Panagiotis Roussos

List of Publications by Year
in descending order

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153	27,524	16437 64	9090 144
papers	citations	h-index	g-index

206	206	206	30808
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. Nature Genetics, 2019, 51, 63-75.	9.4	1,594
2	Identification of common genetic risk variants for autism spectrum disorder. Nature Genetics, 2019, 51, 431-444.	9.4	1,538
3	De novo mutations in schizophrenia implicate synaptic networks. Nature, 2014, 506, 179-184.	13.7	1,510
4	A polygenic burden of rare disruptive mutations in schizophrenia. Nature, 2014, 506, 185-190.	13.7	1,305
5	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	9.4	1,191
6	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
7	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085
8	Gene expression elucidates functional impact of polygenic risk for schizophrenia. Nature Neuroscience, 2016, 19, 1442-1453.	7.1	952
9	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
10	Genome-wide association meta-analysis in 269,867 individuals identifies new genetic and functional links to intelligence. Nature Genetics, 2018, 50, 912-919.	9.4	893
11	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. Science, 2018, 359, 693-697.	6.0	851
12	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35.	9.4	838
13	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. Science, 2018, 362, .	6.0	805
14	Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. Nature Genetics, 2021, 53, 817-829.	9.4	629
15	Comprehensive functional genomic resource and integrative model for the human brain. Science, 2018, 362, .	6.0	618
16	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. American Journal of Human Genetics, 2014, 95, 535-552.	2.6	569
17	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. Science, 2018, 362, .	6.0	516
18	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	5.8	484

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19	The PsychENCODE project. Nature Neuroscience, 2015, 18, 1707-1712.	7.1	371
20	Brain Cell Type Specific Gene Expression and Co-expression Network Architectures. Scientific Reports, 2018, 8, 8868.	1.6	335
21	The Mount Sinai cohort of large-scale genomic, transcriptomic and proteomic data in Alzheimer's disease. Scientific Data, 2018, 5, 180185.	2.4	320
22	Cardiometabolic risk loci share downstream cis- and trans-gene regulation across tissues and diseases. Science, 2016, 353, 827-830.	6.0	241
23	Analysis of Transcriptional Variability in a Large Human iPSC Library Reveals Genetic and Non-genetic Determinants of Heterogeneity. Cell Stem Cell, 2017, 20, 518-532.e9.	5.2	230
24	A Role for Noncoding Variation in Schizophrenia. Cell Reports, 2014, 9, 1417-1429.	2.9	225
25	Integrative network analysis of nineteen brain regions identifies molecular signatures and networks underlying selective regional vulnerability to Alzheimerâ€™s disease. Genome Medicine, 2016, 8, 104.	3.6	224
26	Transcriptome and epigenome landscape of human cortical development modeled in organoids. Science, 2018, 362, .	6.0	220
27	Myelination, oligodendrocytes, and serious mental illness. Glia, 2014, 62, 1856-1877.	2.5	203
28	A Bayesian framework for multiple trait colocalization from summary association statistics. Bioinformatics, 2018, 34, 2538-2545.	1.8	203
29	A functional genomics predictive network model identifies regulators of inflammatory bowel disease. Nature Genetics, 2017, 49, 1437-1449.	9.4	199
30	GWAS meta-analysis reveals novel loci and genetic correlates for general cognitive function: a report from the COGENT consortium. Molecular Psychiatry, 2017, 22, 336-345.	4.1	194
31	Differences in DNA methylation between human neuronal and glial cells are concentrated in enhancers and non-CpG sites. Nucleic Acids Research, 2014, 42, 109-127.	6.5	187
32	Molecular genetic evidence for overlap between general cognitive ability and risk for schizophrenia: a report from the Cognitive Genomics consorTium (COGENT). Molecular Psychiatry, 2014, 19, 168-174.	4.1	178
33	An atlas of chromatin accessibility in the adult human brain. Genome Research, 2018, 28, 1243-1252.	2.4	170
34	Genome-wide DNA methylation profiling in the superior temporal gyrus reveals epigenetic signatures associated with Alzheimerâ€™s disease. Genome Medicine, 2016, 8, 5.	3.6	163
35	Evidence for genetic heterogeneity between clinical subtypes of bipolar disorder. Translational Psychiatry, 2017, 7, e993-e993.	2.4	162
36	Neuron-specific signatures in the chromosomal connectome associated with schizophrenia risk. Science, 2018, 362, .	6.0	162

