. Gastroenterology, 2020, 158, S-131.	0.6	0
53	Methylation of OXT and OXTR genes, central oxytocin, and social behavior in female macaques. Hormones and Behavior, 2020, 126, 104856.	1.0	5
54	Evaluating the impact of trauma and PTSD on epigenetic prediction of lifespan and neural integrity. Neuropsychopharmacology, 2020, 45, 1609-1616.	2.8	63

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55	Neuroendocrine biomarkers of prolonged exposure treatment response in military-related PTSD. Psychoneuroendocrinology, 2020, 119, 104749.	1.3	3
56	Transcription factor AP2A affects sFLT1 expression and decidualization in decidual stromal cells: Implications to preeclampsia pathology. Pregnancy Hypertension, 2020, 21, 152-158.	0.6	4
57	Sex-specific DNA methylation differences in people exposed to polybrominated biphenyl. Epigenomics, 2020, 12, 757-770.	1.0	13
58	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
59	Prenatal antidepressant exposures and gastrointestinal complaints in childhood: A gut–brain axis connection?. Developmental Psychobiology, 2020, 62, 816-828.	0.9	14
60	Longitudinal Changes in DNA Methylation in Relation to the Development, Treatment and Late Onset of PTSD. Biological Psychiatry, 2020, 87, S58.	0.7	0
61	Endometriosis, endocrine disrupters, and epigenetics: an investigation into the complex interplay in women with polybrominated biphenyl exposure and endometriosis. Journal of Assisted Reproduction and Genetics, 2020, 37, 427-436.	1.2	4
62	Examining Reproductive Health Outcomes in Females Exposed to Polychlorinated Biphenyl and Polybrominated Biphenyl. Scientific Reports, 2020, 10, 3314.	1.6	25
63	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.	1.8	45
64	Epigenetic modification of the oxytocin receptor gene: implications for autism symptom severity and brain functional connectivity. Neuropsychopharmacology, 2020, 45, 1150-1158.	2.8	62
65	Glucocorticoid receptor sensitivity in early pregnancy in an African American cohort. American Journal of Reproductive Immunology, 2020, 84, e13252.	1.2	2
66	Associations between the development of PTSD symptoms and longitudinal changes in the DNA methylome of deployed military servicemen: A comparison with polygenic risk scores. Comprehensive Psychoneuroendocrinology, 2020, 4, 100018.	0.7	4
67	Trauma, psychiatric disorders, and treatment history among pregnant African American women Psychological Trauma: Theory, Research, Practice, and Policy, 2020, 12, 138-146.	1.4	15
68	Maternal trauma and fear history predict <i>BDNF</i> methylation and gene expression in newborns. PeerJ, 2020, 8, e8858.	0.9	15
69	15 LONGITUDINAL EVALUATION OF MUCOSAL DNA METHYLATION IN ULCERATIVE COLITIS SHOWS DISEASE-SPECIFIC CHANGES. Gastroenterology, 2020, 158, S50-S51.	0.6	0
70	Maternal Trauma Exposure and Childhood Anxiety Outcomes: Examining Psychosocial Mechanisms of Risk. Journal of Abnormal Child Psychology, 2019, 47, 645-657.	3.5	10
71	Associations Between the Features of Gross Placental Morphology and Birthweight. Pediatric and Developmental Pathology, 2019, 22, 194-204.	0.5	14
72	Correction for multiple testing in candidate-gene methylation studies. Epigenomics, 2019, 11, 1089-1105.	1.0	6

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73	Childhood Adversity, Socioeconomic Instability, Oxytocin-Receptor-Gene Methylation, and Romantic-Relationship Support Among Young African American Men. Psychological Science, 2019, 30, 1234-1244.	1.8	17
74	Association of HLA locus alleles with posttraumatic stress disorder. Brain, Behavior, and Immunity, 2019, 81, 655-658.	2.0	30
