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List of Publications by Year
in descending order

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70	3,350	159585 30	155660 55
papers	citations	h-index	g-index

76	76	76	5848
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Dual methylation and hydroxymethylation study of alcohol use disorder. Addiction Biology, 2022, 27, e13114.	2.6	12
2	Early adversities accelerate epigenetic aging into adulthood: a 10â€year, withinâ€subject analysis. Journal of Child Psychology and Psychiatry and Allied Disciplines, 2022, 63, 1308-1315.	5.2	16
3	Transcriptome-wide association study for postpartum depression implicates altered B-cell activation and insulin resistance. Molecular Psychiatry, 2022, 27, 2858-2867.	7.9	9
4	DNA methylation signatures of childhood trauma predict psychiatric disorders and other adverse outcomes 17 years after exposure. Molecular Psychiatry, 2022, 27, 3367-3373.	7.9	9
5	Methylomic Investigation of Problematic Adolescent Cannabis Use and Its Negative Mental Health Consequences. Journal of the American Academy of Child and Adolescent Psychiatry, 2021, 60, 1524-1532.	0.5	12
6	An integrative study of five biological clocks in somatic and mental health. ELife, 2021, 10, .	6.0	52
7	A methylation study implicates the rewiring of brain neural circuits during puberty in the emergence of sex differences in depression symptoms. Journal of Child Psychology and Psychiatry and Allied Disciplines, 2021, , .	5.2	4
8	A targeted solution for estimating the cell-type composition of bulk samples. BMC Bioinformatics, 2021, 22, 462.	2.6	4
9	DNA methylation of the KLK8 gene in depression symptomatology. Clinical Epigenetics, 2021, 13, 200.	4.1	7
10	Independent Methylome-Wide Association Studies of Schizophrenia Detect Consistent Caseâ€“Control Differences. Schizophrenia Bulletin, 2020, 46, 319-327.	4.3	15
11	Methylome-wide association findings for major depressive disorder overlap in blood and brain and replicate in independent brain samples. Molecular Psychiatry, 2020, 25, 1344-1354.	7.9	61
12	A methylation study of long-term depression risk. Molecular Psychiatry, 2020, 25, 1334-1343.	7.9	56
13	Cell Typeâ€“Specific Methylome-wide Association Studies Implicate Neurotrophin and Innate Immune Signaling in Major Depressive Disorder. Biological Psychiatry, 2020, 87, 431-442.	1.3	35
14	MBD-seq - realities of a misunderstood method for high-quality methylome-wide association studies. Epigenetics, 2020, 15, 431-438.	2.7	17
15	Test-statistic inflation in methylome-wide association studies. Epigenetics, 2020, 15, 1163-1166.	2.7	20
16	DNA methylation and histone acetylation changes to cytochrome P450 2E1 regulation in normal aging and impact on rates of drug metabolism in the liver. GeroScience, 2020, 42, 819-832.	4.6	26
17	The genomics of major psychiatric disorders in a large pedigree from Northern Sweden. Translational Psychiatry, 2019, 9, 60.	4.8	15
18	Epigenetic Aging in Major Depressive Disorder. American Journal of Psychiatry, 2018, 175, 774-782.	7.2	172