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37	Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. Nature Genetics, 2019, 51, 659-674.	9.4	154
38	Non-cell-autonomous disruption of nuclear architecture as a potential cause of COVID-19-induced anosmia. Cell, 2022, 185, 1052-1064.e12.	13.5	154
39	CommonMind Consortium provides transcriptomic and epigenomic data for Schizophrenia and Bipolar Disorder. Scientific Data, 2019, 6, 180.	2.4	149
40	Evaluation of chromatin accessibility in prefrontal cortex of individuals with schizophrenia. Nature Communications, 2018, 9, 3121.	5.8	141
41	Dream: powerful differential expression analysis for repeated measures designs. Bioinformatics, 2021, 37, 192-201.	1.8	138
42	The Genetics of the Mood Disorder Spectrum: Genome-wide Association Analyses of More Than 185,000 Cases and 439,000 Controls. Biological Psychiatry, 2020, 88, 169-184.	0.7	137
43	The methyltransferase SETDB1 regulates a large neuron-specific topological chromatin domain. Nature Genetics, 2017, 49, 1239-1250.	9.4	133
44	Improvement of Prepulse Inhibition and Executive Function by the COMT Inhibitor Tolcapone Depends on COMT Val158Met Polymorphism. Neuropsychopharmacology, 2008, 33, 3058-3068.	2.8	132
45	Landscape of Conditional eQTL in Dorsolateral Prefrontal Cortex and Co-localization with Schizophrenia GWAS. American Journal of Human Genetics, 2018, 102, 1169-1184.	2.6	128
46	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. Nature Communications, 2018, 9, 5141.	5.8	119
47	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. American Journal of Human Genetics, 2018, 102, 1185-1194.	2.6	119
48	Integration of Alzheimerâ€™s disease genetics and myeloid genomics identifies disease risk regulatory elements and genes. Nature Communications, 2021, 12, 1610.	5.8	118
49	Cell-specific histone modification maps in the human frontal lobe link schizophrenia risk to the neuronal epigenome. Nature Neuroscience, 2018, 21, 1126-1136.	7.1	112
50	Common genetic variation influencing human white matter microstructure. Science, 2021, 372, .	6.0	106
51	Large-Scale Cognitive GWAS Meta-Analysis Reveals Tissue-Specific Neural Expression and Potential Nootropic Drug Targets. Cell Reports, 2017, 21, 2597-2613.	2.9	103
52	Genomic and Network Patterns of Schizophrenia Genetic Variation in Human Evolutionary Accelerated Regions. Molecular Biology and Evolution, 2015, 32, 1148-1160.	3.5	98
53	Molecular and Genetic Evidence for Abnormalities in the Nodes of Ranvier in Schizophrenia. Archives of General Psychiatry, 2012, 69, 7.	13.8	97
54	Substantial DNA methylation differences between two major neuronal subtypes in human brain. Nucleic Acids Research, 2016, 44, 2593-2612.	6.5	97

