Rebecca G Smith

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Epigenomic features related to microglia are associated with attenuated effect of <i>APOE</i> ε4 on Alzheimer's disease risk in humans. Alzheimer's and Dementia, 2022, 18, 688-699.	0.4	9
2	The histone modification H3K4me3 is altered at the <i>ANK1</i> locus in Alzheimer's disease brain. Future Science OA, 2021, 7, FSO665.	0.9	10
3	A meta-analysis of epigenome-wide association studies in Alzheimer's disease highlights novel differentially methylated loci across cortex. Nature Communications, 2021, 12, 3517.	5.8	72
4	An epigenome-wide association study of Alzheimer's disease blood highlights robust DNA hypermethylation in the HOXB6 gene. Neurobiology of Aging, 2020, 95, 26-45.	1.5	51
5	Altered DNA methylation profiles in blood from patients with sporadic Creutzfeldt–Jakob disease. Acta Neuropathologica, 2020, 140, 863-879.	3.9	18
6	Recalibrating the epigenetic clock: implications for assessing biological age in the human cortex. Brain, 2020, 143, 3763-3775.	3.7	100
7	Epigenomic features related to microglia are associated with attenuated effect of APOE ε4 on Alzheimer's disease risk in humans. Alzheimer's and Dementia, 2020, 16, e043533.	0.4	2
8	T40. Alzheimer's Disease DNA (Hydroxy)Methylome in the Brain and Blood: Evidence for OXT Methylation as a Preclinical Marker. Biological Psychiatry, 2019, 85, S144.	0.7	1
9	Parallel profiling of DNA methylation and hydroxymethylation highlights neuropathology-associated epigenetic variation in Alzheimer's disease. Clinical Epigenetics, 2019, 11, 52.	1.8	84
10	Genome-wide DNA methylation profiling identifies convergent molecular signatures associated with idiopathic and syndromic autism in post-mortem human brain tissue. Human Molecular Genetics, 2019, 28, 2201-2211.	1.4	70
11	Alzheimer's disease-associated (hydroxy)methylomic changes in the brain and blood. Clinical Epigenetics, 2019, 11, 164.	1.8	88
12	A cross-brain regions study of ANK1 DNA methylation in different neurodegenerative diseases. Neurobiology of Aging, 2019, 74, 70-76.	1.5	58
13	Elevated DNA methylation across a 48â€kb region spanning the <i>HOXA</i> gene cluster is associated with Alzheimer's disease neuropathology. Alzheimer's and Dementia, 2018, 14, 1580-1588.	0.4	138
14	Neonatal DNA methylation and early-onset conduct problems: A genome-wide, prospective study. Development and Psychopathology, 2018, 30, 383-397.	1.4	43
15	Genetic polymorphisms and their association with brain and behavioural measures in heterogeneous stock mice. Scientific Reports, 2017, 7, 41204.	1.6	2
16	DNA Modifications and Alzheimer's Disease. Advances in Experimental Medicine and Biology, 2017, 978, 303-319.	0.8	14
17	Epigenetics and DNA methylomic profiling in Alzheimer's disease and other neurodegenerative diseases. Journal of Neurochemistry, 2017, 143, 158-170.	2.1	65
18	Regional differences in mitochondrial DNA methylation in human post-mortem brain tissue. Clinical Epigenetics, 2017, 9, 47.	1.8	34

