

Darina Czamara

List of Publications by Year in descending order

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Version: 2024-02-01

98
papers

8,438
citations

87888

38
h-index

53230

85
g-index

111
all docs

111
docs citations

111
times ranked

15819
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. <i>Nature Genetics</i> , 2013, 45, 984-994.	21.4	2,067
2	A mega-analysis of genome-wide association studies for major depressive disorder. <i>Molecular Psychiatry</i> , 2013, 18, 497-511.	7.9	1,002
3	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. <i>Nature Genetics</i> , 2013, 45, 145-154.	21.4	675
4	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016, 7, 10023.	12.8	412
5	Joint Analysis of Psychiatric Disorders Increases Accuracy of Risk Prediction for Schizophrenia, Bipolar Disorder, and Major Depressive Disorder. <i>American Journal of Human Genetics</i> , 2015, 96, 283-294.	6.2	225
6	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	21.4	218
7	An epigenetic clock for gestational age at birth based on blood methylation data. <i>Genome Biology</i> , 2016, 17, 206.	8.8	193
8	Dissecting the Association Between Inflammation, Metabolic Dysregulation, and Specific Depressive Symptoms. <i>JAMA Psychiatry</i> , 2021, 78, 161.	11.0	150
9	Maternal Gestational Diabetes Mellitus and Newborn DNA Methylation: Findings From the Pregnancy and Childhood Epigenetics Consortium. <i>Diabetes Care</i> , 2020, 43, 98-105.	8.6	145
10	Glucocorticoid exposure during hippocampal neurogenesis primes future stress response by inducing changes in DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 23280-23285.	7.1	141
11	Meta-analysis of epigenome-wide association studies in neonates reveals widespread differential DNA methylation associated with birthweight. <i>Nature Communications</i> , 2019, 10, 1893.	12.8	140
12	The PedBE clock accurately estimates DNA methylation age in pediatric buccal cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 23329-23335.	7.1	140
13	Novel multiple sclerosis susceptibility loci implicated in epigenetic regulation. <i>Science Advances</i> , 2016, 2, e1501678.	10.3	133
14	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. <i>International Journal of Epidemiology</i> , 2018, 47, 22-23u.	1.9	105
15	Restless Legs Syndrome-associated intronic common variant in <i>Meis1</i> alters enhancer function in the developing telencephalon. <i>Genome Research</i> , 2014, 24, 592-603.	5.5	102
16	Genetic Differences in the Immediate Transcriptome Response to Stress Predict Risk-Related Brain Function and Psychiatric Disorders. <i>Neuron</i> , 2015, 86, 1189-1202.	8.1	102
17	Integrated analysis of environmental and genetic influences on cord blood DNA methylation in new-borns. <i>Nature Communications</i> , 2019, 10, 2548.	12.8	94
18	Genome-wide association scan identifies new variants associated with a cognitive predictor of dyslexia. <i>Translational Psychiatry</i> , 2019, 9, 77.	4.8	82