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55	A System-Level Transcriptomic Analysis of Schizophrenia Using Postmortem Brain Tissue Samples. Archives of General Psychiatry, 2012, 69, 1205.	13.8	94
56	The CACNA1C and ANK3 risk alleles impact on affective personality traits and startle reactivity but not on cognition or gating in healthy males. Bipolar Disorders, 2011, 13, 250-259.	1.1	92
57	Large-Scale Identification of Common Trait and Disease Variants Affecting Gene Expression. American Journal of Human Genetics, 2017, 100, 885-894.	2.6	91
58	Adolescent exposure to Î”9-tetrahydrocannabinol alters the transcriptional trajectory and dendritic architecture of prefrontal pyramidal neurons. Molecular Psychiatry, 2019, 24, 588-600.	4.1	89
59	Pleiotropic Meta-Analysis of Cognition, Education, and Schizophrenia Differentiates Roles of Early Neurodevelopmental and Adult Synaptic Pathways. American Journal of Human Genetics, 2019, 105, 334-350.	2.6	86
60	Single-nucleus transcriptome analysis of human brain immune response in patients with severe COVID-19. Genome Medicine, 2021, 13, 118.	3.6	81
61	Schizophrenia: susceptibility genes and oligodendroglial and myelin related abnormalities. Frontiers in Cellular Neuroscience, 2014, 8, 5.	1.8	78
62	Analyzing the Role of MicroRNAs in Schizophrenia in the Context of Common Genetic Risk Variants. JAMA Psychiatry, 2016, 73, 369.	6.0	78
63	Prepulse inhibition of the startle reflex depends on the catecholO-methyltransferase Val158Met gene polymorphism. Psychological Medicine, 2008, 38, 1651-1658.	2.7	77
64	Striatal H3K27 Acetylation Linked to Glutamatergic Gene Dysregulation in Human Heroin Abusers Holds Promise as Therapeutic Target. Biological Psychiatry, 2017, 81, 585-594.	0.7	77
65	Conserved Higher-Order Chromatin Regulates NMDA Receptor Gene Expression and Cognition. Neuron, 2014, 84, 997-1008.	3.8	76
66	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. Scientific Data, 2020, 7, 340.	2.4	75
67	Planning, decision-making and the COMT rs4818 polymorphism in healthy males. Neuropsychologia, 2008, 46, 757-763.	0.7	72
68	Disproportionate Contributions of Select Genomic Compartments and Cell Types to Genetic Risk for Coronary Artery Disease. PLoS Genetics, 2015, 11, e1005622.	1.5	70
69	The triggering receptor expressed on myeloid cells 2 (TREM2) is associated with enhanced inflammation, neuropathological lesions and increased risk for Alzheimer's dementia. Alzheimer's and Dementia, 2015, 11, 1163-1170.	0.4	70
70	Open chromatin profiling of human postmortem brain infers functional roles for non-coding schizophrenia loci. Human Molecular Genetics, 2017, 26, 1942-1951.	1.4	69
71	Integrative transcriptome imputation reveals tissue-specific and shared biological mechanisms mediating susceptibility to complex traits. Nature Communications, 2019, 10, 3834.	5.8	68
72	Tolcapone Effects on Gating, Working Memory, and Mood Interact with the Synonymous Catechol-O-methyltransferase rs4818C/G Polymorphism. Biological Psychiatry, 2009, 66, 997-1004.	0.7	66

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73	Global landscape and genetic regulation of RNA editing in cortical samples from individuals with schizophrenia. Nature Neuroscience, 2019, 22, 1402-1412.	7.1	63
74	Genome-wide autozygosity is associated with lower general cognitive ability. Molecular Psychiatry, 2016, 21, 837-843.	4.1	62
75	Cognitive and emotional processing in high novelty seeking associated with the L-DRD4 genotype. Neuropsychologia, 2009, 47, 1654-1659.	0.7	61
76	A complete temporal transcription factor series in the fly visual system. Nature, 2022, 604, 316-322.	13.7	60
77	The Influence of Schizophrenia-Related Neuregulin-1 Polymorphisms on Sensorimotor Gating in Healthy Males. Biological Psychiatry, 2011, 69, 479-486.	0.7	58
78	Microvascular anomaly conditions in psychiatric disease. Schizophrenia â€“ angiogenesis connection. Neuroscience and Biobehavioral Reviews, 2017, 77, 327-339.	2.9	58
79	A Risk PRODH Haplotype Affects Sensorimotor Gating, Memory, Schizotypy, and Anxiety in Healthy Male Subjects. Biological Psychiatry, 2009, 65, 1063-1070.	0.7	57
80	The Dopamine D3 Receptor Ser9Gly Polymorphism Modulates Prepulse Inhibition of the Acoustic Startle Reflex. Biological Psychiatry, 2008, 64, 235-240.	0.7	53
81	Common schizophrenia risk variants are enriched in open chromatin regions of human glutamatergic neurons. Nature Communications, 2020, 11, 5581.	5.8	53
82	Common genetic variation and schizophrenia polygenic risk influence neurocognitive performance in young adulthood. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2015, 168, 392-401.	1.1	52
83	A mechanistic framework for cardiometabolic and coronary artery diseases. , 2022, 1, 85-100.		51
84	Glutamate transporter splice variant expression in an enriched pyramidal cell population in schizophrenia. Translational Psychiatry, 2015, 5, e579-e579.	2.4	49
85	Multi-ancestry eQTL meta-analysis of human brain identifies candidate causal variants for brain-related traits. Nature Genetics, 2022, 54, 161-169.	9.4	49
86	Practical Guidelines for High-Resolution Epigenomic Profiling of Nucleosomal Histones in Postmortem Human Brain Tissue. Biological Psychiatry, 2017, 81, 162-170.	0.7	48
87	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. Nature Communications, 2021, 12, 3968.	5.8	48
88	The Role of H3K4me3 in Transcriptional Regulation Is Altered in Huntingtonâ€™s Disease. PLoS ONE, 2015, 10, e0144398.	1.1	47
89	Revealing the brain's molecular architecture. Science, 2018, 362, 1262-1263.	6.0	45
90	The Relationship of Common Risk Variants and Polygenic Risk for Schizophrenia to Sensorimotor Gating. Biological Psychiatry, 2016, 79, 988-996.	0.7	44

