Esther Walton

List of Publications by Year
in descending order

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87 papers	9,274 citations	94381 37 h-index	51562 86 g-index
114 all docs	114 docs citations	114 times ranked	13060 citing authors

#	Article	IF	Citations
1	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. Cell, 2019, 179, 1469-1482.e11.	13.5	935
2	Subcortical brain volume abnormalities in 2028 individuals with schizophrenia and 2540 healthy controls via the ENIGMA consortium. Molecular Psychiatry, 2016, 21, 547-553.	4.1	820
3	Common genetic variants influence human subcortical brain structures. Nature, 2015, 520, 224-229.	13.7	772
4	Genome-wide association study identifies eight risk loci and implicates metabo-psychiatric origins for anorexia nervosa. Nature Genetics, 2019, 51, 1207-1214.	9.4	641
5	Cortical Brain Abnormalities in 4474 Individuals With Schizophrenia and 5098 Control Subjects via the Enhancing Neuro Imaging Genetics Through Meta Analysis (ENIGMA) Consortium. Biological Psychiatry, 2018, 84, 644-654.	0.7	627
6	The genetic architecture of the human cerebral cortex. Science, 2020, 367, .	6.0	450
7	Significant Locus and Metabolic Genetic Correlations Revealed in Genome-Wide Association Study of Anorexia Nervosa. American Journal of Psychiatry, 2017, 174, 850-858.	4.0	410
8	ENIGMA and global neuroscience: A decade of large-scale studies of the brain in health and disease across more than 40 countries. Translational Psychiatry, 2020, 10, 100.	2.4	365
9	Mapping cortical brain asymmetry in 17,141 healthy individuals worldwide via the ENIGMA Consortium. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E5154-E5163.	3.3	299
10	Novel genetic loci associated with hippocampal volume. Nature Communications, 2017, 8, 13624.	5.8	250
11	Correspondence of DNA Methylation Between Blood and Brain Tissue and Its Application to Schizophrenia Research. Schizophrenia Bulletin, 2016, 42, 406-414.	2.3	227
12	Novel genetic loci underlying human intracranial volume identified through genome-wide association. Nature Neuroscience, 2016, 19, 1569-1582.	7.1	213
13	Genetic influences on schizophrenia and subcortical brain volumes: large-scale proof of concept. Nature Neuroscience, 2016, 19, 420-431.	7.1	204
14	Genetic architecture of subcortical brain structures in 38,851 individuals. Nature Genetics, 2019, 51, 1624-1636.	9.4	192
15	Human subcortical brain asymmetries in 15,847 people worldwide reveal effects of age and sex. Brain Imaging and Behavior, 2017, 11, 1497-1514.	1.1	144
16	Cortical thickness across the lifespan: Data from 17,075 healthy individuals aged 3â€“90â€‰years. Human Brain Mapping, 2022, 43, 431-451.	1.9	143
17	Virtual Histology of Cortical Thickness and Shared Neurobiology in 6 Psychiatric Disorders. JAMA Psychiatry, 2021, 78, 47.	6.0	136
18	Epigenetic profiling of ADHD symptoms trajectories: a prospective, methylome-wide study. Molecular Psychiatry, 2017, 22, 250-256.	4.1	124

