

Gene expression elucidates functional impact of polyge

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Genomics implicates adaptive and innate immunity in Alzheimer's and Parkinson's diseases. <i>Annals of Clinical and Translational Neurology</i> , 2016, 3, 924-933.	1.7	84
2	The road to precision psychiatry: translating genetics into disease mechanisms. <i>Nature Neuroscience</i> , 2016, 19, 1397-1407.	7.1	189
3	Translating genome-wide association findings into new therapeutics for psychiatry. <i>Nature Neuroscience</i> , 2016, 19, 1392-1396.	7.1	115
4	Focus on psychiatric disorders. <i>Nature Neuroscience</i> , 2016, 19, 1381-1382.	7.1	3
5	When size matters: CHD8 in autism. <i>Nature Neuroscience</i> , 2016, 19, 1430-1432.	7.1	14
6	Chromosome conformation elucidates regulatory relationships in developing human brain. <i>Nature</i> , 2016, 538, 523-527.	13.7	507
7	Brains, genes and power. <i>Nature Neuroscience</i> , 2016, 19, 1428-1430.	7.1	2
8	Correlated expression analysis of genes implicated in schizophrenia: Identification of putative disease-related pathways. <i>European Journal of Molecular and Clinical Medicine</i> , 2017, 3, 224.	0.5	2
9	Molecular mechanisms underlying noncoding risk variations in psychiatric genetic studies. <i>Molecular Psychiatry</i> , 2017, 22, 497-511.	4.1	43
10	A current view on contactin-4, -5, and -6: Implications in neurodevelopmental disorders. <i>Molecular and Cellular Neurosciences</i> , 2017, 81, 72-83.	1.0	71
11	Predicting gene expression in massively parallel reporter assays: A comparative study. <i>Human Mutation</i> , 2017, 38, 1240-1250.	1.1	39
12	Integrating Gene Expression with Summary Association Statistics to Identify Genes Associated with 30 Complex Traits. <i>American Journal of Human Genetics</i> , 2017, 100, 473-487.	2.6	248
13	The Yin and Yang of Autism Genetics: How Rare De Novo and Common Variations Affect Liability. <i>Annual Review of Genomics and Human Genetics</i> , 2017, 18, 167-187.	2.5	44
14	Systems Research in Psychiatric Neuroscience. <i>JAMA Psychiatry</i> , 2017, 74, 553.	6.0	4
15	Systems biology in the central nervous system: A brief perspective on essential recent advancements. <i>Current Opinion in Systems Biology</i> , 2017, 3, 67-76.	1.3	8
16	qSVA framework for RNA quality correction in differential expression analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7130-7135.	3.3	95
17	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
18	Application of CRISPR/Cas9 to the study of brain development and neuropsychiatric disease. <i>Molecular and Cellular Neurosciences</i> , 2017, 82, 157-166.	1.0	25

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19	Open chromatin profiling of human postmortem brain infers functional roles for non-coding schizophrenia loci. <i>Human Molecular Genetics</i> , 2017, 26, 1942-1951.	1.4	69
20	Transcriptome Alterations in Prefrontal Pyramidal Cells Distinguish Schizophrenia From Bipolar and Major Depressive Disorders. <i>Biological Psychiatry</i> , 2017, 82, 594-600.	0.7	73
21	Genetic insights into the neurodevelopmental origins of schizophrenia. <i>Nature Reviews Neuroscience</i> , 2017, 18, 727-740.	4.9	377
22	Genetic variation and gene expression across multiple tissues and developmental stages in a nonhuman primate. <i>Nature Genetics</i> , 2017, 49, 1714-1721.	9.4	57
23	THC Treatment Alters Glutamate Receptor Gene Expression in Human Stem Cell-Derived Neurons. <i>Molecular Neuropsychiatry</i> , 2017, 3, 73-84.	3.0	5
24	Testing high-dimensional covariance matrices, with application to detecting schizophrenia risk genes. <i>Annals of Applied Statistics</i> , 2017, 11, 1810-1831.	0.5	20
25	Genome-wide association analysis identifies 30 new susceptibility loci for schizophrenia. <i>Nature Genetics</i> , 2017, 49, 1576-1583.	9.4	395
26	Predicting causal variants affecting expression by using whole-genome sequencing and RNA-seq from multiple human tissues. <i>Nature Genetics</i> , 2017, 49, 1747-1751.	9.4	88
27	A ratiometric electrochemical strategy for sensitive determination of Furin activity based on dual signal amplification and antifouling nanosurfaces. <i>Analyst, The</i> , 2017, 142, 4215-4220.	1.7	18
28	Modeling a linkage between blood transcriptional expression and activity in brain regions to infer the phenotype of schizophrenia patients. <i>NPJ Schizophrenia</i> , 2017, 3, 25.	2.0	8
29	Gene-wide Association Study Reveals RNF122 Ubiquitin Ligase as a Novel Susceptibility Gene for Attention Deficit Hyperactivity Disorder. <i>Scientific Reports</i> , 2017, 7, 5407.	1.6	11
30	The epigenomics of schizophrenia, in the mouse. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2017, 174, 631-640.	1.1	12
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36	Epigenetic mechanisms during ageing and neurogenesis as novel therapeutic avenues in human brain disorders. <i>Clinical Epigenetics</i> , 2017, 9, 67.	1.8	108