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91	The expression of long noncoding RNA NEAT1 is reduced in schizophrenia and modulates oligodendrocytes transcription. NPJ Schizophrenia, 2019, 5, 3.	2.0	44
92	The CSMD1 genome-wide associated schizophrenia risk variant rs10503253 affects general cognitive ability and executive function in healthy males. Schizophrenia Research, 2014, 154, 42-47.	1.1	42
93	Downregulation of exhausted cytotoxic T cells in gene expression networks of multisystem inflammatory syndrome in children. Nature Communications, 2021, 12, 4854.	5.8	42
94	Activity-Dependent Changes in Gene Expression in Schizophrenia Human-Induced Pluripotent Stem Cell Neurons. JAMA Psychiatry, 2016, 73, 1180.	6.0	40
95	Differential activity of transcribed enhancers in the prefrontal cortex of 537 cases with schizophrenia and controls. Molecular Psychiatry, 2019, 24, 1685-1695.	4.1	40
96	Functional interpretation of genetic variants using deep learning predicts impact on chromatin accessibility and histone modification. Nucleic Acids Research, 2019, 47, 10597-10611.	6.5	39
97	mGluR5 hypofunction is integral to glutamatergic dysregulation in schizophrenia. Molecular Psychiatry, 2020, 25, 750-760.	4.1	39
98	Sex Differences in the Human Brain Transcriptome of Cases With Schizophrenia. Biological Psychiatry, 2022, 91, 92-101.	0.7	38
99	A unique gene expression signature associated with serotonin 2C receptor RNA editing in the prefrontal cortex and altered in suicide. Human Molecular Genetics, 2014, 23, 4801-4813.	1.4	37
100	Common variants contribute to intrinsic human brain functional networks. Nature Genetics, 2022, 54, 508-517.	9.4	37
101	CACNA1C as a risk factor for schizotypal personality disorder and schizotypy in healthy individuals. Psychiatry Research, 2013, 206, 122-123.	1.7	35
102	Analysis of exome sequence in 604 trios for recessive genotypes in schizophrenia. Translational Psychiatry, 2015, 5, e607-e607.	2.4	35
103	THC exposure of human iPSC neurons impacts genes associated with neuropsychiatric disorders. Translational Psychiatry, 2018, 8, 89.	2.4	35
104	The Association of Schizophrenia Risk D-Amino Acid Oxidase Polymorphisms With Sensorimotor Gating, Working Memory and Personality in Healthy Males. Neuropsychopharmacology, 2011, 36, 1677-1688.	2.8	34
105	Stress-Dependent Association Between Polygenic Risk for Schizophrenia and Schizotypal Traits in Young Army Recruits. Schizophrenia Bulletin, 2018, 44, 338-347.	2.3	33
106	Functional annotation of rare structural variation in the human brain. Nature Communications, 2020, 11, 2990.	5.8	32
107	A chromosomal connectome for psychiatric and metabolic risk variants in adult dopaminergic neurons. Genome Medicine, 2020, 12, 19.	3.6	31
108	Use of the PsycheMERGE Network to Investigate the Association Between Depression Polygenic Scores and White Blood Cell Count. JAMA Psychiatry, 2021, 78, 1365.	6.0	31

