

Laura M Huckins

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4966637/publications.pdf>

Version: 2024-02-01

46
papers

9,333
citations

201674

27
h-index

214800

47
g-index

70
all docs

70
docs citations

70
times ranked

14973
citing authors

#	ARTICLE	IF	CITATIONS
1	Induction of dopaminergic neurons for neuronal subtype-specific modeling of psychiatric disease risk. <i>Molecular Psychiatry</i> , 2023, 28, 1970-1982.	7.9	13
2	Mapping anorexia nervosa genes to clinical phenotypes. <i>Psychological Medicine</i> , 2023, 53, 2619-2633.	4.5	9
3	Comparison of confound adjustment methods in the construction of gene co-expression networks. <i>Genome Biology</i> , 2022, 23, 44.	8.8	4
4	Integration with systems biology approaches and -omics data to characterize risk variation. , 2022, , 289-315.		4
5	Altered gene expression and PTSD symptom dimensions in World Trade Center responders. <i>Molecular Psychiatry</i> , 2022, 27, 2225-2246.	7.9	9
6	Using phenotype risk scores to enhance gene discovery for generalized anxiety disorder and posttraumatic stress disorder. <i>Molecular Psychiatry</i> , 2022, 27, 2206-2215.	7.9	22
7	Predicted gene expression in ancestrally diverse populations leads to discovery of susceptibility loci for lifestyle and cardiometabolic traits. <i>American Journal of Human Genetics</i> , 2022, 109, 669-679.	6.2	5
8	What next for eating disorder genetics? Replacing myths with facts to sharpen our understanding. <i>Molecular Psychiatry</i> , 2022, 27, 3929-3938.	7.9	5
9	Exploring the clinical and genetic associations of adult weight trajectories using electronic health records in a racially diverse biobank: a phenome-wide and polygenic risk study. <i>The Lancet Digital Health</i> , 2022, 4, e604-e614.	12.3	6
10	Shared genetic risk between eating disorder and substance use-related phenotypes: Evidence from genome-wide association studies. <i>Addiction Biology</i> , 2021, 26, e12880.	2.6	28
11	Common Genetic Variation in Humans Impacts In Vitro Susceptibility to SARS-CoV-2 Infection. <i>Stem Cell Reports</i> , 2021, 16, 505-518.	4.8	39
12	Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. <i>Nature Genetics</i> , 2021, 53, 817-829.	21.4	629
13	Identifying nootropic drug targets via large-scale cognitive GWAS and transcriptomics. <i>Neuropsychopharmacology</i> , 2021, 46, 1788-1801.	5.4	12
14	Multi-ethnic genome-wide association analyses of white blood cell and platelet traits in the Population Architecture using Genomics and Epidemiology (PAGE) study. <i>BMC Genomics</i> , 2021, 22, 432.	2.8	6
15	Examining Sex-Differentiated Genetic Effects Across Neuropsychiatric and Behavioral Traits. <i>Biological Psychiatry</i> , 2021, 89, 1127-1137.	1.3	48
16	The Genetics of the Mood Disorder Spectrum: Genome-wide Association Analyses of More Than 185,000 Cases and 439,000 Controls. <i>Biological Psychiatry</i> , 2020, 88, 169-184.	1.3	137
17	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. <i>Scientific Data</i> , 2020, 7, 340.	5.3	75
18	Massively parallel techniques for cataloguing the regulome of the human brain. <i>Nature Neuroscience</i> , 2020, 23, 1509-1521.	14.8	39