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38	A group II metabotropic glutamate receptor 3 (mGlu3, GRM3) isoform implicated in schizophrenia interacts with canonical mGlu3 and reduces ligand binding. <i>Journal of Psychopharmacology</i> , 2017, 31, 1519-1526.	2.0	8
39	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
40	A deep learning based scoring system for prioritizing susceptibility variants for mental disorders. , 2017, , .		2
41	Applying meta-analysis to genotype-tissue expression data from multiple tissues to identify eQTLs and increase the number of eGenes. <i>Bioinformatics</i> , 2017, 33, i67-i74.	1.8	21
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53	MIR137 schizophrenia-associated locus controls synaptic function by regulating synaptogenesis, synapse maturation and synaptic transmission. <i>Human Molecular Genetics</i> , 2018, 27, 1879-1891.	1.4	58
54	Non-coding RNA dysregulation in the amygdala region of schizophrenia patients contributes to the pathogenesis of the disease. <i>Translational Psychiatry</i> , 2018, 8, 44.	2.4	55
55	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. <i>Science</i> , 2018, 359, 693-697.	6.0	851

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57	Mapping regulatory variants in hiPSC models. <i>Nature Genetics</i> , 2018, 50, 1-2.	9.4	33
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67	A comprehensive review of the genetic and biological evidence supports a role for MicroRNA-137 in the etiology of schizophrenia. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2018, 177, 242-256.	1.1	30
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76	Investigation of common, low-frequency and rare genome-wide variation in anorexia nervosa. <i>Molecular Psychiatry</i> , 2018, 23, 1169-1180.	4.1	32
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78	iMEGES: integrated mental-disorder GENome score by deep neural network for prioritizing the susceptibility genes for mental disorders in personal genomes. <i>BMC Bioinformatics</i> , 2018, 19, 501.	1.2	10
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86	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. <i>Science</i> , 2018, 362, .	6.0	805
87	Comprehensive functional genomic resource and integrative model for the human brain. <i>Science</i> , 2018, 362, .	6.0	618
88	The <i>DGCR5</i> long noncoding RNA may regulate expression of several schizophrenia-related genes. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	65
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90	Temporal proteomic profiling of postnatal human cortical development. <i>Translational Psychiatry</i> , 2018, 8, 267.	2.4	22
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109	Unperturbed expression bias of imprinted genes in schizophrenia. <i>Nature Communications</i> , 2018, 9, 2914.	5.8	6

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113	Altered Expression Profile of IgLON Family of Neural Cell Adhesion Molecules in the Dorsolateral Prefrontal Cortex of Schizophrenic Patients. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 8.	1.4	43
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125	Building a schizophrenia genetic network: transcription factor 4 regulates genes involved in neuronal development and schizophrenia risk. <i>Human Molecular Genetics</i> , 2018, 27, 3246-3256.	1.4	33
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135	A critical review of zebrafish schizophrenia models: Time for validation?. <i>Neuroscience and Biobehavioral Reviews</i> , 2019, 107, 6-22.	2.9	29
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150	<p>Large-scale GWAS reveals genetic architecture of brain white matter microstructure and genetic overlap with cognitive and mental health traits (n=17,706). Molecular Psychiatry, 2021, 26, 3943-3955.</p>	4.1	100
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152	<p>Integrate GWAS, eQTL, and mQTL Data to Identify Alzheimer's Disease-Related Genes. Frontiers in Genetics, 2019, 10, 1021.</p>	1.1	40
153	<p>Shared genetics of asthma and mental health disorders: a large-scale genome-wide cross-trait analysis. European Respiratory Journal, 2019, 54, 1901507.</p>	3.1	106
154	<p>Global landscape and genetic regulation of RNA editing in cortical samples from individuals with schizophrenia. Nature Neuroscience, 2019, 22, 1402-1412.</p>	7.1	63
155	<p>Integrative transcriptome imputation reveals tissue-specific and shared biological mechanisms mediating susceptibility to complex traits. Nature Communications, 2019, 10, 3834.</p>	5.8	68
156	<p>POTENTIAL ASSOCIATION OF MIR-137 WITH AGE OF ONSET OF SCHIZOPHRENIA. European Neuropsychopharmacology, 2019, 29, S1012-S1013.</p>	0.3	0
157	<p>Availability of public databases for triangulation of findings. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 15766-15767.</p>	3.3	2
158	<p>Using Transcriptomic Hidden Variables to Infer Context-Specific Genotype Effects in the Brain. American Journal of Human Genetics, 2019, 105, 562-572.</p>	2.6	7
159	<p>Deconvolution of transcriptional networks identifies TCF4 as a master regulator in schizophrenia. Science Advances, 2019, 5, eaau4139.</p>	4.7	59
160	<p>CommonMind Consortium provides transcriptomic and epigenomic data for Schizophrenia and Bipolar Disorder. Scientific Data, 2019, 6, 180.</p>	2.4	149
161	<p>Exploring genetic variation that influences brain methylation in attention-deficit/hyperactivity disorder. Translational Psychiatry, 2019, 9, 242.</p>	2.4	21
162	<p>Synergistic effects of common schizophrenia risk variants. Nature Genetics, 2019, 51, 1475-1485.</p>	9.4	184
163	<p>Functional interpretation of genetic variants using deep learning predicts impact on chromatin accessibility and histone modification. Nucleic Acids Research, 2019, 47, 10597-10611.</p>	6.5	39

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