7 5	Protocol for the Emory University African American maternal stress and infant gut microbiome cohort study. BMC Pediatrics, 2019, 19, 246.	0.7	24
76	Glucocorticoid-induced leucine zipper "quantifies―stressors and increases male susceptibility to PTSD. Translational Psychiatry, 2019, 9, 178.	2.4	25
77	Methylomic profiles reveal sex-specific differences in leukocyte composition associated with post-traumatic stress disorder. Brain, Behavior, and Immunity, 2019, 81, 280-291.	2.0	14
78	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
79	Accuracy of self-reported menstrual cycle characteristics and infertility in a cohort highly exposed to endocrine-disruptingÂcompounds (EDCs). Fertility and Sterility, 2019, 112, e341-e342.	0.5	O
80	EPIGENOME-WIDE META-ANALYSES OF PTSD HIGHLIGHT THE ROLE OF SEX AND TRAUMA-TYPE AS A POTENTIAL SOURCE OF HETEROGENEITY. European Neuropsychopharmacology, 2019, 29, S42.	0.3	0
81	S15ASSOCIATION OF DIFFERENTIALLY METHYLATED REGIONS WITH PTSD IN A TRAUMATIZED CIVILIAN COHORT. European Neuropsychopharmacology, 2019, 29, S121.	0.3	O
82	F95. Effect of HLA Alleles on Suicide Attempts and Chronic Pain in Women. Biological Psychiatry, 2019, 85, S249-S250.	0.7	2
83	Thyroid hormone levels associate with exposure to polychlorinated biphenyls and polybrominated biphenyls in adults exposed as children. Environmental Health, 2019, 18, 75.	1.7	41
84	Tu1159 – Blood Mqtl Effects are Consistent During the Course of the Disease Regardless of Remission Or Relapse Status in Pediatric Crohn's Disease Patients. Gastroenterology, 2019, 156, S-967.	0.6	0
85	O41. Longitudinal Changes in Genome-Wide DNA Methylation Levels Related to Treatment Outcomes and Recovery From Post-Traumatic Stress Disorder. Biological Psychiatry, 2019, 85, S122-S123.	0.7	1
86	O13. DNA Methylation Biomarkers Predict Antenatal and Postpartum Depression and Associate With Postpartum Changes in Resting State Functional Connectivity. Biological Psychiatry, 2019, 85, S110.	0.7	0
87	S152. Genetic Risk for Hospitalization in Serious Mental Illness. Biological Psychiatry, 2019, 85, S355-S356.	0.7	O
88	Exposure to polybrominated biphenyl (PBB) associates with genome-wide DNA methylation differences in peripheral blood. Epigenetics, 2019, 14, 52-66.	1.3	38
89	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.	0.8	7
90	28. An Epigenome-Wide Association Study of PTSD in Veterans Implicates Several New DNA Methylation Loci. Biological Psychiatry, 2019, 85, S12.	0.7	2

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91	25. Longitudinal Epigenome-Wide Changes From Trauma to PTSD Diagnosis. Biological Psychiatry, 2019, 85, S10-S11.	0.7	o
92	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.	1.3	14
93	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.	3.3	193
94	462: Effects of periconception and current stress on perinatal outcomes: A Grady Trauma Project study. American Journal of Obstetrics and Gynecology, 2019, 220, S309-S310.	0.7	0
95	Oxytocin receptor DNA methylation and alterations of brain volumes in maltreated children. Neuropsychopharmacology, 2019, 44, 2045-2053.	2.8	49
96	Blood-Derived DNA Methylation Signatures of Crohn's Disease and Severity of Intestinal Inflammation. Gastroenterology, 2019, 156, 2254-2265.e3.	0.6	91
97	P108 LONGITUDINAL MQTL STUDY IN BLOOD FROM PEDIATRIC CROHN'S DISEASE PATIENTS. Gastroenterology, 2019, 156, S75-S76.	0.6	0
98	Epigenetic Biomarkers Of PTSD: Updates From The EWAS Working Group of The PTSD PGC. European Neuropsychopharmacology, 2019, 29, S750.	0.3	2
99	Decidual cells from women with preeclampsia exhibit inadequate decidualization and reduced sFlt1 suppression. Pregnancy Hypertension, 2019, 15, 64-71.	0.6	25
