

Rosie M Walker

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

2,352
citations

331670

21
h-index

289244

40
g-index

94
all docs

94
docs citations

94
times ranked

3734
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	21.4	218
3	Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. <i>Genome Medicine</i> , 2019, 11, 54.	8.2	191
4	Epigenetic prediction of complex traits and death. <i>Genome Biology</i> , 2018, 19, 136.	8.8	146
5	An epigenome-wide association study of sex-specific chronological ageing. <i>Genome Medicine</i> , 2020, 12, 1.	8.2	117
6	Epigenetic measures of ageing predict the prevalence and incidence of leading causes of death and disease burden. <i>Clinical Epigenetics</i> , 2020, 12, 115.	4.1	109
7	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.	2.4	93
8	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021, 22, 194.	8.8	90
9	A meta-analysis of genome-wide association studies of epigenetic age acceleration. <i>PLoS Genetics</i> , 2019, 15, e1008104.	3.5	83
10	DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons. <i>JAMA Psychiatry</i> , 2018, 75, 949.	11.0	78
11	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.	8.2	76
12	Epigenetic signatures of starting and stopping smoking. <i>EBioMedicine</i> , 2018, 37, 214-220.	6.1	67
13	Structural brain correlates of serum and epigenetic markers of inflammation in major depressive disorder. <i>Brain, Behavior, and Immunity</i> , 2021, 92, 39-48.	4.1	53
14	Epigenetic prediction of major depressive disorder. <i>Molecular Psychiatry</i> , 2021, 26, 5112-5123.	7.9	44
15	Bayesian reassessment of the epigenetic architecture of complex traits. <i>Nature Communications</i> , 2020, 11, 2865.	12.8	43
16	Association analysis of Neuregulin 1 candidate regions in schizophrenia and bipolar disorder. <i>Neuroscience Letters</i> , 2010, 478, 9-13.	2.1	41
17	The DISC1 promoter: characterization and regulation by FOXP2. <i>Human Molecular Genetics</i> , 2012, 21, 2862-2872.	2.9	39
18	Characterisation of an inflammation-related epigenetic score and its association with cognitive ability. <i>Clinical Epigenetics</i> , 2020, 12, 113.	4.1	38

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19	Parent of origin genetic effects on methylation in humans are common and influence complex trait variation. <i>Nature Communications</i> , 2019, 10, 1383.	12.8	37
20	Epigenetic scores for the circulating proteome as tools for disease prediction. <i>ELife</i> , 2022, 11, .	6.0	37
21	Epigenome-wide association study and multi-tissue replication of individuals with alcohol use disorder: evidence for abnormal glucocorticoid signaling pathway gene regulation. <i>Molecular Psychiatry</i> , 2021, 26, 2224-2237.	7.9	32
22	Meta-analyses identify DNA methylation associated with kidney function and damage. <i>Nature Communications</i> , 2021, 12, 7174.	12.8	30
23	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.	3.4	25
24	A catalogue of omics biological ageing clocks reveals substantial commonality and associations with disease risk. <i>Aging</i> , 2022, 14, 623-659.	3.1	22
25	Identification of novel differentially methylated sites with potential as clinical predictors of impaired respiratory function and COPD. <i>EBioMedicine</i> , 2019, 43, 576-586.	6.1	21
26	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.	7.9	21
27	Assessment of dried blood spots for DNA methylation profiling. <i>Wellcome Open Research</i> , 2019, 4, 44.	1.8	20
28	Blood-based epigenome-wide analyses of cognitive abilities. <i>Genome Biology</i> , 2022, 23, 26.	8.8	20
29	Associations between alcohol use and accelerated biological ageing. <i>Addiction Biology</i> , 2022, 27, e13100.	2.6	19
30	Birth weight associations with DNA methylation differences in an adult population. <i>Epigenetics</i> , 2021, 16, 783-796.	2.7	18
31	Epigenome-wide association study of alcohol consumption in N=8161 individuals and relevance to alcohol use disorder pathophysiology: identification of the cystine/glutamate transporter SLC7A11 as a top target. <i>Molecular Psychiatry</i> , 2022, 27, 1754-1764.	7.9	18
32	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.	4.1	17
33	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.	3.6	16
34	DNA methylome-wide association study of genetic risk for depression implicates antigen processing and immune responses. <i>Genome Medicine</i> , 2022, 14, 36.	8.2	16
35	Pulmonary Function and Blood DNA Methylation: A Multiancestry Epigenome-Wide Association Meta-analysis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2022, 206, 321-336.	5.6	15
36	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.	3.7	14

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37	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.	1.9	14
38	Methylome-wide association study of antidepressant use in Generation Scotland and the Netherlands Twin Register implicates the innate immune system. <i>Molecular Psychiatry</i> , 2022, 27, 1647-1657.	7.9	10
39	Altered DNA methylation associated with a translocation linked to major mental illness. <i>NPJ Schizophrenia</i> , 2018, 4, 5.	3.6	9
40	Methylome-wide association study of early life stressors and adult mental health. <i>Human Molecular Genetics</i> , 2022, 31, 651-664.	2.9	7
41	Genome-wide methylation data improves dissection of the effect of smoking on body mass index. <i>PLoS Genetics</i> , 2021, 17, e1009750.	3.5	7
42	Alcohol use disorder is associated with DNA methylation-based shortening of telomere length and regulated by TESPA1: implications for aging. <i>Molecular Psychiatry</i> , 2022, 27, 3875-3884.	7.9	7
43	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.	4.1	6
44	Lifestyle and Genetic Factors Modify Parent-of-Origin Effects on the Human Methylome. <i>EBioMedicine</i> , 2021, 74, 103730.	6.1	5
45	Loss of SORCS2 is Associated with Neuronal DNA Double-Strand Breaks. <i>Cellular and Molecular Neurobiology</i> , 2023, 43, 237-249.	3.3	4
46	Genome- and epigenome-wide studies of plasma protein biomarkers for Alzheimer's disease implicate TBCA and TREM2 in disease risk. <i>Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring</i> , 2022, 14, e12280.	2.4	4
47	Complex trait methylation scores in the prediction of major depressive disorder. <i>EBioMedicine</i> , 2022, 79, 104000.	6.1	4
48	Epigenome-wide association study of global cortical volumes in generation Scotland: Scottish family health study. <i>Epigenetics</i> , 2022, 17, 1143-1158.	2.7	3