

Pamela Sklar

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2258098/publications.pdf>

Version: 2024-02-01

68
papers

38,847
citations

44444

50
h-index

104191

69
g-index

84
all docs

84
docs citations

84
times ranked

58500
citing authors

#	ARTICLE	IF	CITATIONS
1	Dissecting the Shared Genetic Architecture of Suicide Attempt, Psychiatric Disorders, and Known Risk Factors. <i>Biological Psychiatry</i> , 2022, 91, 313-327.	0.7	114
2	Rare coding variants in ten genes confer substantial risk for schizophrenia. <i>Nature</i> , 2022, 604, 509-516.	13.7	326
3	Investigating rare pathogenic/likely pathogenic exonic variation in bipolar disorder. <i>Molecular Psychiatry</i> , 2021, 26, 5239-5250.	4.1	15
4	Contributions of common genetic variants to risk of schizophrenia among individuals of African and Latino ancestry. <i>Molecular Psychiatry</i> , 2020, 25, 2455-2467.	4.1	82
5	Characterization of Single Gene Copy Number Variants in Schizophrenia. <i>Biological Psychiatry</i> , 2020, 87, 736-744.	0.7	10
6	Analysis of Genetically Regulated Gene Expression Identifies a Prefrontal PTSD Gene, SNRNP35, Specific to Military Cohorts. <i>Cell Reports</i> , 2020, 31, 107716.	2.9	44
7	A molecular approach to treating cognition in schizophrenia by calcium channel blockade. <i>Schizophrenia Research: Cognition</i> , 2020, 21, 100180.	0.7	4
8	Differential activity of transcribed enhancers in the prefrontal cortex of 537 cases with schizophrenia and controls. <i>Molecular Psychiatry</i> , 2019, 24, 1685-1695.	4.1	40
9	O1.3. DIFFERENTIAL HISTONE MODIFICATIONS IN 250 SCHIZOPHRENIA CASES AND 330 CONTROLS. <i>Schizophrenia Bulletin</i> , 2019, 45, S159-S160.	2.3	0
10	Global landscape and genetic regulation of RNA editing in cortical samples from individuals with schizophrenia. <i>Nature Neuroscience</i> , 2019, 22, 1402-1412.	7.1	63
11	Synergistic effects of common schizophrenia risk variants. <i>Nature Genetics</i> , 2019, 51, 1475-1485.	9.4	184
12	GWAS of Suicide Attempt in Psychiatric Disorders and Association With Major Depression Polygenic Risk Scores. <i>American Journal of Psychiatry</i> , 2019, 176, 651-660.	4.0	186
13	Genome-wide association study identifies 30 loci associated with bipolar disorder. <i>Nature Genetics</i> , 2019, 51, 793-803.	9.4	1,191
14	Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. <i>Nature Genetics</i> , 2019, 51, 659-674.	9.4	154
15	Comparative genetic architectures of schizophrenia in East Asian and European populations. <i>Nature Genetics</i> , 2019, 51, 1670-1678.	9.4	440
16	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. <i>Nature Genetics</i> , 2019, 51, 63-75.	9.4	1,594
17	Contribution of Rare Copy Number Variants to Bipolar Disorder Risk Is Limited to Schizoaffective Cases. <i>Biological Psychiatry</i> , 2019, 86, 110-119.	0.7	45
18	Common schizophrenia alleles are enriched in mutation-intolerant genes and in regions under strong background selection. <i>Nature Genetics</i> , 2018, 50, 381-389.	9.4	1,332