100	Associations Between Features of Placental Morphology and Birth Weight in Dichorionic Twins. American Journal of Epidemiology, 2019, 188, 518-526.	1.6	9
101	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.	2.9	39
102	Environmental exposure to polybrominated biphenyl (PBB) associates with an increased rate of biological aging. Aging, 2019, 11, 5498-5517.	1.4	14
103	Stability of the vaginal, oral, and gut microbiota across pregnancy among African American women: the effect of socioeconomic status and antibiotic exposure. PeerJ, 2019, 7, e8004.	0.9	31
104	OR23-2 Increased Exposure to Brominated Flame Retardant Associates with Differences in DNA Methylation Similar to Natural Estrogen. Journal of the Endocrine Society, 2019, 3, .	0.1	0
105	Genomic Approaches to Posttraumatic Stress Disorder: The Psychiatric Genomic Consortium Initiative. Biological Psychiatry, 2018, 83, 831-839.	0.7	47
106	10 EPIGENOME-WIDE ASSOCIATION STUDY IDENTIFIED SHARED METHYLOMIC CONTRIBUTIONS TO SUSCEPTIBILITY AND PROGRESSION IN PEDIATRIC CROHN'S DISEASE. Gastroenterology, 2018, 154, S101.	0.6	0
107	Traumatic stress and accelerated DNA methylation age: A meta-analysis. Psychoneuroendocrinology, 2018, 92, 123-134.	1.3	190
108	Kernel machine methods for integrative analysis of genomeâ€wide methylation and genotyping studies. Genetic Epidemiology, 2018, 42, 156-167.	0.6	8

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109	<i>SLC9B1</i> methylation predicts fetal intolerance of labor. Epigenetics, 2018, 13, 33-39.	1.3	16
110	Relationship between Epigenetic Maturity and Respiratory Morbidity in Preterm Infants. Journal of Pediatrics, 2018, 198, 168-173.e2.	0.9	23
111	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.	0.3	78
112	A DNA methylation biomarker of alcohol consumption. Molecular Psychiatry, 2018, 23, 422-433.	4.1	280
113	Estrogen-dependent association of HDAC4 with fear in female mice and women with PTSD. Molecular Psychiatry, 2018, 23, 658-665.	4.1	77
114	Methylation differences reveal heterogeneity in preterm pathophysiology: results from bipartite network analyses. Journal of Perinatal Medicine, 2018, 46, 509-521.	0.6	13
115	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.	0.3	6
116	Problematic alcohol use associates with sodium channel and clathrin linker 1 (⟨i⟩SCLT1⟨/i⟩) in traumaâ€exposed populations. Addiction Biology, 2018, 23, 1145-1159.	1.4	9
117	The neural correlates of visual imagery vividness – An fMRI study and literature review. Cortex, 2018, 105, 26-40.	1.1	104
118	Examining polychlorinated biphenyl exposure and reproductive health outcomes. Fertility and Sterility, 2018, 110, e171.	0.5	0
119	Association between one-carbon metabolism indices and DNA methylation status in maternal and cord blood. Scientific Reports, 2018, 8, 16873.	1.6	21
120	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.	1.0	39
121	Characterization of gene expression changes over healthy term pregnancies. PLoS ONE, 2018, 13, e0204228.	1.1	13
122	Epigenetic Modification of <i>OXTR</i> is Associated with Openness to Experience. Personality Neuroscience, 2018, 1, e7.	1.3	6
123	216. Thyroid Hormones and Their Influence on Expression in Humans and an Animal Model of Trauma Exposure. Biological Psychiatry, 2018, 83, S87.	0.7	0
124	F62. Neonate BDNF Gene Regulation Associates With Maternal Trauma and Fear History. Biological Psychiatry, 2018, 83, S261-S262.	0.7	0
125	Oxytocin receptor gene methylation and substance use problems among young African American men. Drug and Alcohol Dependence, 2018, 192, 309-315.	1.6	20