REBECCA G SMITH

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19	DNA methylation and substance-use risk: a prospective, genome-wide study spanning gestation to adolescence. Translational Psychiatry, 2016, 6, e976-e976.	2.4	86
20	O2â€06â€05: Hydroxymethylomic Profiling Implicates Cortical Deregulation of <i>ANK1</i> and <i>APP</i> in the Alzheimer's Disease Brain. Alzheimer's and Dementia, 2016, 12, P240.	0.4	0
21	Epigenetic signatures of childhood abuse and neglect: Implications for psychiatric vulnerability. Journal of Psychiatric Research, 2016, 83, 184-194.	1.5	99
22	Increased DNA methylation near TREM2 is consistently seen in the superior temporal gyrus in Alzheimer's disease brain. Neurobiology of Aging, 2016, 47, 35-40.	1.5	79
23	Elucidating novel dysfunctional pathways in Alzheimer's disease by integrating loci identified in genetic and epigenetic studies. Neuroepigenetics, 2016, 6, 32-50.	2.8	17
24	Variation in 5-hydroxymethylcytosine across human cortex and cerebellum. Genome Biology, 2016, 17, 27.	3.8	83
25	Tissue-specific patterns of allelically-skewed DNA methylation. Epigenetics, 2016, 11, 24-35.	1.3	32
26	Effects of advanced paternal age on trajectories of social behavior in offspring. Genes, Brain and Behavior, 2015, 14, 443-453.	1.1	22
27	Methylomic trajectories across human fetal brain development. Genome Research, 2015, 25, 338-352.	2.4	250
28	Blood methylomic signatures of presymptomatic dementia in elderly subjects with type 2 diabetes mellitus. Neurobiology of Aging, 2015, 36, 1600.e1-1600.e4.	1.5	21
29	TEMPORARY REMOVAL: Blood methylomic signatures of presymptomatic dementia in elderly subjects with type 2 diabetes mellitus. Neurobiology of Aging, 2014, , .	1.5	1
30	Transcriptomic changes in the frontal cortex associated with paternal age. Molecular Autism, 2014, 5, 24.	2.6	11
31	Genetic differences in cytochrome P450 enzymes and antidepressant treatment response. Journal of Psychopharmacology, 2014, 28, 133-141.	2.0	75
32	Environmental risk, Oxytocin Receptor Gene (OXTR) methylation and youth callous-unemotional traits: a 13-year longitudinal study. Molecular Psychiatry, 2014, 19, 1071-1077.	4.1	192
33	Methylomic profiling implicates cortical deregulation of ANK1 in Alzheimer's disease. Nature Neuroscience, 2014, 17, 1164-1170.	7.1	488
34	O3-04-03: CROSS-TISSUE METHYLOMIC PROFILING IN ALZHEIMER'S DISEASE. , 2014, 10, P215-P215.		0
35	Advanced paternal age is associated with altered DNA methylation at brain-expressed imprinted loci in inbred mice: implications for neuropsychiatric disease. Molecular Psychiatry, 2013, 18, 635-636.	4.1	31
36	DNA methylation in interleukin-11 predicts clinical response to antidepressants in GENDEP. Translational Psychiatry, 2013, 3, e300-e300.	2.4	71

REBECCA G SMITH

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37	<i>CYP2C19</i> genotype predicts steady state escitalopram concentration in GENDEP. Journal of Psychopharmacology, 2012, 26, 398-407.	2.0	69
38	DNA methylation at the lgf2/H19 imprinting control region is associated with cerebellum mass in outbred mice. Molecular Brain, 2012, 5, 42.	1.3	15
39	Epigenetics and Chronic Diseases: An Overview. , 2011, , 1-20.		4
40	Interaction between serotonin transporter gene variants and life events predicts response to antidepressants in the GENDEP project. Pharmacogenomics Journal, 2011, 11, 138-145.	0.9	70
41	Allelic Skewing of DNA Methylation Is Widespread across the Genome. American Journal of Human Genetics, 2010, 86, 196-212.	2.6	228
42	No association between genetic markers inBDNFgene and lithium prophylaxis in a Greek sample. International Journal of Psychiatry in Clinical Practice, 2010, 14, 154-157.	1.2	7
43	Moderation of antidepressant response by the serotonin transporter gene. British Journal of Psychiatry, 2009, 195, 30-38.	1.7	143
44	Genetic predictors of response to antidepressants in the GENDEP project. Pharmacogenomics Journal, 2009, 9, 225-233.	0.9	188
45	Genetic Predictors of Increase in Suicidal Ideation During Antidepressant Treatment in the GENDEP Project. Neuropsychopharmacology, 2009, 34, 2517-2528.	2.8	105
46	Advancing Paternal Age Is Associated with Deficits in Social and Exploratory Behaviors in the Offspring: A Mouse Model. PLoS ONE, 2009, 4, e8456.	1.1	77