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19	RaMWAS: fast methylome-wide association study pipeline for enrichment platforms. Bioinformatics, 2018, 34, 2283-2285.	4.1	42
20	Methyl-CpG-Binding Domain Sequencing: MBD-seq. Methods in Molecular Biology, 2018, 1708, 171-189.	0.9	21
21	Association of Childhood Trauma Exposure With Adult Psychiatric Disorders and Functional Outcomes. JAMA Network Open, 2018, 1, e184493.	5.9	285
22	Successes and Challenges in Precision Medicine in Psychiatry. JAMA Psychiatry, 2018, 75, 1269.	11.0	4
23	A Whole Methylome Study of Ethanol Exposure in Brain and Blood: An Exploration of the Utility of Peripheral Blood as Proxy Tissue for Brain in Alcohol Methylation Studies. Alcoholism: Clinical and Experimental Research, 2018, 42, 2360-2368.	2.4	12
24	Convergence of evidence from a methylome-wide CpG-SNP association study and GWAS of major depressive disorder. Translational Psychiatry, 2018, 8, 162.	4.8	16
25	Correcting for cell-type effects in DNA methylation studies: reference-based method outperforms latent variable approaches in empirical studies. Genome Biology, 2017, 18, 24.	8.8	25
26	Deep Sequencing of 71 Candidate Genes to Characterize Variation Associated with Alcohol Dependence. Alcoholism: Clinical and Experimental Research, 2017, 41, 711-718.	2.4	13
27	Enrichment methods provide a feasible approach to comprehensive and adequately powered investigations of the brain methylome. Nucleic Acids Research, 2017, 45, e97-e97.	14.5	32
28	A MBD-seq protocol for large-scale methylome-wide studies with (very) low amounts of DNA. Epigenetics, 2017, 12, 743-750.	2.7	42
29	A Whole Methylome CpG-SNP Association Study of Psychosis in Blood and Brain Tissue. Schizophrenia Bulletin, 2016, 42, 1018-1026.	4.3	41
30	Deep Sequencing of Three Loci Implicated in Large-Scale Genome-Wide Association Study Smoking Meta-Analyses. Nicotine and Tobacco Research, 2016, 18, 626-631.	2.6	10
31	Combined Whole Methylome and Genomewide Association Study ImplicatesCNTN4in Alcohol Use. Alcoholism: Clinical and Experimental Research, 2015, 39, 1396-1405.	2.4	15
32	High density methylation QTL analysis in human blood via next-generation sequencing of the methylated genomic DNA fraction. Genome Biology, 2015, 16, 291.	8.8	112
33	Refinement of schizophrenia GWAS loci using methylome-wide association data. Human Genetics, 2015, 134, 77-87.	3.8	25
34	Candidate gene methylation studies are at high risk of erroneous conclusions. Epigenomics, 2015, 7, 13-15.	2.1	14
35	Systematic Integration of Brain eQTL and GWAS IdentifiesZNF323as a Novel Schizophrenia Risk Gene and Suggests Recent Positive Selection Based on Compensatory Advantage on Pulmonary Function. Schizophrenia Bulletin, 2015, 41, 1294-1308.	4.3	48
36	Common Variants in the MKL1 Gene Confer Risk of Schizophrenia. Schizophrenia Bulletin, 2015, 41, 715-727.	4.3	15

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37	Evaluation of Methyl-Binding Domain Based Enrichment Approaches Revisited. PLoS ONE, 2015, 10, e0132205.	2.5	26
38	Could monitoring methylation markers aid the management of schizophrenia?. Biomarkers in Medicine, 2014, 8, 607-611.	1.4	0
39	Family-Based Replication Study of Schizophrenia Genes. JAMA Psychiatry, 2014, 71, 1195.	11.0	0
40	Methylome-Wide Association Study of Schizophrenia. JAMA Psychiatry, 2014, 71, 255.	11.0	210
41	A methylome-wide study of aging using massively parallel sequencing of the methyl-CpG-enriched genomic fraction from blood in over 700 subjects. Human Molecular Genetics, 2014, 23, 1175-1185.	2.9	147
42	MethylPCA: a toolkit to control for confounders in methylome-wide association studies. BMC Bioinformatics, 2013, 14, 74.	2.6	16
43	Estimation of CpG coverage in whole methylome next-generation sequencing studies. BMC Bioinformatics, 2013, 14, 50.	2.6	24
44	A Comprehensive Family-Based Replication Study of Schizophrenia Genes. JAMA Psychiatry, 2013, 70, 573.	11.0	138
45	Testing two models describing how methylome-wide studies in blood are informative for psychiatric conditions. Epigenomics, 2013, 5, 367-377.	2.1	81
46	High quality methylome-wide investigations through next-generation sequencing of DNA from a single archived dry blood spot. Epigenetics, 2013, 8, 542-547.	2.7	31
47	Genome-wide association study of patient-rated and clinician-rated global impression of severity during antipsychotic treatment. Pharmacogenetics and Genomics, 2013, 23, 69-77.	1.5	43
48	Genotype-Based Ancestral Background Consistently Predicts Efficacy and Side Effects across Treatments in CATIE and STAR*D. PLoS ONE, 2013, 8, e55239.	2.5	6
49	Genome-wide pharmacogenomic study of citalopram-induced side effects in STAR*D. Translational Psychiatry, 2012, 2, e129-e129.	4.8	41
50	Genome-wide association study of antipsychotic-induced QTc interval prolongation. Pharmacogenomics Journal, 2012, 12, 165-172.	2.0	78
51	Pharmacogenomic study of side-effects for antidepressant treatment options in STAR*D. Psychological Medicine, 2012, 42, 1151-1162.	4.5	60
52	MBD-seq as a cost-effective approach for methylome-wide association studies: demonstration in 1500 caseâ€“control samples. Epigenomics, 2012, 4, 605-621.	2.1	86
53	Methylome-wide comparison of human genomic DNA extracted from whole blood and from EBV-transformed lymphocyte cell lines. European Journal of Human Genetics, 2012, 20, 953-955.	2.8	25
54	SNP-based analysis of neuroactive ligandâ€“receptor interaction pathways implicates PGE2 as a novel mediator of antipsychotic treatment response: Data from the CATIE study. Schizophrenia Research, 2012, 135, 200-201.	2.0	47