126	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.	0.5	36

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127	T33. Polyepigenetic Prediction of PTSD Physiology Based on Estrogen Status. Biological Psychiatry, 2018, 83, S141.	0.7	1
128	127. The Epigenetic Clock at Birth: Associations With Maternal Antenatal Depression and Child Psychiatric Problems. Biological Psychiatry, 2018, 83, S52.	0.7	0
129	CD4 ⁺ and CD8 ⁺ T ellâ€5pecific DNA Cytosine Methylation Differences Associated With Obesity. Obesity, 2018, 26, 1312-1321.	1.5	4
130	Comparison of diameter-based and image-based measures of surface area from gross placental pathology for use in epidemiologic studies. Placenta, 2018, 69, 82-85.	0.7	1
131	An integrated -omics analysis of the epigenetic landscape of gene expression in human blood cells. BMC Genomics, 2018, 19, 476.	1.2	35
132	215. DNA Methylation Across the Genome Associates With Serum Estrogen Levels and PTSD. Biological Psychiatry, 2018, 83, S86-S87.	0.7	0
133	Maternal depression and cortisol in pregnancy predict offspring emotional reactivity in the preschool period. Developmental Psychobiology, 2018, 60, 557-566.	0.9	23
134	Neuroepigenetics of Post-Traumatic Stress Disorder. Progress in Molecular Biology and Translational Science, 2018, 158, 227-253.	0.9	30
135	Intergenerational effects of endocrine-disrupting compounds: a review of the Michigan polybrominated biphenyl registry. Epigenomics, 2018, 10, 845-858.	1.0	18
136	Translational studies support a role for serotonin 2B receptor (HTR2B) gene in aggression-related cannabis response. Molecular Psychiatry, 2018, 23, 2277-2286.	4.1	20
137	DNA methylation analysis from saliva samples for epidemiological studies. Epigenetics, 2018, 13, 352-362.	1.3	28
138	Dynamic Patterns of Threat-Associated Gene Expression in the Amygdala and Blood. Frontiers in Psychiatry, 2018, 9, 778.	1.3	15
139	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
140	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.	0.6	32
141	Gestational age predicted by DNA methylation: potential clinical and research utility. Epigenomics, 2017, 9, 101-104.	1.0	8
142	894. Suicide Prediction Using Machine Learning Techniques in Screening and Clinician-Derived Data. Biological Psychiatry, 2017, 81, S361.	0.7	2
143	489. Examination of an Acute Role for Thyroid Hormone Regulation of Trauma-Related Plasticity and Memory Formation in the Amygdala. Biological Psychiatry, 2017, 81, S199.	0.7	0
144	Accelerated placental aging in early onset preeclampsia pregnancies identified by DNA methylation. Epigenomics, 2017, 9, 279-289.	1.0	91

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145	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.	1.8	68
146	Non-linear patterns in age-related DNA methylation may reflect CD4 ⁺ T cell differentiation. Epigenetics, 2017, 12, 492-503.	1.3	24
147	The correlation of methylation levels measured using Illumina 450K and EPIC BeadChips in blood samples. Epigenomics, 2017, 9, 1363-1371.	1.0	102
148	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.	1.1	69
149	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.	0.8	13
150	58. Experiencing Violence Accelerates Epigenetic Aging in Children. Biological Psychiatry, 2017, 81, S24.	0.7	1
151	60. Dynamic Patterns of Fear-Associated Gene Expression in the Amygdala and Blood. Biological Psychiatry, 2017, 81, S25.	0.7	0
152	345. Hippocampal Activation and COMT Genotype Mediate the Relationship between Childhood Trauma and Resilience. Biological Psychiatry, 2017, 81, S141-S142.	0.7	0