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19	Retrospective cohort study of clinical characteristics of 2199 hospitalised patients with COVID-19 in New York City. <i>BMJ Open</i> , 2020, 10, e040736.	1.9	50
20	Analysis of Genetically Regulated Gene Expression Identifies a Prefrontal PTSD Gene, SNRNP35, Specific to Military Cohorts. <i>Cell Reports</i> , 2020, 31, 107716.	6.4	44
21	Implicit bias of encoded variables: frameworks for addressing structured bias in EHRâ€™GWAS data. <i>Human Molecular Genetics</i> , 2020, 29, R33-R41.	2.9	15
22	A chromosomal connectome for psychiatric and metabolic risk variants in adult dopaminergic neurons. <i>Genome Medicine</i> , 2020, 12, 19.	8.2	31
23	Machine Learning to Predict Mortality and Critical Events in a Cohort of Patients With COVID-19 in New York City: Model Development and Validation. <i>Journal of Medical Internet Research</i> , 2020, 22, e24018.	4.3	174
24	Penetrance and Pleiotropy of Polygenic Risk Scores for Schizophrenia in 106,160 Patients Across Four Health Care Systems. <i>American Journal of Psychiatry</i> , 2019, 176, 846-855.	7.2	168
25	Pleiotropic Meta-Analysis of Cognition, Education, and Schizophrenia Differentiates Roles of Early Neurodevelopmental and Adult Synaptic Pathways. <i>American Journal of Human Genetics</i> , 2019, 105, 334-350.	6.2	86
26	Genome-wide association study identifies eight risk loci and implicates metabo-psychiatric origins for anorexia nervosa. <i>Nature Genetics</i> , 2019, 51, 1207-1214.	21.4	641
27	Synergistic effects of common schizophrenia risk variants. <i>Nature Genetics</i> , 2019, 51, 1475-1485.	21.4	184
28	International Society of Psychiatric Genetics Ethics Committee: Issues facing us. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2019, 180, 543-554.	1.7	16
29	Genome-wide association study implicates CHRNA2 in cannabis use disorder. <i>Nature Neuroscience</i> , 2019, 22, 1066-1074.	14.8	94
30	Genetic analyses of diverse populations improves discovery for complex traits. <i>Nature</i> , 2019, 570, 514-518.	27.8	679
31	Associations Between Attention-Deficit/Hyperactivity Disorder and Various Eating Disorders: A Swedish Nationwide Population Study Using Multiple Genetically Informative Approaches. <i>Biological Psychiatry</i> , 2019, 86, 577-586.	1.3	43
32	Genome-wide association study identifies 30 loci associated with bipolar disorder. <i>Nature Genetics</i> , 2019, 51, 793-803.	21.4	1,191
33	Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. <i>Nature Genetics</i> , 2019, 51, 659-674.	21.4	154
34	Common schizophrenia alleles are enriched in mutation-intolerant genes and in regions under strong background selection. <i>Nature Genetics</i> , 2018, 50, 381-389.	21.4	1,332
35	Recent Genetics and Epigenetics Approaches to PTSD. <i>Current Psychiatry Reports</i> , 2018, 20, 30.	4.5	89
36	Landscape of Conditional eQTL in Dorsolateral Prefrontal Cortex and Co-localization with Schizophrenia GWAS. <i>American Journal of Human Genetics</i> , 2018, 102, 1169-1184.	6.2	128

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37	Analysis of shared heritability in common disorders of the brain. <i>Science</i> , 2018, 360, .	12.6	1,085
38	Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics. <i>Nature Communications</i> , 2018, 9, 1825.	12.8	748
39	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. <i>Cell</i> , 2018, 173, 1705-1715.e16.	28.9	623
40	Significant Locus and Metabolic Genetic Correlations Revealed in Genome-Wide Association Study of Anorexia Nervosa. <i>American Journal of Psychiatry</i> , 2017, 174, 850-858.	7.2	410
41	Linking cannabis use to depression and suicidal thoughts and behaviours. <i>Lancet Psychiatry</i> , the, 2017, 4, 654-656.	7.4	5
42	Integrated Bayesian analysis of rare exonic variants to identify risk genes for schizophrenia and neurodevelopmental disorders. <i>Genome Medicine</i> , 2017, 9, 114.	8.2	86
43	Summaries of plenary, symposia, and oral sessions at the XXII World Congress of Psychiatric Genetics, Copenhagen, Denmark, 12â€“16 October 2014. <i>Psychiatric Genetics</i> , 2016, 26, 1-47.	1.1	0
44	Using ancestry-informative markers to identify fine structure across 15 populations of European origin. <i>European Journal of Human Genetics</i> , 2014, 22, 1190-1200.	2.8	32
45	Olfaction and olfactory-mediated behaviour in psychiatric disease models. <i>Cell and Tissue Research</i> , 2013, 354, 69-80.	2.9	15
46	Analysis of Genetically Regulated Gene Expression Identifies a Trauma Type Specific PTSD Gene, SNRNP35. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0