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55	Reply to: Epstein-Barr Virus Transformed DNA as a Source of False Positive Findings in Methylation Studies of Psychiatric Conditions. Biological Psychiatry, 2011, 70, e27-e28.	1.3	5
56	Genome-wide pharmacogenomic analysis of response to treatment with antipsychotics. Molecular Psychiatry, 2011, 16, 76-85.	7.9	141
57	Genomewide pharmacogenomic study of metabolic side effects to antipsychotic drugs. Molecular Psychiatry, 2011, 16, 321-332.	7.9	141
58	Genome-Wide Pharmacogenomic Study of Neurocognition As an Indicator of Antipsychotic Treatment Response in Schizophrenia. Neuropsychopharmacology, 2011, 36, 616-626.	5.4	103
59	Genomewide Association Study of Movement-Related Adverse Antipsychotic Effects. Biological Psychiatry, 2010, 67, 279-282.	1.3	122
60	A Genomewide Association Study of Citalopram Response in Major Depressive Disorderâ€"A Psychometric Approach. Biological Psychiatry, 2010, 68, e25-e27.	1.3	18
61	Suggestive linkage detected for blood pressure related traits on 2q and 22q in the population on the Samoan islands. BMC Medical Genetics, 2009, 10, 107.	2.1	13
62	Susceptibility Loci for Adiposity Phenotypes on 8p, 9p, and 16q in American Samoa and Samoa. Obesity, 2009, 17, 518-524.	3.0	28
63	Support for schizophrenia susceptibility locus on chromosome 2q detected in a Swedish isolate using a dense map of microsatellites and SNPs. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2008, 147B, 1238-1244.	1.7	8
64	Merging microsatellite data: enhanced methodology and software to combine genotype data for linkage and association analysis. BMC Bioinformatics, 2008, 9, 317.	2.6	5
65	Applying Novel Genome-Wide Linkage Strategies to Search for Loci Influencing Type 2 Diabetes and Adult Height in American Samoa. Human Biology, 2008, 80, 99-123.	0.2	4
66	A genome-wide linkage scan identifies multiple chromosomal regions influencing serum lipid levels in the population on the Samoan islands. Journal of Lipid Research, 2008, 49, 2169-2178.	4.2	29
67	Human QKI, a new candidate gene for schizophrenia involved in myelination. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2006, 141B, 84-90.	1.7	95
68	Human QKI, a potential regulator of mRNA expression of human oligodendrocyte-related genes involved in schizophrenia. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 7482-7487.	7.1	193
69	Serotonin receptor 2C (HTR2C) and schizophrenia: Examination of possible medication and genetic influences on expression levels. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2005, 134B, 84-89.	1.7	32
70	Reconstruction of ancestral haplotypes in a 12-generation schizophrenia pedigree. Psychiatric Genetics, 2004, 14, 1-8.	1.1	22