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List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3315511/publications.pdf>

Version: 2024-02-01

31
papers

16,151
citations

257450

24
h-index

414414

32
g-index

42
all docs

42
docs citations

42
times ranked

21374
citing authors

#	ARTICLE	IF	CITATIONS
1	Biological insights from 108 schizophrenia-associated genetic loci. <i>Nature</i> , 2014, 511, 421-427.	27.8	6,934
2	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018, 50, 668-681.	21.4	2,224
3	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. <i>Nature</i> , 2022, 604, 502-508.	27.8	929
4	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. <i>Nature Genetics</i> , 2017, 49, 27-35.	21.4	838
5	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. <i>Science</i> , 2018, 362, .	12.6	805
6	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
7	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. <i>Cell</i> , 2018, 173, 1705-1715.e16.	28.9	623
8	Comprehensive functional genomic resource and integrative model for the human brain. <i>Science</i> , 2018, 362, .	12.6	618
9	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. <i>Science</i> , 2018, 362, .	12.6	516
10	Genetic identification of brain cell types underlying schizophrenia. <i>Nature Genetics</i> , 2018, 50, 825-833.	21.4	497
11	The Mouse Universal Genotyping Array: From Substrains to Subspecies. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 263-279.	1.8	199
12	Genomes of the Mouse Collaborative Cross. <i>Genetics</i> , 2017, 206, 537-556.	2.9	189
13	Evaluation of chromatin accessibility in prefrontal cortex of individuals with schizophrenia. <i>Nature Communications</i> , 2018, 9, 3121.	12.8	141
14	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. <i>American Journal of Human Genetics</i> , 2018, 102, 1185-1194.	6.2	119
15	Robust Hi-C Maps of Enhancer-Promoter Interactions Reveal the Function of Non-coding Genome in Neural Development and Diseases. <i>Molecular Cell</i> , 2020, 79, 521-534.e15.	9.7	110
16	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. <i>Biological Psychiatry</i> , 2021, 90, 611-620.	1.3	103
17	Non-coding variability at the APOE locus contributes to the Alzheimer's risk. <i>Nature Communications</i> , 2019, 10, 3310.	12.8	91
18	The genomics of schizophrenia: update and implications. <i>Journal of Clinical Investigation</i> , 2013, 123, 4557-4563.	8.2	87

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19	A meta-analysis of gene expression quantitative trait loci in brain. <i>Translational Psychiatry</i> , 2014, 4, e459-e459.	4.8	77
20	Activity-Dependent p25 Generation Regulates Synaptic Plasticity and A β -Induced Cognitive Impairment. <i>Cell</i> , 2014, 157, 486-498.	28.9	74
21	Increased burden of ultra-rare structural variants localizing to boundaries of topologically associated domains in schizophrenia. <i>Nature Communications</i> , 2020, 11, 1842.	12.8	56
22	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. <i>Nature Communications</i> , 2021, 12, 3968.	12.8	48
23	Revealing the brain's molecular architecture. <i>Science</i> , 2018, 362, 1262-1263.	12.6	45
24	Synaptic Deficits Are Rescued in the p25/Cdk5 Model of Neurodegeneration by the Reduction of β -Secretase (BACE1). <i>Journal of Neuroscience</i> , 2011, 31, 15751-15756.	3.6	29
25	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
26	Comparative genomic evidence for the involvement of schizophrenia risk genes in antipsychotic effects. <i>Molecular Psychiatry</i> , 2018, 23, 708-712.	7.9	27
27	Gene expression changes following chronic antipsychotic exposure in single cells from mouse striatum. <i>Molecular Psychiatry</i> , 2022, 27, 2803-2812.	7.9	10
28	THUNDER: A reference-free deconvolution method to infer cell type proportions from bulk Hi-C data. <i>PLoS Genetics</i> , 2022, 18, e1010102.	3.5	9
29	Common-variant associations with fragile X syndrome. <i>Molecular Psychiatry</i> , 2019, 24, 338-344.	7.9	8
30	Bayesian modeling of skewed X inactivation in genetically diverse mice identifies a novel Xce allele associated with copy number changes. <i>Genetics</i> , 2021, 218, .	2.9	5
31	Antipsychotic Behavioral Phenotypes in the Mouse Collaborative Cross Recombinant Inbred Inter-Crosses (RIX). <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3165-3177.	1.8	4