

Rosie M Walker

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

2,352
citations

377584

21
h-index

325983

40
g-index

94
all docs

94
docs citations

94
times ranked

4069
citing authors

#	ARTICLE	IF	CITATIONS
1	Loss of SORCS2 is Associated with Neuronal DNA Double-Strand Breaks. Cellular and Molecular Neurobiology, 2023, 43, 237-249.	1.7	4
2	Methylome-wide association study of early life stressors and adult mental health. Human Molecular Genetics, 2022, 31, 651-664.	1.4	7
3	Associations between alcohol use and accelerated biological ageing. Addiction Biology, 2022, 27, e13100.	1.4	19
4	Epigenome-wide association study of global cortical volumes in generation Scotland: Scottish family health study. Epigenetics, 2022, 17, 1143-1158.	1.3	3
5	Epigenome-wide association study of alcohol consumption in 8161 individuals and relevance to alcohol use disorder pathophysiology: identification of the cystine/glutamate transporter SLC7A11 as a top target. Molecular Psychiatry, 2022, 27, 1754-1764.	4.1	18
6	Blood-based epigenome-wide analyses of cognitive abilities. Genome Biology, 2022, 23, 26.	3.8	20
7	A catalogue of omics biological ageing clocks reveals substantial commonality and associations with disease risk. Aging, 2022, 14, 623-659.	1.4	22
8	Epigenetic scores for the circulating proteome as tools for disease prediction. ELife, 2022, 11, .	2.8	37
9	DNA methylome-wide association study of genetic risk for depression implicates antigen processing and immune responses. Genome Medicine, 2022, 14, 36.	3.6	16
10	Methylome-wide association study of antidepressant use in Generation Scotland and the Netherlands Twin Register implicates the innate immune system. Molecular Psychiatry, 2022, 27, 1647-1657.	4.1	10
11	Genome- and epigenome-wide studies of plasma protein biomarkers for Alzheimer's disease implicate TBCA and TREM2 in disease risk. Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2022, 14, e12280.	1.2	4
12	Pulmonary Function and Blood DNA Methylation: A Multiancestry Epigenome-Wide Association Meta-analysis. American Journal of Respiratory and Critical Care Medicine, 2022, 206, 321-336.	2.5	15
13	Complex trait methylation scores in the prediction of major depressive disorder. EBioMedicine, 2022, 79, 104000.	2.7	4
14	Alcohol use disorder is associated with DNA methylation-based shortening of telomere length and regulated by TESPA1: implications for aging. Molecular Psychiatry, 2022, 27, 3875-3884.	4.1	7
15	Birth weight associations with DNA methylation differences in an adult population. Epigenetics, 2021, 16, 783-796.	1.3	18
16	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
17	Epigenetic prediction of major depressive disorder. Molecular Psychiatry, 2021, 26, 5112-5123.	4.1	44
18	Structural brain correlates of serum and epigenetic markers of inflammation in major depressive disorder. Brain, Behavior, and Immunity, 2021, 92, 39-48.	2.0	53