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109	Meta-analysis on the association between genetic polymorphisms and prepulse inhibition of the acoustic startle response. Schizophrenia Research, 2018, 198, 52-59.	1.1	29
110	Chromatin domain alterations linked to 3D genome organization in a large cohort of schizophrenia and bipolar disorder brains. Nature Neuroscience, 2022, 25, 474-483.	7.1	25
111	Sustained Attention and Working Memory Deficits Follow a Familial Pattern in Schizophrenia. Archives of Clinical Neuropsychology, 2011, 26, 687-695.	0.3	23
112	Understanding the genetic liability to schizophrenia through the neuroepigenome. Schizophrenia Research, 2016, 177, 115-124.	1.1	22
113	Parahippocampal gyrus expression of endothelial and insulin receptor signaling pathway genes is modulated by Alzheimerâ€™s disease and normalized by treatment with anti-diabetic agents. PLoS ONE, 2018, 13, e0206547.	1.1	22
114	Chromatin accessibility mapping of the striatum identifies tyrosine kinase FYN as a therapeutic target for heroin use disorder. Nature Communications, 2020, 11, 4634.	5.8	21
115	scGRNom: a computational pipeline of integrative multi-omics analyses for predicting cell-type disease genes and regulatory networks. Genome Medicine, 2021, 13, 95.	3.6	21
116	NeuN+ neuronal nuclei in non-human primate prefrontal cortex and subcortical white matter after clozapine exposure. Schizophrenia Research, 2016, 170, 235-244.	1.1	20
117	The relationship between dopamine receptor D1 and cognitive performance. NPJ Schizophrenia, 2015, 1, 14002.	2.0	18
118	Cognitive profiles of schizotypal dimensions in a community cohort: Common properties of differential manifestations. Journal of Clinical and Experimental Neuropsychology, 2016, 38, 1050-1063.	0.8	18
119	A bidirectional competitive interaction between circHomer1 and Homer1b within the orbitofrontal cortex regulates reversal learning. Cell Reports, 2022, 38, 110282.	2.9	17
120	Tolcapone, COMT polymorphisms and pharmacogenomic treatment of schizophrenia. Pharmacogenomics, 2011, 12, 559-566.	0.6	16
121	Assessment of somatic single-nucleotide variation in brain tissue of cases with schizophrenia. Translational Psychiatry, 2019, 9, 21.	2.4	16
122	The Future of Neuroepigenetics in the Human Brain. Progress in Molecular Biology and Translational Science, 2014, 128, 199-228.	0.9	14
123	Differential gene regulatory pattern in the human brain from schizophrenia using transcriptomic-causal network. BMC Bioinformatics, 2020, 21, 469.	1.2	14
124	The effects of theCACNA1Crs1006737 A/G on affective startle modulation in healthy males. European Psychiatry, 2015, 30, 492-498.	0.1	13
125	Sex Differences in Molecular Rhythms in the Human Cortex. Biological Psychiatry, 2022, 91, 152-162.	0.7	12
126	Identifying nootropic drug targets via large-scale cognitive GWAS and transcriptomics. Neuropsychopharmacology, 2021, 46, 1788-1801.	2.8	12