153	86. Epigenetic Signatures of PTSD: Results from the Psychiatric Genomics Consortium PTSD Epigenetics Workgroup. Biological Psychiatry, 2017, 81, S36.	0.7	0
154	Genomewide <scp>DNA</scp> methylation analysis in combat veterans reveals a novel locus for <scp>PTSD</scp> . Acta Psychiatrica Scandinavica, 2017, 136, 493-505.	2.2	53
155	Exposure to Violence Accelerates Epigenetic Aging in Children. Scientific Reports, 2017, 7, 8962.	1.6	131
156	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.	2.0	6
157	Locus-specific DNA methylation changes and phenotypic variability in children with attention-deficit hyperactivity disorder. Psychiatry Research, 2017, 256, 298-304.	1.7	23
158	Comparison of different cell type correction methods for genome-scale epigenetics studies. BMC Bioinformatics, 2017, 18, 216.	1.2	80
159	A Gene-Based Analysis of Acoustic Startle Latency. Frontiers in Psychiatry, 2017, 8, 117.	1.3	7
160	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.	2.8	62
161	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.	0.6	5
162	Resilience and biomarkers of health risk in Black smokers and nonsmokers Health Psychology, 2017, 36, 1047-1058.	1.3	12

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163	DECOY: Documenting Experiences with Cigarettes and Other Tobacco in Young Adults. American Journal of Health Behavior, 2016, 40, 310-321.	0.6	39
164	Epigenetic Biomarkers of Preterm Birth and Its Risk Factors. Genes, 2016, 7, 15.	1.0	32
165	Childhood Trauma and COMT Genotype Interact to Increase Hippocampal Activation in Resilient Individuals. Frontiers in Psychiatry, 2016, 7, 156.	1.3	40
166	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. Genome Biology, 2016, 17, 255.	3.8	251
167	Genome-wide gene-based analysis suggests an association between Neuroligin 1 (NLGN1) and post-traumatic stress disorder. Translational Psychiatry, 2016, 6, e820-e820.	2.4	62
168	Stress vulnerability and epigenetic variation of SKA2, potential causes and consequences. Psychoneuroendocrinology, 2016, 71, 11.	1.3	0
169	An epigenetic clock for gestational age at birth based on blood methylation data. Genome Biology, 2016, 17, 206.	3.8	193
170	A genome-wide association study of emotion dysregulation: Evidence for interleukin 2 receptor alpha. Journal of Psychiatric Research, 2016, 83, 195-202.	1.5	23
171	Oxytocin Receptor Genetic and Epigenetic Variations: Association With Child Abuse and Adult Psychiatric Symptoms. Child Development, 2016, 87, 122-134.	1.7	127
172	Epigenetic Signatures of Cigarette Smoking. Circulation: Cardiovascular Genetics, 2016, 9, 436-447.	5.1	678
173	Discovery and replication of a peripheral tissue DNA methylation biosignature to augment a suicide prediction model. Clinical Epigenetics, 2016, 8, 113.	1.8	47
174	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.	3.3	79
175	SKA2 methylation is associated with decreased prefrontal cortical thickness and greater PTSD severity among trauma-exposed veterans. Molecular Psychiatry, 2016, 21, 357-363.	4.1	86
176	Preschool Outcomes Following Prenatal Serotonin Reuptake Inhibitor Exposure. Journal of Clinical Psychiatry, 2016, 77, e176-e182.	1.1	34
177	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.	1.1	70
178	Insights into genetic susceptibility in the etiology of spontaneous preterm birth. The Application of Clinical Genetics, 2015, 8, 283.	1.4	11
179	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
180	DICER1 and microRNA regulation in post-traumatic stress disorder with comorbid depression. Nature Communications, 2015, 6, 10106.	5.8	81