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19	Epigenome-wide meta-analysis of blood DNA methylation in newborns and children identifies numerous loci related to gestational age. <i>Genome Medicine</i> , 2020, 12, 25.	8.2	81
20	The Epigenetic Clock at Birth: Associations With Maternal Antenatal Depression and Child Psychiatric Problems. <i>Journal of the American Academy of Child and Adolescent Psychiatry</i> , 2018, 57, 321-328.e2.	0.5	78
21	FoxO1, A2M, and TGF- β 1: three novel genes predicting depression in gene X environment interactions are identified using cross-species and cross-tissues transcriptomic and miRNomic analyses. <i>Molecular Psychiatry</i> , 2018, 23, 2192-2208.	7.9	73
22	Hypertensive Disorders of Pregnancy and DNA Methylation in Newborns. <i>Hypertension</i> , 2019, 74, 375-383.	2.7	73
23	Children with ADHD Symptoms Have a Higher Risk for Reading, Spelling and Math Difficulties in the GINIplus and LISApplus Cohort Studies. <i>PLoS ONE</i> , 2013, 8, e63859.	2.5	72
24	Associations between maternal risk factors of adverse pregnancy and birth outcomes and the offspring epigenetic clock of gestational age at birth. <i>Clinical Epigenetics</i> , 2017, 9, 49.	4.1	68
25	Polygenic Risk: Predicting Depression Outcomes in Clinical and Epidemiological Cohorts of Youths. <i>American Journal of Psychiatry</i> , 2019, 176, 615-625.	7.2	67
26	Genome-wide mapping of genetic determinants influencing DNA methylation and gene expression in human hippocampus. <i>Nature Communications</i> , 2017, 8, 1511.	12.8	60
27	Genetic analysis of dyslexia candidate genes in the European cross-linguistic NeuroDys cohort. <i>European Journal of Human Genetics</i> , 2014, 22, 675-680.	2.8	59
28	Genome-wide association study of panic disorder reveals genetic overlap with neuroticism and depression. <i>Molecular Psychiatry</i> , 2021, 26, 4179-4190.	7.9	58
29	Methodological challenges in constructing DNA methylation risk scores. <i>Epigenetics</i> , 2020, 15, 1-11.	2.7	57
30	IRGM Variants and Susceptibility to Inflammatory Bowel Disease in the German Population. <i>PLoS ONE</i> , 2013, 8, e54338.	2.5	57
31	<i>ABC1</i> gene variants and antidepressant treatment outcome: A meta-analysis. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2015, 168, 274-283.	1.7	56
32	A genetic risk score combining 32 SNPs is associated with body mass index and improves obesity prediction in people with major depressive disorder. <i>BMC Medicine</i> , 2015, 13, 86.	5.5	56
33	Genome-wide association study reveals new insights into the heritability and genetic correlates of developmental dyslexia. <i>Molecular Psychiatry</i> , 2021, 26, 3004-3017.	7.9	56
34	Association between DNA methylation and ADHD symptoms from birth to school age: a prospective meta-analysis. <i>Translational Psychiatry</i> , 2020, 10, 398.	4.8	54
35	The brain's hemodynamic response function rapidly changes under acute psychosocial stress in association with genetic and endocrine stress response markers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E10206-E10215.	7.1	53
36	Treatment response classes in major depressive disorder identified by model-based clustering and validated by clinical prediction models. <i>Translational Psychiatry</i> , 2019, 9, 187.	4.8	51

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37	Interaction between the <i>FTO</i> gene, body mass index and depression: meta-analysis of 13701 individuals. <i>British Journal of Psychiatry</i> , 2017, 211, 70-76.	2.8	49
38	Maternal blood contamination of collected cord blood can be identified using DNA methylation at three CpGs. <i>Clinical Epigenetics</i> , 2017, 9, 75.	4.1	49
39	Identification of dynamic glucocorticoid-induced methylation changes at the <i>FKBP5</i> locus. <i>Clinical Epigenetics</i> , 2019, 11, 83.	4.1	49
40	The epigenetic clock and pubertal, neuroendocrine, psychiatric, and cognitive outcomes in adolescents. <i>Clinical Epigenetics</i> , 2018, 10, 96.	4.1	43
41	Multi-omics analysis identifies mitochondrial pathways associated with anxiety-related behavior. <i>PLoS Genetics</i> , 2019, 15, e1008358.	3.5	43
42	â€œDNA Methylation signatures in panic disorderâ€. <i>Translational Psychiatry</i> , 2017, 7, 1287.	4.8	42
43	Single-cell molecular profiling of all three components of the HPA axis reveals adrenal <i>ABCB1</i> as a regulator of stress adaptation. <i>Science Advances</i> , 2021, 7, .	10.3	42
44	DNA methylation and body mass index from birth to adolescence: meta-analyses of epigenome-wide association studies. <i>Genome Medicine</i> , 2020, 12, 105.	8.2	41
45	<i>PTGER4</i> Expression-Modulating Polymorphisms in the 5p13.1 Region Predispose to Crohn's Disease and Affect <i>NF-Î²</i> and <i>XBP1</i> Binding Sites. <i>PLoS ONE</i> , 2012, 7, e52873.	2.5	39
46	DNA methylation levels are associated with <i>CRF1</i> receptor antagonist treatment outcome in women with post-traumatic stress disorder. <i>Clinical Epigenetics</i> , 2018, 10, 136.	4.1	36
47	The biological classification of mental disorders (BeCOME) study: a protocol for an observational deep-phenotyping study for the identification of biological subtypes. <i>BMC Psychiatry</i> , 2020, 20, 213.	2.6	36
48	The <i>P2RX7</i> polymorphism rs2230912 is associated with depression: A meta-analysis. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2018, 82, 272-277.	4.8	34
49	Time-dependent effects of dexamethasone plasma concentrations on glucocorticoid receptor challenge tests. <i>Psychoneuroendocrinology</i> , 2016, 69, 161-171.	2.7	33
50	Genetic comorbidity between major depression and cardioâ€œmetabolic traits, stratified by age at onset of major depression. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2020, 183, 309-330.	1.7	33
51	Cell-Type-Specific Impact of Glucocorticoid Receptor Activation on the Developing Brain: A Cerebral Organoid Study. <i>American Journal of Psychiatry</i> , 2022, 179, 375-387.	7.2	33
52	Dilution of candidates: the case of iron-related genes in restless legs syndrome. <i>European Journal of Human Genetics</i> , 2013, 21, 410-414.	2.8	32
53	Polygenic risk for immuno-metabolic markers and specific depressive symptoms: A multi-sample network analysis study. <i>Brain, Behavior, and Immunity</i> , 2021, 95, 256-268.	4.1	31
54	A genome-wide association study identifies key modulators of complement factor H binding to malondialdehyde-epitopes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 9942-9951.	7.1	29

