# Panagiotis Roussos

List of Publications by Year
in descending order



| 153 | 27,524 | 16451 64 | 9103 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. | 21.4 | 1,594 |
| 2 | Identification of common genetic risk variants for autism spectrum disorder. Nature Genetics, 2019, 51, 431-444. | 21.4 | 1,538 |
| 3 | De novo mutations in schizophrenia implicate synaptic networks. Nature, 2014, 506, 179-184. | 27.8 | 1,510 |
| 4 | A polygenic burden of rare disruptive mutations in schizophrenia. Nature, 2014, 506, 185-190. | 27.8 | 1,305 |
| 5 | Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803. | 21.4 | 1,191 |
| 6 | Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592. | 6.2 | 1,098 |
| 7 | Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, . | 12.6 | 1,085 |
| 8 | Gene expression elucidates functional impact of polygenic risk for schizophrenia. Nature Neuroscience, 2016, 19, 1442-1453. | 14.8 | 952 |
| 9 | Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508. | 27.8 | 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. | 21.4 | 893 |
| 11 | Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. Science, 2018, 359, 693-697. | 12.6 | 851 |
| 12 | Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35. | 21.4 | 838 |
| 13 | Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. Science, 2018, 362, . | 12.6 | 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. | 21.4 | 629 |
| 15 | Comprehensive functional genomic resource and integrative model for the human brain. Science, 2018, 362, . | 12.6 | 618 |
| 16 | Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. American Journal of Human Genetics, 2014, 95, 535-552. | 6.2 | 569 |
| 17 | Integrative functional genomic analysis of human brain development and neuropsychiatric risks. Science, 2018, 362, . | 12.6 | 516 |
| 18 | Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098. | 12.8 | 484 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | The PsychENCODE project. Nature Neuroscience, 2015, 18, 1707-1712. | 14.8 | 371 |
| 20 | Brain Cell Type Specific Gene Expression and Co-expression Network Architectures. Scientific Reports, 2018, 8, 8868. | 3.3 | 335 |
| 21 | The Mount Sinai cohort of large-scale genomic, transcriptomic and proteomic data in Alzheimer's disease. Scientific Data, 2018, 5, 180185. | 5.3 | 320 |
| 22 | Cardiometabolic risk loci share downstream cis- and trans-gene regulation across tissues and diseases. Science, 2016, 353, 827-830. | 12.6 | 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. | 11.1 | 230 |
| 24 | A Role for Noncoding Variation in Schizophrenia. Cell Reports, 2014, 9, 1417-1429. | 6.4 | 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. | 8.2 | 224 |
| 26 | Transcriptome and epigenome landscape of human cortical development modeled in organoids. Science, 2018, 362, . | 12.6 | 220 |
| 27 | Myelination, oligodendrocytes, and serious mental illness. Glia, 2014, 62, 1856-1877. | 4.9 | 203 |
| 28 | A Bayesian framework for multiple trait colocalization from summary association statistics. Bioinformatics, 2018, 34, 2538-2545. | 4.1 | 203 |
| 29 | A functional genomics predictive network model identifies regulators of inflammatory bowel disease. Nature Genetics, 2017, 49, 1437-1449. | 21.4 | 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. | 7.9 | 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. | 14.5 | 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. | 7.9 | 178 |
| 33 | An atlas of chromatin accessibility in the adult human brain. Genome Research, 2018, 28, 1243-1252. | 5.5 | 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. | 8.2 | 163 |
| 35 | Evidence for genetic heterogeneity between clinical subtypes of bipolar disorder. Translational Psychiatry, 2017, 7, e993-e993. | 4.8 | 162 |
| 36 | Neuron-specific signatures in the chromosomal connectome associated with schizophrenia risk. Science, 2018, 362, . | 12.6 | 162 |

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|---|---|---|---|
| 37 | Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. Nature Genetics, 2019, 51, 659-674. | 21.4 | 154 |
| 38 | Non-cell-autonomous disruption of nuclear architecture as a potential cause of COVID-19-induced anosmia. Cell, 2022, 185, 1052-1064.e12. | 28.9 | 154 |
| 39 | CommonMind Consortium provides transcriptomic and epigenomic data for Schizophrenia and Bipolar Disorder. Scientific Data, 2019, 6, 180. | 5.3 | 149 |
| 40 | Evaluation of chromatin accessibility in prefrontal cortex of individuals with schizophrenia. Nature Communications, 2018, 9, 3121. | 12.8 | 141 |