#	Article	IF	CITATIONS
181	Epigenetic and genetic variation at SKA2 predict suicidal behavior and post-traumatic stress disorder. Translational Psychiatry, 2015, 5, e627-e627.	2.4	100
182	Lifetime stress accelerates epigenetic aging in an urban, African American cohort: relevance of glucocorticoid signaling. Genome Biology, 2015, 16, 266.	3.8	340
183	Down-regulation of PRKCB1 expression in Han Chinese patients with subsyndromal symptomatic depression. Journal of Psychiatric Research, 2015, 69, 1-6.	1.5	6
184	DNA methylation provides insight into intergenerational risk for preterm birth in African Americans. Epigenetics, 2015, 10, 784-792.	1.3	47
185	Oxytocin, vasopressin, and Williams syndrome: epigenetic effects on abnormal social behavior. Frontiers in Genetics, 2015, 6, 28.	1.1	17
186	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
187	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.	0.7	51
188	The transcriptional landscape of age in human peripheral blood. Nature Communications, 2015, 6, 8570.	5.8	533
189	39: Fetal DNA methylation of autism spectrum disorders (ASD) candidate genes: association with spontaneous preterm birth. American Journal of Obstetrics and Gynecology, 2015, 212, S27.	0.7	1
190	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.	1.1	281
191	Ancestry Dependent DNA Methylation and Influence of Maternal Nutrition. PLoS ONE, 2015, 10, e0118466.	1.1	40
192	Preterm Birth and Its Long-Term Effects: Methylation to Mechanisms. Biology, 2014, 3, 498-513.	1.3	40
193	Accounting for Population Stratification in DNA Methylation Studies. Genetic Epidemiology, 2014, 38, 231-241.	0.6	207
194	14: Methylation differences reveal heterogeneity in spontaneous preterm birth pathophysiology: a visual analytical approach. American Journal of Obstetrics and Gynecology, 2014, 210, S9-S10.	0.7	0
195	Epigenetic changes associated with inflammation in breast cancer patients treated with chemotherapy. Brain, Behavior, and Immunity, 2014, 38, 227-236.	2.0	59
196	Methylation quantitative trait loci (meQTLs) are consistently detected across ancestry, developmental stage, and tissue type. BMC Genomics, 2014, 15, 145.	1.2	217
197	Genetic approaches to understanding post-traumatic stress disorder. International Journal of Neuropsychopharmacology, 2014, 17, 355-370.	1.0	97
198	Epigenetics of Psychopathology. , 2014, , 283-309.		4

#	Article	IF	Citations
199	Geneâ€specific changes in DNA methylation in response to chronic folic acid supplementation in normal weight and obese women of childâ€bearing age (817.3). FASEB Journal, 2014, 28, 817.3.	0.2	0
200	Genomeâ€wide DNA methylation in whole blood and CD16 + cells in response to chronic folic acid supplementation in women of childâ€bearing age (817.1). FASEB Journal, 2014, 28, 817.1.	0.2	0
201	Epigenomic association analysis identifies smoking-related DNA methylation sites in African Americans. Human Genetics, 2013, 132, 1027-1037.	1.8	153
202	Fetal DNA Methylation Associates with Early Spontaneous Preterm Birth and Gestational Age. PLoS ONE, 2013, 8, e67489.	1.1	84
203	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.	1.1	32
204	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.	3.3	482
205	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.	1.0	93
206	Biomarker Development for Brain-Based Disorders: Recent Progress in Psychiatry. Journal of Neurology and Psychology, 2013, 01, 7.	2.0	11
207	CpGassoc: an R function for analysis of DNA methylation microarray data. Bioinformatics, 2012, 28, 1280-1281.	1.8	207
208	DNA methylation in neonates born to women receiving psychiatric care. Epigenetics, 2012, 7, 409-414.	1.3	68