#	ARTICLE	IF	CITATIONS
19	Genetic validation of bipolar disorder identified by automated phenotyping using electronic health records. <i>Translational Psychiatry</i> , 2018, 8, 86.	2.4	24
20	Integrative transcriptome analyses of the aging brain implicate altered splicing in Alzheimer's disease susceptibility. <i>Nature Genetics</i> , 2018, 50, 1584-1592.	9.4	307
21	20.4 MODELING THE CONTRIBUTION OF COMMON VARIANTS TO SCHIZOPHRENIA RISK. <i>Schizophrenia Bulletin</i> , 2018, 44, S34-S34.	2.3	0
22	Expression-based drug screening of neural progenitor cells from individuals with schizophrenia. <i>Nature Communications</i> , 2018, 9, 4412.	5.8	63
23	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.	2.6	128
24	Evaluation of chromatin accessibility in prefrontal cortex of individuals with schizophrenia. <i>Nature Communications</i> , 2018, 9, 3121.	5.8	141
25	Cell-specific histone modification maps in the human frontal lobe link schizophrenia risk to the neuronal epigenome. <i>Nature Neuroscience</i> , 2018, 21, 1126-1136.	7.1	112
26	Analysis of shared heritability in common disorders of the brain. <i>Science</i> , 2018, 360, .	6.0	1,085
27	Examining the role of common and rare mitochondrial variants in schizophrenia. <i>PLoS ONE</i> , 2018, 13, e0191153.	1.1	23
28	Practical Guidelines for High-Resolution Epigenomic Profiling of Nucleosomal Histones in Postmortem Human Brain Tissue. <i>Biological Psychiatry</i> , 2017, 81, 162-170.	0.7	48
29	Large-Scale Identification of Common Trait and Disease Variants Affecting Gene Expression. <i>American Journal of Human Genetics</i> , 2017, 100, 885-894.	2.6	91
30	Institutional profile: translational pharmacogenomics at the Icahn School of Medicine at Mount Sinai. <i>Pharmacogenomics</i> , 2017, 18, 1381-1386.	0.6	20
31	Mutation intolerant genes and targets of FMRP are enriched for nonsynonymous alleles in schizophrenia. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2017, 174, 724-731.	1.1	19
32	The contribution of rare variants to risk of schizophrenia in individuals with and without intellectual disability. <i>Nature Genetics</i> , 2017, 49, 1167-1173.	9.4	200
33	10 Years of GWAS Discovery: Biology, Function, and Translation. <i>American Journal of Human Genetics</i> , 2017, 101, 5-22.	2.6	2,793
34	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. <i>Nature Genetics</i> , 2017, 49, 27-35.	9.4	838
35	Transcriptional signatures of schizophrenia in hiPSC-derived NPCs and neurons are concordant with post-mortem adult brains. <i>Nature Communications</i> , 2017, 8, 2225.	5.8	143
36	Integrated Bayesian analysis of rare exonic variants to identify risk genes for schizophrenia and neurodevelopmental disorders. <i>Genome Medicine</i> , 2017, 9, 114.	3.6	86