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19	Prefrontal cortical thinning links to negative symptoms in schizophrenia via the ENIGMA consortium. Psychological Medicine, 2018, 48, 82-94.	2.7	121
20	Methylation Patterns in Whole Blood Correlate With Symptoms in Schizophrenia Patients. Schizophrenia Bulletin, 2014, 40, 769-776.	2.3	115
21	Epigenetic signatures of childhood abuse and neglect: Implications for psychiatric vulnerability. Journal of Psychiatric Research, 2016, 83, 184-194.	1.5	99
22	Annual Research Review: DNA methylation as a mediator in the association between risk exposure and child and adolescent psychopathology. Journal of Child Psychology and Psychiatry and Allied Disciplines, 2018, 59, 303-322.	3.1	92
23	DNA methylation and substance-use risk: a prospective, genome-wide study spanning gestation to adolescence. Translational Psychiatry, 2016, 6, e976-e976.	2.4	86
24	An epigenome-wide association meta-analysis of prenatal maternal stress in neonates: A model approach for replication. Epigenetics, 2016, 11, 140-149.	1.3	80
25	Positive symptoms associate with cortical thinning in the superior temporal gyrus via the ENIGMA Schizophrenia consortium. Acta Psychiatrica Scandinavica, 2017, 135, 439-447.	2.2	80
26	Subcortical volumes across the lifespan: Data from 18,605 healthy individuals aged 3â€“90â€‰years. Human Brain Mapping, 2022, 43, 452-469.	1.9	72
27	Prenatal unhealthy diet, insulinâ€like growth factor 2 gene (<scp>IGF</scp>2) methylation, and attention deficit hyperactivity disorder symptoms in youth with earlyâ€onset conduct problems. Journal of Child Psychology and Psychiatry and Allied Disciplines, 2017, 58, 19-27.	3.1	70
28	MB-COMTpromoter DNA methylation is associated with working-memory processing in schizophrenia patients and healthy controls. Epigenetics, 2014, 9, 1101-1107.	1.3	65
29	Multiâ€Polygenic Score Approach to Identifying Individual Vulnerabilities Associated With the Risk of Exposure to Bullying. JAMA Psychiatry, 2019, 76, 730.	6.0	65
30	Epigenome-wide change and variation in DNA methylation in childhood: trajectories from birth to late adolescence. Human Molecular Genetics, 2021, 30, 119-134.	1.4	65
31	Brain structure and function correlates of cognitive subtypes in schizophrenia. Psychiatry Research - Neuroimaging, 2015, 234, 74-83.	0.9	64
32	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. Nature Communications, 2020, 11, 4796.	5.8	61
33	Cumulative Genetic Risk and Prefrontal Activity in Patients With Schizophrenia. Schizophrenia Bulletin, 2013, 39, 703-711.	2.3	55
34	Association between DNA methylation and ADHD symptoms from birth to school age: a prospective meta-analysis. Translational Psychiatry, 2020, 10, 398.	2.4	54
35	A cross-disorder PRS-pheWAS of 5 major psychiatric disorders in UK Biobank. PLoS Genetics, 2020, 16, e1008185.	1.5	54
36	Prefrontal Inefficiency Is Associated With Polygenic Risk for Schizophrenia. Schizophrenia Bulletin, 2014, 40, 1263-1271.	2.3	53