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19	DNA methylation signatures of aggression and closely related constructs: A meta-analysis of epigenome-wide studies across the lifespan. <i>Molecular Psychiatry</i> , 2021, 26, 2148-2162.	4.1	21
20	Creating and Validating a DNA Methylation-Based Proxy for Interleukin-6. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2021, 76, 2284-2292.	1.7	16
21	Assessing the role of genome-wide DNA methylation between smoking and risk of lung cancer using repeated measurements: the HUNT study. <i>International Journal of Epidemiology</i> , 2021, 50, 1482-1497.	0.9	14
22	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021, 22, 194.	3.8	90
23	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	9.4	218
24	Genome-wide methylation data improves dissection of the effect of smoking on body mass index. <i>PLoS Genetics</i> , 2021, 17, e1009750.	1.5	7
25	Identification of epigenome-wide DNA methylation differences between carriers of APOE ϵ 4 and APOE ϵ 2 alleles. <i>Genome Medicine</i> , 2021, 13, 1.	3.6	76
26	Lifestyle and Genetic Factors Modify Parent-of-Origin Effects on the Human Methylome. <i>EBioMedicine</i> , 2021, 74, 103730.	2.7	5
27	Meta-analyses identify DNA methylation associated with kidney function and damage. <i>Nature Communications</i> , 2021, 12, 7174.	5.8	30
28	An epigenome-wide association study of sex-specific chronological ageing. <i>Genome Medicine</i> , 2020, 12, 1.	3.6	117
29	Characterisation of an inflammation-related epigenetic score and its association with cognitive ability. <i>Clinical Epigenetics</i> , 2020, 12, 113.	1.8	38
30	Epigenetic measures of ageing predict the prevalence and incidence of leading causes of death and disease burden. <i>Clinical Epigenetics</i> , 2020, 12, 115.	1.8	109
31	DNA methylation in APOE: The relationship with Alzheimer's and with cardiovascular health. <i>Alzheimer's and Dementia: Translational Research and Clinical Interventions</i> , 2020, 6, e12026.	1.8	14
32	Bayesian reassessment of the epigenetic architecture of complex traits. <i>Nature Communications</i> , 2020, 11, 2865.	5.8	43
33	Identifying epigenetic biomarkers of established prognostic factors and survival in a clinical cohort of individuals with oropharyngeal cancer. <i>Clinical Epigenetics</i> , 2020, 12, 95.	1.8	6
34	DNA methylation outlier burden, health, and ageing in Generation Scotland and the Lothian Birth Cohorts of 1921 and 1936. <i>Clinical Epigenetics</i> , 2020, 12, 49.	1.8	17
35	Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. <i>Genome Medicine</i> , 2019, 11, 54.	3.6	191
36	Parent of origin genetic effects on methylation in humans are common and influence complex trait variation. <i>Nature Communications</i> , 2019, 10, 1383.	5.8	37

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37	An epigenetic score for BMI based on DNA methylation correlates with poor physical health and major disease in the Lothian Birth Cohort. <i>International Journal of Obesity</i> , 2019, 43, 1795-1802.	1.6	25
38	Identification of novel differentially methylated sites with potential as clinical predictors of impaired respiratory function and COPD. <i>EBioMedicine</i> , 2019, 43, 576-586.	2.7	21
39	A meta-analysis of genome-wide association studies of epigenetic age acceleration. <i>PLoS Genetics</i> , 2019, 15, e1008104.	1.5	83
40	Assessment of dried blood spots for DNA methylation profiling. <i>Wellcome Open Research</i> , 2019, 4, 44.	0.9	20
41	Altered DNA methylation associated with a translocation linked to major mental illness. <i>NPJ Schizophrenia</i> , 2018, 4, 5.	2.0	9
42	Epigenetic signatures of starting and stopping smoking. <i>EBioMedicine</i> , 2018, 37, 214-220.	2.7	67
43	Epigenetic prediction of complex traits and death. <i>Genome Biology</i> , 2018, 19, 136.	3.8	146
44	Investigating the relationship between DNA methylation age acceleration and risk factors for Alzheimer's disease. <i>Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring</i> , 2018, 10, 429-437.	1.2	93
45	DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons. <i>JAMA Psychiatry</i> , 2018, 75, 949.	6.0	78
46	Identification of polymorphic and off-target probe binding sites on the Illumina Infinium MethylationEPIC BeadChip. <i>Genomics Data</i> , 2016, 9, 22-24.	1.3	264
47	The DISC1 promoter: characterization and regulation by FOXP2. <i>Human Molecular Genetics</i> , 2012, 21, 2862-2872.	1.4	39
48	Association analysis of Neuregulin 1 candidate regions in schizophrenia and bipolar disorder. <i>Neuroscience Letters</i> , 2010, 478, 9-13.	1.0	41