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55	The pediatric buccal epigenetic clock identifies significant ageing acceleration in children with internalizing disorder and maltreatment exposure. <i>Neurobiology of Stress</i> , 2021, 15, 100394.	4.0	28
56	Combined effects of genotype and childhood adversity shape variability of DNA methylation across age. <i>Translational Psychiatry</i> , 2021, 11, 88.	4.8	27
57	Supportive evidence for <i>FOXP1</i> , <i>BARX1</i> , and <i>FOXF1</i> as genetic risk loci for the development of esophageal adenocarcinoma. <i>Cancer Medicine</i> , 2015, 4, 1700-1704.	2.8	26
58	Characteristics of epigenetic aging across gestational and perinatal tissues. <i>Clinical Epigenetics</i> , 2021, 13, 97.	4.1	25
59	Maternal anxiety during pregnancy and newborn epigenome-wide DNA methylation. <i>Molecular Psychiatry</i> , 2021, 26, 1832-1845.	7.9	24
60	An EPIC predictor of gestational age and its application to newborns conceived by assisted reproductive technologies. <i>Clinical Epigenetics</i> , 2021, 13, 82.	4.1	24
61	Meta-analysis of epigenome-wide association studies in newborns and children show widespread sex differences in blood DNA methylation. <i>Mutation Research - Reviews in Mutation Research</i> , 2022, 789, 108415.	5.5	24
62	Stable longitudinal associations of family income with children's hippocampal volume and memory persist after controlling for polygenic scores of educational attainment. <i>Developmental Cognitive Neuroscience</i> , 2019, 40, 100720.	4.0	22
63	Intestinal DMBT1 Expression Is Modulated by Crohn's Disease-Associated IL23R Variants and by a DMBT1 Variant Which Influences Binding of the Transcription Factors CREB1 and ATF-2. <i>PLoS ONE</i> , 2013, 8, e77773.	2.5	22
64	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
65	Childhood adversity correlates with stable changes in DNA methylation trajectories in children and converges with epigenetic signatures of prenatal stress. <i>Neurobiology of Stress</i> , 2021, 15, 100336.	4.0	19
66	Possible Associations of NTRK2 Polymorphisms with Antidepressant Treatment Outcome: Findings from an Extended Tag SNP Approach. <i>PLoS ONE</i> , 2013, 8, e64947.	2.5	17
67	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. <i>Communications Biology</i> , 2022, 5, .	4.4	17
68	Rare Variants in PLXNA4 and Parkinson's Disease. <i>PLoS ONE</i> , 2013, 8, e79145.	2.5	16
69	Sex-related differential response to dexamethasone in endocrine and immune measures in depressed in-patients and healthy controls. <i>Journal of Psychiatric Research</i> , 2018, 98, 107-115.	3.1	15
70	Toll-like receptor 4 methylation grade is linked to depressive symptom severity. <i>Translational Psychiatry</i> , 2021, 11, 371.	4.8	13
71	The role of environmental stress and DNA methylation in the longitudinal course of bipolar disorder. <i>International Journal of Bipolar Disorders</i> , 2020, 8, 9.	2.2	13
72	Meta-analysis of epigenome-wide associations between DNA methylation at birth and childhood cognitive skills. <i>Molecular Psychiatry</i> , 2022, 27, 2126-2135.	7.9	13