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37	Neonatal DNA methylation and early-onset conduct problems: A genome-wide, prospective study. Development and Psychopathology, 2018, 30, 383-397.	1.4	43
38	Associations Between Attention-Deficit/Hyperactivity Disorder and Various Eating Disorders: A Swedish Nationwide Population Study Using Multiple Genetically Informative Approaches. Biological Psychiatry, 2019, 86, 577-586.	0.7	43
39	Inflammation-related epigenetic risk and child and adolescent mental health: A prospective study from pregnancy to middle adolescence. Development and Psychopathology, 2018, 30, 1145-1156.	1.4	39
40	A <scp>meta€analysis</scp> of deep brain structural shape and asymmetry abnormalities in 2,833 individuals with schizophrenia compared with 3,929 healthy volunteers via the <scp>ENIGMA Consortium</scp>. Human Brain Mapping, 2022, 43, 352-372.	1.9	39
41	Brain Structure in Acutely Underweight and Partially Weight-Restored Individuals With Anorexia Nervosa: A Coordinated Analysis by the ENIGMA Eating Disorders Working Group. Biological Psychiatry, 2022, 92, 730-738.	0.7	37
42	DRD4 methylation as a potential biomarker for physical aggression: An epigenome€wide, cross€tissue investigation. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2018, 177, 746-764.	1.1	33
43	Investigation of common, low-frequency and rare genome-wide variation in anorexia nervosa. Molecular Psychiatry, 2018, 23, 1169-1180.	4.1	32
44	Epigenetics of Addiction: Current Knowledge, Challenges, and Future Directions. Journal of Studies on Alcohol and Drugs, 2016, 77, 688-691.	0.6	31
45	Smoking, but Not Malnutrition, Influences Promoter-Specific DNA Methylation of the Proopiomelanocortin Gene in Patients with and without Anorexia Nervosa. Canadian Journal of Psychiatry, 2012, 57, 168-176.	0.9	29
46	Associations between DNA methylation and schizophrenia-related intermediate phenotypes â€" A gene set enrichment analysis. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2015, 59, 31-39.	2.5	29
47	The association of DNA methylation and brain volume in healthy individuals and schizophrenia patients. Schizophrenia Research, 2015, 169, 447-452.	1.1	29
48	Cross-Tissue Exploration of Genetic and Epigenetic Effects on Brain Gray Matter in Schizophrenia. Schizophrenia Bulletin, 2018, 44, 443-452.	2.3	29
49	Longitudinal epigenetic predictors of amygdala:hippocampus volume ratio. Journal of Child Psychology and Psychiatry and Allied Disciplines, 2017, 58, 1341-1350.	3.1	28
50	Shared genetic risk between eating disorder€•and substance€use€related phenotypes: Evidence from genome€wide association studies. Addiction Biology, 2021, 26, e12880.	1.4	28
51	DNA methylation signature of chronic low-grade inflammation and its role in cardio-respiratory diseases. Nature Communications, 2022, 13, 2408.	5.8	26
52	A Genome-Wide Association Study Suggests Novel Loci Associated with a Schizophrenia-Related Brain-Based Phenotype. PLoS ONE, 2013, 8, e64872.	1.1	21
53	DNA Methylation, Substance Use and Addiction: a Systematic Review of Recent Animal and Human Research from a Developmental Perspective. Current Addiction Reports, 2015, 2, 331-346.	1.6	21
54	The Impact of Genome-Wide Supported Schizophrenia Risk Variants in the Neurogranin Gene on Brain Structure and Function. PLoS ONE, 2013, 8, e76815.	1.1	21

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55	Complexin2 modulates working memory-related neural activity in patients with schizophrenia. European Archives of Psychiatry and Clinical Neuroscience, 2015, 265, 137-145.	1.8	19
56	An overlapping pattern of cerebral cortical thinning is associated with both positive symptoms and aggression in schizophrenia via the ENIGMA consortium. Psychological Medicine, 2020, 50, 2034-2045.	2.7	18
57	A Methylomeâ€Wide Association Study of Trajectories of Oppositional Defiant Behaviors and Biological Overlap With Attention Deficit Hyperactivity Disorder. Child Development, 2018, 89, 1839-1855.	1.7	17
58	The Genetics of Endophenotypes of Neurofunction to Understand Schizophrenia (GENUS) consortium: A collaborative cognitive and neuroimaging genetics project. Schizophrenia Research, 2018, 195, 306-317.	1.1	17
59	Obesity and brain structure in schizophrenia â€“ ENIGMA study in 3021 individuals. Molecular Psychiatry, 2022, 27, 3731-3737.	4.1	17
60	Reproducibility in the absence of selective reporting: AnÂillustration from largeâ€scale brain asymmetry research. Human Brain Mapping, 2022, 43, 244-254.	1.9	16
61	Epigenomics of being bullied: changes in DNA methylation following bullying exposure. Epigenetics, 2020, 15, 750-764.	1.3	16
62	Exploration of Shared Genetic Architecture Between Subcortical Brain Volumes and Anorexia Nervosa. Molecular Neurobiology, 2019, 56, 5146-5156.	1.9	15
63	Genetic influences on cognitive endophenotypes in schizophrenia. Schizophrenia Research, 2014, 156, 71-75.	1.1	14
64	Neuroimaging as a potential biomarker to optimize psychiatric research and treatment. International Review of Psychiatry, 2013, 25, 619-631.	1.4	13
65	Using Openly Accessible Resources to Strengthen Causal Inference in Epigenetic Epidemiology of Neurodevelopment and Mental Health. Genes, 2019, 10, 193.	1.0	13
66	Hidden hypotheses in â€˜hypothesis-freeâ€™ genome-wide epigenetic associations. Current Opinion in Psychology, 2019, 27, 13-17.	2.5	12
67	Epigenome-wide association study of seizures in childhood and adolescence. Clinical Epigenetics, 2020, 12, 8.	1.8	12
68	Population neuroimaging: generation of a comprehensive data resource within the ALSPAC pregnancy and birth cohort. Wellcome Open Research, 2020, 5, 203.	0.9	12
69	Peripheral serotonin transporter DNA methylation is linked to increased salience network connectivity in females with anorexia nervosa. Journal of Psychiatry and Neuroscience, 2020, 45, 206-213.	1.4	11
70	A Structured Approach to Evaluating Life-Course Hypotheses: Moving Beyond Analyses of Exposed Versus Unexposed in the -Omics Context. American Journal of Epidemiology, 2021, 190, 1101-1112.	1.6	11
71	Common Genetic Variation and Age of Onset of Anorexia Nervosa. Biological Psychiatry Global Open Science, 2022, 2, 368-378.	1.0	10
72	Genetic variation in GAD1 is associated with cortical thickness in the parahippocampal gyrus. Journal of Psychiatric Research, 2013, 47, 872-879.	1.5	9

