

Edwin J C G Van Den Oord

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

1,823
citations

394421

19
h-index

361022

35
g-index

36
all docs

36
docs citations

36
times ranked

3364
citing authors

#	ARTICLE	IF	CITATIONS
1	Association of Childhood Trauma Exposure With Adult Psychiatric Disorders and Functional Outcomes. <i>JAMA Network Open</i> , 2018, 1, e184493.	5.9	285
2	Methylome-Wide Association Study of Schizophrenia. <i>JAMA Psychiatry</i> , 2014, 71, 255.	11.0	210
3	Epigenetic Aging in Major Depressive Disorder. <i>American Journal of Psychiatry</i> , 2018, 175, 774-782.	7.2	172
4	Clozapine-induced agranulocytosis is associated with rare HLA-DQB1 and HLA-B alleles. <i>Nature Communications</i> , 2014, 5, 4757.	12.8	153
5	False discoveries and models for gene discovery. <i>Trends in Genetics</i> , 2003, 19, 537-542.	6.7	133
6	Genomewide Association Analysis Followed by a Replication Study Implicates a Novel Candidate Gene for Neuroticism. <i>Archives of General Psychiatry</i> , 2008, 65, 1062.	12.3	120
7	High density methylation QTL analysis in human blood via next-generation sequencing of the methylated genomic DNA fraction. <i>Genome Biology</i> , 2015, 16, 291.	8.8	112
8	Methylome-wide association findings for major depressive disorder overlap in blood and brain and replicate in independent brain samples. <i>Molecular Psychiatry</i> , 2020, 25, 1344-1354.	7.9	61
9	Controlling false discoveries in genetic studies. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2008, 147B, 637-644.	1.7	60
10	A methylation study of long-term depression risk. <i>Molecular Psychiatry</i> , 2020, 25, 1334-1343.	7.9	56
11	RaMWAS: fast methylome-wide association study pipeline for enrichment platforms. <i>Bioinformatics</i> , 2018, 34, 2283-2285.	4.1	42
12	A Whole Methylome CpG-SNP Association Study of Psychosis in Blood and Brain Tissue. <i>Schizophrenia Bulletin</i> , 2016, 42, 1018-1026.	4.3	41
13	Cell Type-Specific Methylome-wide Association Studies Implicate Neurotrophin and Innate Immune Signaling in Major Depressive Disorder. <i>Biological Psychiatry</i> , 2020, 87, 431-442.	1.3	35
14	Enrichment methods provide a feasible approach to comprehensive and adequately powered investigations of the brain methylome. <i>Nucleic Acids Research</i> , 2017, 45, e97-e97.	14.5	32
15	Genome-Wide Meta-Analysis of Longitudinal Alcohol Consumption Across Youth and Early Adulthood. <i>Twin Research and Human Genetics</i> , 2015, 18, 335-347.	0.6	26
16	Evaluation of Methyl-Binding Domain Based Enrichment Approaches Revisited. <i>PLoS ONE</i> , 2015, 10, e0132205.	2.5	26
17	Correcting for cell-type effects in DNA methylation studies: reference-based method outperforms latent variable approaches in empirical studies. <i>Genome Biology</i> , 2017, 18, 24.	8.8	25
18	Estimation of CpG coverage in whole methylome next-generation sequencing studies. <i>BMC Bioinformatics</i> , 2013, 14, 50.	2.6	24

#	ARTICLE	IF	CITATIONS
19	The NLSY Kinship Links: Using the NLSY79 and NLSY-Children Data to Conduct Genetically-Informed and Family-Oriented Research. <i>Behavior Genetics</i> , 2016, 46, 538-551.	2.1	24
20	Methyl-CpG-Binding Domain Sequencing: MBD-seq. <i>Methods in Molecular Biology</i> , 2018, 1708, 171-189.	0.9	21
21	Test-statistic inflation in methylome-wide association studies. <i>Epigenetics</i> , 2020, 15, 1163-1166.	2.7	20
22	MBD-seq - realities of a misunderstood method for high-quality methylome-wide association studies. <i>Epigenetics</i> , 2020, 15, 431-438.	2.7	17
23	Convergence of evidence from a methylome-wide CpG-SNP association study and GWAS of major depressive disorder. <i>Translational Psychiatry</i> , 2018, 8, 162.	4.8	16
24	Early adversities accelerate epigenetic aging into adulthood: a 10-year, within-subject analysis. <i>Journal of Child Psychology and Psychiatry and Allied Disciplines</i> , 2022, 63, 1308-1315.	5.2	16
25	Combined Whole Methylome and Genomewide Association Study Implicates <i>CNTN4</i> in Alcohol Use. <i>Alcoholism: Clinical and Experimental Research</i> , 2015, 39, 1396-1405.	2.4	15
26	Independent Methylome-Wide Association Studies of Schizophrenia Detect Consistent Case-Control Differences. <i>Schizophrenia Bulletin</i> , 2020, 46, 319-327.	4.3	15
27	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. <i>Alcoholism: Clinical and Experimental Research</i> , 2018, 42, 2360-2368.	2.4	12
28	Dual methylation and hydroxymethylation study of alcohol use disorder. <i>Addiction Biology</i> , 2022, 27, e13114.	2.6	12
29	Transcriptome-wide association study for postpartum depression implicates altered B-cell activation and insulin resistance. <i>Molecular Psychiatry</i> , 2022, 27, 2858-2867.	7.9	9
30	DNA methylation signatures of childhood trauma predict psychiatric disorders and other adverse outcomes 17 years after exposure. <i>Molecular Psychiatry</i> , 2022, 27, 3367-3373.	7.9	9
31	DNA methylation of the <i>KLK8</i> gene in depression symptomatology. <i>Clinical Epigenetics</i> , 2021, 13, 200.	4.1	7
32	Genetics and diagnostic refinement. <i>Behavior Genetics</i> , 2007, 37, 535-545.	2.1	5
33	Successes and Challenges in Precision Medicine in Psychiatry. <i>JAMA Psychiatry</i> , 2018, 75, 1269.	11.0	4
34	A methylation study implicates the rewiring of brain neural circuits during puberty in the emergence of sex differences in depression symptoms. <i>Journal of Child Psychology and Psychiatry and Allied Disciplines</i> , 2021, , .	5.2	4
35	A targeted solution for estimating the cell-type composition of bulk samples. <i>BMC Bioinformatics</i> , 2021, 22, 462.	2.6	4
36	Family-Based Replication Study of Schizophrenia Genes. <i>JAMA Psychiatry</i> , 2014, 71, 1195.	11.0	0