| 41 | Dream: powerful differential expression analysis for repeated measures designs. Bioinformatics, 2021, 37, 192-201. | 4.1 | 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. | 1.3 | 137 |
| 43 | The methyltransferase SETDB1 regulates a large neuron-specific topological chromatin domain. Nature Genetics, 2017, 49, 1239-1250. | 21.4 | 133 |
| 44 | Improvement of Prepulse Inhibition and Executive Function by the COMT Inhibitor Tolcapone Depends on COMT Val158Met Polymorphism. Neuropsychopharmacology, 2008, 33, 3058-3068. | 5.4 | 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. | 6.2 | 128 |
| 46 | GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. Nature Communications, 2018, 9, 5141. | 12.8 | 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. | 6.2 | 119 |
| 48 | Integration of Alzheimerâ€™s disease genetics and myeloid genomics identifies disease risk regulatory elements and genes. Nature Communications, 2021, 12, 1610. | 12.8 | 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. | 14.8 | 112 |
| 50 | Common genetic variation influencing human white matter microstructure. Science, 2021, 372, . | 12.6 | 106 |
| 51 | Large-Scale Cognitive GWAS Meta-Analysis Reveals Tissue-Specific Neural Expression and Potential Nootropic Drug Targets. Cell Reports, 2017, 21, 2597-2613. | 6.4 | 103 |
| 52 | Genomic and Network Patterns of Schizophrenia Genetic Variation in Human Evolutionary Accelerated Regions. Molecular Biology and Evolution, 2015, 32, 1148-1160. | 8.9 | 98 |
| 53 | Molecular and Genetic Evidence for Abnormalities in the Nodes of Ranvier in Schizophrenia. Archives of General Psychiatry, 2012, 69, 7. | 12.3 | 97 |
| 54 | Substantial DNA methylation differences between two major neuronal subtypes in human brain. Nucleic Acids Research, 2016, 44, 2593-2612. | 14.5 | 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. | 12.3 | 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. | 1.9 | 92 |
| 57 | Large-Scale Identification of Common Trait and Disease Variants Affecting Gene Expression. American Journal of Human Genetics, 2017, 100, 885-894. | 6.2 | 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. | 7.9 | 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. | 6.2 | 86 |
| 60 | Single-nucleus transcriptome analysis of human brain immune response in patients with severe COVID-19. Genome Medicine, 2021, 13, 118. | 8.2 | 81 |
| 61 | Schizophrenia: susceptibility genes and oligodendroglial and myelin related abnormalities. Frontiers in Cellular Neuroscience, 2014, 8, 5. | 3.7 | 78 |
| 62 | Analyzing the Role of MicroRNAs in Schizophrenia in the Context of Common Genetic Risk Variants. JAMA Psychiatry, 2016, 73, 369. | 11.0 | 78 |
| 63 | Prepulse inhibition of the startle reflex depends on the catecholO-methyltransferase Val158Met gene polymorphism. Psychological Medicine, 2008, 38, 1651-1658. | 4.5 | 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. | 1.3 | 77 |
| 65 | Conserved Higher-Order Chromatin Regulates NMDA Receptor Gene Expression and Cognition. Neuron, 2014, 84, 997-1008. | 8.1 | 76 |
| 66 | Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. Scientific Data, 2020, 7, 340. | 5.3 | 75 |
| 67 | Planning, decision-making and the COMT rs4818 polymorphism in healthy males. Neuropsychologia, 2008, 46, 757-763. | 1.6 | 72 |
| 68 | Disproportionate Contributions of Select Genomic Compartments and Cell Types to Genetic Risk for Coronary Artery Disease. PLoS Genetics, 2015, 11, e1005622. | 3.5 | 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. | 0.8 | 70 |
| 70 | Open chromatin profiling of human postmortem brain infers functional roles for non-coding schizophrenia loci. Human Molecular Genetics, 2017, 26, 1942-1951. | 2.9 | 69 |
| 71 | Integrative transcriptome imputation reveals tissue-specific and shared biological mechanisms mediating susceptibility to complex traits. Nature Communications, 2019, 10, 3834. | 12.8 | 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. | 1.3 | 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. | 14.8 | 63 |
| 74 | Genome-wide autozygosity is associated with lower general cognitive ability. Molecular Psychiatry, 2016, 21, 837-843. | 7.9 | 62 |
| 75 | Cognitive and emotional processing in high novelty seeking associated with the L-DRD4 genotype. Neuropsychologia, 2009, 47, 1654-1659. | 1.6 | 61 |
| 76 | A complete temporal transcription factor series in the fly visual system. Nature, 2022, 604, 316-322. | 27.8 | 60 |
| 77 | The Influence of Schizophrenia-Related Neuregulin-1 Polymorphisms on Sensorimotor Gating in Healthy Males. Biological Psychiatry, 2011, 69, 479-486. | 1.3 | 58 |