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73	Prenatal diet and childhood ADHD: exploring the potential role of IGF2 methylation. Epigenomics, 2016, 8, 1573-1576.	1.0	9
74	Identifying causative mechanisms linking early-life stress to psycho-cardio-metabolic multi-morbidity: The EarlyCause project. PLoS ONE, 2021, 16, e0245475.	1.1	9
75	Updates to data versions and analytic methods influence the reproducibility of results from epigenome-wide association studies. Epigenetics, 2022, 17, 1373-1388.	1.3	9
76	Identifying risk factors involved in the common versus specific liabilities to substance use: A genetically informed approach. Addiction Biology, 2021, 26, e12944.	1.4	7
77	Genetic underpinnings of left superior temporal gyrus thickness in patients with schizophrenia. World Journal of Biological Psychiatry, 2015, 16, 430-440.	1.3	5
78	Epigenome-wide Associations With Attention-Deficit/Hyperactivity Disorder in Adults: The Need for a Longitudinal Life Course Approach in Epigenetic Psychiatry. Biological Psychiatry, 2019, 86, 570-572.	0.7	5
79	Reply to: New Meta- and Mega-analyses of Magnetic Resonance Imaging Findings in Schizophrenia: Do They Really Increase Our Knowledge About the Nature of the Disease Process?. Biological Psychiatry, 2019, 85, e35-e39.	0.7	5
80	Examining the possible causal relationship between lung function, COPD and Alzheimerâ€™s disease: a Mendelian randomisation study. BMJ Open Respiratory Research, 2021, 8, e000759.	1.2	5
81	Genetic underpinnings of left superior temporal gyrus thickness in patients with schizophrenia. World Journal of Biological Psychiatry, 2015, , 1-11.	1.3	5
82	Machine Learning for Large-Scale Quality Control of 3D Shape Models in Neuroimaging. Lecture Notes in Computer Science, 2017, 10541, 371-378.	1.0	4
83	DNA methylation of ghrelin and leptin receptors in underweight and recovered patients with anorexia nervosa. Journal of Psychiatric Research, 2020, 131, 271-278.	1.5	3
84	Sensitive Periods for the Effect of Childhood Adversity on DNA Methylation: Updated Results From a Prospective, Longitudinal Study. Biological Psychiatry Global Open Science, 2023, 3, 567-571.	1.0	3
85	Neonatal DNA methylation and childhood low prosocial behavior: An epigenomeâ€wide association metaâ€analysis. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2021, 186, 228-241.	1.1	2
86	Examining the epigenetic mechanisms of childhood adversity and sensitive periods: A gene set-based approach. Psychoneuroendocrinology, 2022, 144, 105854.	1.3	2
87	Epigenome-wide contributions to individual differences in childhood phenotypes: a GREML approach. Clinical Epigenetics, 2022, 14, 53.	1.8	1