#	ARTICLE	IF	CITATIONS
37	Analysis of 589,306 genomes identifies individuals resilient to severe Mendelian childhood diseases. <i>Nature Biotechnology</i> , 2016, 34, 531-538.	9.4	273
38	Exome Sequencing of Familial Bipolar Disorder. <i>JAMA Psychiatry</i> , 2016, 73, 590.	6.0	97
39	Gene expression elucidates functional impact of polygenic risk for schizophrenia. <i>Nature Neuroscience</i> , 2016, 19, 1442-1453.	7.1	952
40	Increased burden of ultra-rare protein-altering variants among 4,877 individuals with schizophrenia. <i>Nature Neuroscience</i> , 2016, 19, 1433-1441.	7.1	427
41	Ultra-rare disruptive and damaging mutations influence educational attainment in the general population. <i>Nature Neuroscience</i> , 2016, 19, 1563-1565.	7.1	90
42	Nicotine dependence and psychosis in Bipolar disorder and Schizoaffective disorder, Bipolar type. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2016, 171, 521-524.	1.1	7
43	Analysis of protein-coding genetic variation in 60,706 humans. <i>Nature</i> , 2016, 536, 285-291.	13.7	9,051
44	Constance E. Lieber, Theodore R. Stanley, and the Enduring Impact of Philanthropy on Psychiatry Research. <i>Biological Psychiatry</i> , 2016, 80, 84-86.	0.7	2
45	Translating genome-wide association findings into new therapeutics for psychiatry. <i>Nature Neuroscience</i> , 2016, 19, 1392-1396.	7.1	115
46	Dysregulation of miRNA-9 in a Subset of Schizophrenia Patient-Derived Neural Progenitor Cells. <i>Cell Reports</i> , 2016, 15, 1024-1036.	2.9	107
47	Quantifying prion disease penetrance using large population control cohorts. <i>Science Translational Medicine</i> , 2016, 8, 322ra9.	5.8	289
48	Rare loss-of-function variants in SETD1A are associated with schizophrenia and developmental disorders. <i>Nature Neuroscience</i> , 2016, 19, 571-577.	7.1	388
49	Prevalence of Huntington's disease gene CAG trinucleotide repeat alleles in patients with bipolar disorder. <i>Bipolar Disorders</i> , 2015, 17, 403-408.	1.1	6
50	Genetic analysis of schizophrenia and bipolar disorder reveals polygenicity but also suggests new directions for molecular interrogation. <i>Current Opinion in Neurobiology</i> , 2015, 30, 131-138.	2.0	61
51	No evidence for rare recessive and compound heterozygous disruptive variants in schizophrenia. <i>European Journal of Human Genetics</i> , 2015, 23, 555-557.	1.4	21
52	The PsychENCODE project. <i>Nature Neuroscience</i> , 2015, 18, 1707-1712.	7.1	371
53	A Role for Noncoding Variation in Schizophrenia. <i>Cell Reports</i> , 2014, 9, 1417-1429.	2.9	225
54	Specific Glial Functions Contribute to Schizophrenia Susceptibility. <i>Schizophrenia Bulletin</i> , 2014, 40, 925-935.	2.3	105

#	ARTICLE	IF	CITATIONS
55	Conserved Higher-Order Chromatin Regulates NMDA Receptor Gene Expression and Cognition. <i>Neuron</i> , 2014, 84, 997-1008.	3.8	76
56	De novo CNVs in bipolar affective disorder and schizophrenia. <i>Human Molecular Genetics</i> , 2014, 23, 6677-6683.	1.4	70
57	Reciprocal Duplication of the Williams-Beuren Syndrome Deletion on Chromosome 7q11.23 Is Associated with Schizophrenia. <i>Biological Psychiatry</i> , 2014, 75, 371-377.	0.7	66
58	De novo mutations in schizophrenia implicate synaptic networks. <i>Nature</i> , 2014, 506, 179-184.	13.7	1,510
59	A polygenic burden of rare disruptive mutations in schizophrenia. <i>Nature</i> , 2014, 506, 185-190.	13.7	1,305
60	Synaptic, transcriptional and chromatin genes disrupted in autism. <i>Nature</i> , 2014, 515, 209-215.	13.7	2,254
61	Polygenic dissection of diagnosis and clinical dimensions of bipolar disorder and schizophrenia. <i>Molecular Psychiatry</i> , 2014, 19, 1017-1024.	4.1	333
62	Most genetic risk for autism resides with common variation. <i>Nature Genetics</i> , 2014, 46, 881-885.	9.4	977
63	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. <i>Nature Genetics</i> , 2013, 45, 1150-1159.	9.4	1,395
64	Genetics of bipolar disorder. <i>Lancet</i> , The, 2013, 381, 1654-1662.	6.3	499
65	zCall: a rare variant caller for array-based genotyping. <i>Bioinformatics</i> , 2012, 28, 2543-2545.	1.8	195
66	Common polygenic variation contributes to risk of schizophrenia and bipolar disorder. <i>Nature</i> , 2009, 460, 748-752.	13.7	4,345
67	Collaborative genome-wide association analysis supports a role for ANK3 and CACNA1C in bipolar disorder. <i>Nature Genetics</i> , 2008, 40, 1056-1058.	9.4	1,102
68	Analysis of Genetically Regulated Gene Expression Identifies a Trauma Type Specific PTSD Gene, SNRNP35. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0