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73	Polygenic prediction of the risk of perinatal depressive symptoms. <i>Depression and Anxiety</i> , 2020, 37, 862-875.	4.1	12
74	The endocrine stress response is linked to one specific locus on chromosome 3 in a mouse model based on extremes in trait anxiety. <i>BMC Genomics</i> , 2012, 13, 579.	2.8	11
75	Factor H-related protein 1 (FHR-1) is associated with atherosclerotic cardiovascular disease. <i>Scientific Reports</i> , 2021, 11, 22511.	3.3	11
76	Early adversity as the prototype gene–environment interaction in mental disorders?. <i>Pharmacology Biochemistry and Behavior</i> , 2022, 215, 173371.	2.9	11
77	Investigation of MORC1 DNA methylation as biomarker of early life stress and depressive symptoms. <i>Journal of Psychiatric Research</i> , 2020, 120, 154-162.	3.1	9
78	Cord blood DNA methylation reflects cord blood C-reactive protein levels but not maternal levels: a longitudinal study and meta-analysis. <i>Clinical Epigenetics</i> , 2020, 12, 60.	4.1	9
79	Betamethasone administration during pregnancy is associated with placental epigenetic changes with implications for inflammation. <i>Clinical Epigenetics</i> , 2021, 13, 165.	4.1	9
80	A polyepigenetic glucocorticoid exposure score at birth and childhood mental and behavioral disorders. <i>Neurobiology of Stress</i> , 2020, 13, 100275.	4.0	8
81	Reliability of a novel approach for reference-based cell type estimation in human placental DNA methylation studies. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, 115.	5.4	7
82	Exposure-induced changes of plasma metabolome and gene expression in patients with panic disorder. <i>Depression and Anxiety</i> , 2019, 36, 1173-1181.	4.1	6
83	Connecting Anxiety and Genomic Copy Number Variation: A Genome-Wide Analysis in CD-1 Mice. <i>PLoS ONE</i> , 2015, 10, e0128465.	2.5	5
84	Cohort profile: InTraUterine sampling in early pregnancy (ITU), a prospective pregnancy cohort study in Finland: study design and baseline characteristics. <i>BMJ Open</i> , 2022, 12, e049231.	1.9	4
85	DNA-methylation dynamics across short-term, exposure-containing CBT in patients with panic disorder. <i>Translational Psychiatry</i> , 2022, 12, 46.	4.8	4
86	The Maternal Immunome as a Potential Biomarker for the Child's Neurodevelopmental Trajectory. <i>Biological Psychiatry</i> , 2020, 87, 868-869.	1.3	3
87	Maternal haemoglobin levels in pregnancy and child DNA methylation: a study in the pregnancy and childhood epigenetics consortium. <i>Epigenetics</i> , 2022, 17, 19-31.	2.7	3
88	Effects of stressful life-events on DNA methylation in panic disorder and major depressive disorder. <i>Clinical Epigenetics</i> , 2022, 14, 55.	4.1	3
89	141. FOXO1, A2M and TGFB1: Three Novel Genes Predicting Depression in Gene X Environment Interactions Are Identified Using Cross-Species and Cross-Tissues Transcriptomic and Mirnomic Analyses. <i>Biological Psychiatry</i> , 2017, 81, S59.	1.3	0
90	566. Acute Psychosocial Stress Impacts the Hemodynamic Response latency: A Novel Brain Phenotype that Relates to Markers of Acute and Chronic Stress. <i>Biological Psychiatry</i> , 2017, 81, S229.	1.3	0

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91	16.4 EFFECT OF GENOTYPE AND EARLY ADVERSITY ENVIRONMENT ON DNA METHYLATION. Schizophrenia Bulletin, 2018, 44, S26-S27.	4.3	0
92	F63. Polygenic Risk: Predicting Depressive Symptoms in Clinical and Epidemiological Cohorts of Adolescents. Biological Psychiatry, 2018, 83, S262.	1.3	0
93	127. The Epigenetic Clock at Birth: Associations With Maternal Antenatal Depression and Child Psychiatric Problems. Biological Psychiatry, 2018, 83, S52.	1.3	0
94	F179. Epigenetic Biomarkers in Women With Posttraumatic Stress Disorder After CRF1 Receptor Antagonist Treatment. Biological Psychiatry, 2018, 83, S308.	1.3	0
95	GWAS of Behavioral Traits. Current Topics in Behavioral Neurosciences, 2019, 42, 1-34.	1.7	0
96	GENOTYPE, PRENATAL ENVIRONMENT OR BOTHâ€“WHAT SHAPES THE NEWBORN'S EPIGENOME?. European Neuropsychopharmacology, 2019, 29, S1036-S1037.	0.7	0
97	S10FOXO1 MODIFIES ASSOCIATIONS BETWEEN MATERNAL DEPRESSION AND ANXIETY DURING PREGNANCY AND OFFSPRING PSYCHIATRIC PROBLEMS IN EARLY CHILDHOOD. European Neuropsychopharmacology, 2019, 29, S118-S119.	0.7	0
98	INTERACTIONS BETWEEN GENOTYPE AND ENVIRONMENT HAVE A STRONG EFFECT ON VARIABILITY IN DNA METHYLATION IN PSYCHIATRIC PATIENTS. European Neuropsychopharmacology, 2019, 29, S984.	0.7	0