| 78 | Microvascular anomaly conditions in psychiatric disease. Schizophrenia â€“ angiogenesis connection. Neuroscience and Biobehavioral Reviews, 2017, 77, 327-339. | 6.1 | 58 |
| 79 | A Risk PRODH Haplotype Affects Sensorimotor Gating, Memory, Schizotypy, and Anxiety in Healthy Male Subjects. Biological Psychiatry, 2009, 65, 1063-1070. | 1.3 | 57 |
| 80 | The Dopamine D3 Receptor Ser9Gly Polymorphism Modulates Prepulse Inhibition of the Acoustic Startle Reflex. Biological Psychiatry, 2008, 64, 235-240. | 1.3 | 53 |
| 81 | Common schizophrenia risk variants are enriched in open chromatin regions of human glutamatergic neurons. Nature Communications, 2020, 11, 5581. | 12.8 | 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. | 1.7 | 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. | 4.8 | 49 |
| 85 | Multi-ancestry eQTL meta-analysis of human brain identifies candidate causal variants for brain-related traits. Nature Genetics, 2022, 54, 161-169. | 21.4 | 49 |
| 86 | Practical Guidelines for High-Resolution Epigenomic Profiling of Nucleosomal Histones in Postmortem Human Brain Tissue. Biological Psychiatry, 2017, 81, 162-170. | 1.3 | 48 |
| 87 | Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. Nature Communications, 2021, 12, 3968. | 12.8 | 48 |
| 88 | The Role of H3K4me3 in Transcriptional Regulation Is Altered in Huntingtonâ€™s Disease. PLoS ONE, 2015, 10, e0144398. | 2.5 | 47 |
| 89 | Revealing the brain's molecular architecture. Science, 2018, 362, 1262-1263. | 12.6 | 45 |
| 90 | The Relationship of Common Risk Variants and Polygenic Risk for Schizophrenia to Sensorimotor Gating. Biological Psychiatry, 2016, 79, 988-996. | 1.3 | 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. | 3.6 | 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. | 2.0 | 42 |
| 93 | Downregulation of exhausted cytotoxic T cells in gene expression networks of multisystem inflammatory syndrome in children. Nature Communications, 2021, 12, 4854. | 12.8 | 42 |
| 94 | Activity-Dependent Changes in Gene Expression in Schizophrenia Human-Induced Pluripotent Stem Cell Neurons. JAMA Psychiatry, 2016, 73, 1180. | 11.0 | 40 |
| 95 | Differential activity of transcribed enhancers in the prefrontal cortex of 537 cases with schizophrenia and controls. Molecular Psychiatry, 2019, 24, 1685-1695. | 7.9 | 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. | 14.5 | 39 |
| 97 | mGluR5 hypofunction is integral to glutamatergic dysregulation in schizophrenia. Molecular Psychiatry, 2020, 25, 750-760. | 7.9 | 39 |
| 98 | Sex Differences in the Human Brain Transcriptome of Cases With Schizophrenia. Biological Psychiatry, 2022, 91, 92-101. | 1.3 | 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. | 2.9 | 37 |
| 100 | Common variants contribute to intrinsic human brain functional networks. Nature Genetics, 2022, 54, 508-517. | 21.4 | 37 |
| 101 | CACNA1C as a risk factor for schizotypal personality disorder and schizotypy in healthy individuals. Psychiatry Research, 2013, 206, 122-123. | 3.3 | 35 |
| 102 | Analysis of exome sequence in 604 trios for recessive genotypes in schizophrenia. Translational Psychiatry, 2015, 5, e607-e607. | 4.8 | 35 |
| 103 | THC exposure of human iPSC neurons impacts genes associated with neuropsychiatric disorders. Translational Psychiatry, 2018, 8, 89. | 4.8 | 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. | 5.4 | 34 |
| 105 | Stress-Dependent Association Between Polygenic Risk for Schizophrenia and Schizotypal Traits in Young Army Recruits. Schizophrenia Bulletin, 2018, 44, 338-347. | 4.3 | 33 |
| 106 | Functional annotation of rare structural variation in the human brain. Nature Communications, 2020, 11, 2990. | 12.8 | 32 |
| 107 | A chromosomal connectome for psychiatric and metabolic risk variants in adult dopaminergic neurons. Genome Medicine, 2020, 12, 19. | 8.2 | 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. | 11.0 | 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. | 2.0 | 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. | 14.8 | 25 |
| 111 | Sustained Attention and Working Memory Deficits Follow a Familial Pattern in Schizophrenia. Archives of Clinical Neuropsychology, 2011, 26, 687-695. | 0.5 | 23 |
| 112 | Understanding the genetic liability to schizophrenia through the neuroepigenome. Schizophrenia Research, 2016, 177, 115-124. | 2.0 | 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. | 2.5 | 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. | 12.8 | 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. | 8.2 | 21 |