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127	Cognitive and emotional processing associated with the Season of Birth and dopamine D4 receptor gene. Neuropsychologia, 2010, 48, 3926-3933.	0.7	11
128	decorate: differential epigenetic correlation test. Bioinformatics, 2020, 36, 2856-2861.	1.8	11
129	Unbiased identification of novel transcription factors in striatal compartmentation and striosome maturation. ELife, 2021, 10, .	2.8	9
130	Altered gene expression and PTSD symptom dimensions in World Trade Center responders. Molecular Psychiatry, 2022, 27, 2225-2246.	4.1	9
131	minepath.org: a free interactive pathway analysis web server. Nucleic Acids Research, 2017, 45, W116-W121.	6.5	8
132	Winter birth, urbanicity and immigrant status predict psychometric schizotypy dimensions in adolescents. European Psychiatry, 2018, 47, 9-18.	0.1	8
133	Cognitive and personality analysis of startle reactivity in a large cohort of healthy males. Biological Psychology, 2013, 94, 582-591.	1.1	7
134	Associations of differential schizotypal dimensions with executive working memory: A moderated-mediation analysis. Comprehensive Psychiatry, 2016, 71, 39-48.	1.5	7
135	Frontal and temporal cortical volume, white matter tract integrity, and hemispheric asymmetry in schizotypal personality disorder. Schizophrenia Research, 2018, 197, 226-232.	1.1	7
136	Dimensional Traits of Schizotypy Associated With Glycine Receptor GLRA1 Polymorphism: An Exploratory Candidate-Gene Association Study. Journal of Personality Disorders, 2018, 32, 421-432.	0.8	7
137	Association between genes regulating neural pathways for quantitative traits of speech and language disorders. Npj Genomic Medicine, 2021, 6, 64.	1.7	7
138	Comparison of brain connectomes by MRI and genomics and its implication in Alzheimerâ€™s disease. BMC Medicine, 2020, 18, 23.	2.3	6
139	The Neuroepigenome: Implications of Chemical and Physical Modifications of Genomic DNA in Schizophrenia. Biological Psychiatry, 2022, 92, 443-449.	0.7	6
140	Impact of schizophrenia GWAS loci converge onto distinct pathways in cortical interneurons vs glutamatergic neurons during development. Molecular Psychiatry, 2022, 27, 4218-4233.	4.1	6
141	Engagement of vascular early response genes typifies mild cognitive impairment. Alzheimer's and Dementia, 2022, 18, 1357-1369.	0.4	5
142	Azoles and antidepressants: a miniâ€review of the tolerability of coâ€administration. Mycoses, 2009, 52, 433-439.	1.8	4
143	Transcription factor 4 as an important determinant of gating function in schizophrenia. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 5915-5916.	3.3	3
144	Multi-Trait Analysis of GWAS and Biological Insights Into Cognition: A Response to Hill (2018). Twin Research and Human Genetics, 2018, 21, 394-397.	0.3	3

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145	Genetic Variation in Long-Range Enhancers. Current Topics in Behavioral Neurosciences, 2019, 42, 35-50.	0.8	2
146	Populationâ€based identityâ€byâ€descent mapping combined with exome sequencing to detect rare risk variants for schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 223-231.	1.1	2
147	S4â€02â€03: Accelerating Medicines Partnership: Coâ€Expression Networks. Alzheimer's and Dementia, 2016, 12, P322.	0.4	0
148	T185. DIFFERENTIAL ACTIVITY OF TRANSCRIBED ENHANCERS IN THE PREFRONTAL CORTEX OF 592 CASES WITH SCHIZOPHRENIA AND CONTROLS. Schizophrenia Bulletin, 2018, 44, S188-S188.	2.3	0
149	Cell- and layer-specific transcriptomic strategy for characterizing the molecular phenotype of rat cortical neurons using laser capture microdissection and massively parallel RNA sequencing. Molecular Psychiatry, 2019, 24, 473-473.	4.1	0
150	Genetic studies of Alzheimer's disease risk implicate clearance of lipid rich debris in myeloid cells. Alzheimer's and Dementia, 2020, 16, e040601.	0.4	0
151	Integration of Alzheimerâ€™s disease genetics and myeloid genomics reveals novel disease risk mechanisms. Alzheimer's and Dementia, 2020, 16, e043897.	0.4	0
152	ATAC-seq and psychiatric disorders. , 2021, , 143-162.		0
153	Big Data Analysis and Genetic Liability to Neuropsychiatric Disease. Advances in Experimental Medicine and Biology, 2020, 1194, 455-455.	0.8	0