209	Prenatal antiepileptic exposure associates with neonatal DNA methylation differences. Epigenetics, 2012, 7, 458-463.	1.3	46
210	Association of a polymorphism in the indoleamine- 2,3-dioxygenase gene and interferon- \hat{l} ±-induced depression in patients with chronic hepatitis C. Molecular Psychiatry, 2012, 17, 781-789.	4.1	74
211	MethLAB: A graphical user interface package for the analysis of array-based DNA methylation data. Epigenetics, 2012, 7, 225-229.	1.3	38
212	DNA Methylation: An Epigenetic Risk Factor in Preterm Birth. Reproductive Sciences, 2012, 19, 6-13.	1.1	53
213	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.	2.4	246
214	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.	1.1	57
215	Interactions between the COMT Val108/158Met polymorphism and maternal prenatal smoking predict aggressive behavior outcomes. Biological Psychology, 2011, 87, 99-105.	1.1	38
216	Predictors of neonatal hypothalamic–pituitary–adrenal axis activity at delivery. Clinical Endocrinology, 2011, 75, 90-95.	1.2	30

#	Article	IF	CITATIONS
217	Post-traumatic stress disorder is associated with PACAP and the PAC1 receptor. Nature, 2011, 470, 492-497.	13.7	695
218	Posttraumatic stress disorder is a risk factor for metabolic syndrome in an impoverished urban population. General Hospital Psychiatry, 2011, 33, 135-142.	1.2	73
219	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.	1.1	294
220	Neonatal DNA methylation patterns associate with gestational age. Epigenetics, 2011, 6, 1498-1504.	1.3	95
221	Convergent Genomic Studies Identify Association of GRIK2 and NPAS2 with Chronic Fatigue Syndrome. Neuropsychobiology, 2011, 64, 183-194.	0.9	60
222	Polymorphisms in <i>CRHR1</i> and the serotonin transporter loci: Gene × Gene × Environn interactions on depressive symptoms. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2010, 153B, 812-824.	nent 1.1	83
223	A serotonin transporter gene polymorphism predicts peripartum depressive symptoms in an at-risk psychiatric cohort. Journal of Psychiatric Research, 2010, 44, 640-646.	1.5	49
224	The impact of maternal childhood abuse on maternal and infant HPA axis function in the postpartum period. Psychoneuroendocrinology, 2010, 35, 686-693.	1.3	125
225	Nocturnal sleep architecture disturbances in early methadone treatment patients. Psychiatry Research, 2010, 179, 91-95.	1.7	41
226	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.	1.3	24
227	Trauma exposure and stress-related disorders in inner city primary care patients. General Hospital Psychiatry, 2009, 31, 505-514.	1.2	401
228	Advances in genetic studies of attention-deficit/hyperactivity disorder. Current Psychiatry Reports, 2009, 11, 143-148.	2.1	36
229	CLINICAL STUDY: Alterations in pituitaryâ€thyroid axis function among opioidâ€dependent subjects after acute and protracted abstinence. Addiction Biology, 2009, 14, 310-314.	1.4	6
230	Association of polymorphisms in <i>CASP10</i> and <i>CASP8</i> with FEV ₁ /FVC and bronchial hyperresponsiveness in ethnically diverse asthmatics. Clinical and Experimental Allergy, 2008, 38, 1738-1744.	1.4	4
231	Genetic evaluation of the serotonergic system in chronic fatigue syndrome. Psychoneuroendocrinology, 2008, 33, 188-197.	1.3	65
232	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.	1.1	37
233	Glucocorticoid receptor polymorphisms and haplotypes associated with chronic fatigue syndrome. Genes, Brain and Behavior, 2007, 6, 167-176.	1.1	68
234	Polymorphisms in genes regulating the HPA axis associated with empirically delineated classes of unexplained chronic fatigue. Pharmacogenomics, 2006, 7, 387-394.	0.6	65