| 116 | NeuN+ neuronal nuclei in non-human primate prefrontal cortex and subcortical white matter after clozapine exposure. Schizophrenia Research, 2016, 170, 235-244. | 2.0 | 20 |
| 117 | The relationship between dopamine receptor D1 and cognitive performance. NPJ Schizophrenia, 2015, 1, 14002. | 3.6 | 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. | 1.3 | 18 |
| 119 | A bidirectional competitive interaction between circHomer1 and Homer1b within the orbitofrontal cortex regulates reversal learning. Cell Reports, 2022, 38, 110282. | 6.4 | 17 |
| 120 | Tolcapone, COMT polymorphisms and pharmacogenomic treatment of schizophrenia. Pharmacogenomics, 2011, 12, 559-566. | 1.3 | 16 |
| 121 | Assessment of somatic single-nucleotide variation in brain tissue of cases with schizophrenia. Translational Psychiatry, 2019, 9, 21. | 4.8 | 16 |
| 122 | The Future of Neuroepigenetics in the Human Brain. Progress in Molecular Biology and Translational Science, 2014, 128, 199-228. | 1.7 | 14 |
| 123 | Differential gene regulatory pattern in the human brain from schizophrenia using transcriptomic-causal network. BMC Bioinformatics, 2020, 21, 469. | 2.6 | 14 |
| 124 | The effects of theCACNA1Crs1006737 A/G on affective startle modulation in healthy males. European Psychiatry, 2015, 30, 492-498. | 0.2 | 13 |
| 125 | Sex Differences in Molecular Rhythms in the Human Cortex. Biological Psychiatry, 2022, 91, 152-162. | 1.3 | 12 |
| 126 | Identifying nootropic drug targets via large-scale cognitive GWAS and transcriptomics. Neuropsychopharmacology, 2021, 46, 1788-1801. | 5.4 | 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. | 1.6 | 11 |
| 128 | decorate: differential epigenetic correlation test. Bioinformatics, 2020, 36, 2856-2861. | 4.1 | 11 |
| 129 | Unbiased identification of novel transcription factors in striatal compartmentation and striosome maturation. ELife, 2021, 10, . | 6.0 | 9 |
| 130 | Altered gene expression and PTSD symptom dimensions in World Trade Center responders. Molecular Psychiatry, 2022, 27, 2225-2246. | 7.9 | 9 |
| 131 | minepath.org: a free interactive pathway analysis web server. Nucleic Acids Research, 2017, 45, W116-W121. | 14.5 | 8 |
| 132 | Winter birth, urbanicity and immigrant status predict psychometric schizotypy dimensions in adolescents. European Psychiatry, 2018, 47, 9-18. | 0.2 | 8 |
| 133 | Cognitive and personality analysis of startle reactivity in a large cohort of healthy males. Biological Psychology, 2013, 94, 582-591. | 2.2 | 7 |
| 134 | Associations of differential schizotypal dimensions with executive working memory: A moderated-mediation analysis. Comprehensive Psychiatry, 2016, 71, 39-48. | 3.1 | 7 |
| 135 | Frontal and temporal cortical volume, white matter tract integrity, and hemispheric asymmetry in schizotypal personality disorder. Schizophrenia Research, 2018, 197, 226-232. | 2.0 | 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. | 1.4 | 7 |
| 137 | Association between genes regulating neural pathways for quantitative traits of speech and language disorders. Npj Genomic Medicine, 2021, 6, 64. | 3.8 | 7 |
| 138 | Comparison of brain connectomes by MRI and genomics and its implication in Alzheimerâ€™s disease. BMC Medicine, 2020, 18, 23. | 5.5 | 6 |
| 139 | The Neuroepigenome: Implications of Chemical and Physical Modifications of Genomic DNA in Schizophrenia. Biological Psychiatry, 2022, 92, 443-449. | 1.3 | 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. | 7.9 | 6 |
| 141 | Engagement of vascular early response genes typifies mild cognitive impairment. Alzheimer's and Dementia, 2022, 18, 1357-1369. | 0.8 | 5 |
| 142 | Azoles and antidepressants: a miniâ€review of the tolerability of coâ€administration. Mycoses, 2009, 52, 433-439. | 4.0 | 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. | 7.1 | 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. | 0.6 | 3 |

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|---|---|---|---|
| 145 | Genetic Variation in Long-Range Enhancers. Current Topics in Behavioral Neurosciences, 2019, 42, 35-50. | 1.7 | 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. | 1.7 | 2 |
| 147 | S4â€02â€03: Accelerating Medicines Partnership: Coâ€Expression Networks. Alzheimer's and Dementia, 2016, 12, P322. | 0.8 | 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. | 4.3 | 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. | 7.9 | 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. | 0.8 | 0 |
| 151 | Integration of Alzheimerâ€™s disease genetics and myeloid genomics reveals novel disease risk mechanisms. Alzheimer's and Dementia, 2020, 16, e043897. | 0.8 | 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. | 1.6 | 0 |