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	Sex Differences in the Human Brain Transcriptome of Cases With Schizophrenia. Biological Psychiatry, 2022, 91, 92-101.	0.7	38
2	Sex Differences in Molecular Rhythms in the Human Cortex. Biological Psychiatry, 2022, 91, 152-162.	0.7	12
3	Engagement of vascular early response genes typifies mild cognitive impairment. Alzheimer's and Dementia, 2022, 18, 1357-1369.	0.4	5
4	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
5	A bidirectional competitive interaction between circHomer1 and Homer1b within the orbitofrontal cortex regulates reversal learning. Cell Reports, 2022, 38, 110282.	2.9	17
6	A mechanistic framework for cardiometabolic and coronary artery diseases. , 2022, 1, 85-100.		51
7	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
8	Altered gene expression and PTSD symptom dimensions in World Trade Center responders. Molecular Psychiatry, 2022, 27, 2225-2246.	4.1	9
9	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
10	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
11	Common variants contribute to intrinsic human brain functional networks. Nature Genetics, 2022, 54, 508-517.	9.4	37
12	A complete temporal transcription factor series in the fly visual system. Nature, 2022, 604, 316-322.	13.7	60
13	The Neuroepigenome: Implications of Chemical and Physical Modifications of Genomic DNA in Schizophrenia. Biological Psychiatry, 2022, 92, 443-449.	0.7	6
14	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
15	Dream: powerful differential expression analysis for repeated measures designs. Bioinformatics, 2021, 37, 192-201.	1.8	138
16	ATAC-seq and psychiatric disorders. , 2021, , 143-162.		0
17	Integration of Alzheimerâ€™s disease genetics and myeloid genomics identifies disease risk regulatory elements and genes. Nature Communications, 2021, 12, 1610.	5.8	118
18	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

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19	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
20	Identifying nootropic drug targets via large-scale cognitive GWAS and transcriptomics. Neuropsychopharmacology, 2021, 46, 1788-1801.	2.8	12
21	Common genetic variation influencing human white matter microstructure. Science, 2021, 372, .	6.0	106
22	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. Nature Communications, 2021, 12, 3968.	5.8	48
23	Single-nucleus transcriptome analysis of human brain immune response in patients with severe COVID-19. Genome Medicine, 2021, 13, 118.	3.6	81
24	Association between genes regulating neural pathways for quantitative traits of speech and language disorders. Npj Genomic Medicine, 2021, 6, 64.	1.7	7
25	Downregulation of exhausted cytotoxic T cells in gene expression networks of multisystem inflammatory syndrome in children. Nature Communications, 2021, 12, 4854.	5.8	42
26	Unbiased identification of novel transcription factors in striatal compartmentation and striosome maturation. ELife, 2021, 10, .	2.8	9
27	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
28	mGluR5 hypofunction is integral to glutamatergic dysregulation in schizophrenia. Molecular Psychiatry, 2020, 25, 750-760.	4.1	39
29	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
30	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. Scientific Data, 2020, 7, 340.	2.4	75
31	Differential gene regulatory pattern in the human brain from schizophrenia using transcriptomic-causal network. BMC Bioinformatics, 2020, 21, 469.	1.2	14
32	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
33	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
34	Integration of Alzheimerâ€™s disease genetics and myeloid genomics reveals novel disease risk mechanisms. Alzheimer's and Dementia, 2020, 16, e043897.	0.4	0
35	Common schizophrenia risk variants are enriched in open chromatin regions of human glutamatergic neurons. Nature Communications, 2020, 11, 5581.	5.8	53
36	Functional annotation of rare structural variation in the human brain. Nature Communications, 2020, 11, 2990.	5.8	32

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37	decorate: differential epigenetic correlation test. Bioinformatics, 2020, 36, 2856-2861.	1.8	11
38	A chromosomal connectome for psychiatric and metabolic risk variants in adult dopaminergic neurons. Genome Medicine, 2020, 12, 19.	3.6	31
39	Comparison of brain connectomes by MRI and genomics and its implication in Alzheimerâ€™s disease. BMC Medicine, 2020, 18, 23.	2.3	6
40	Big Data Analysis and Genetic Liability to Neuropsychiatric Disease. Advances in Experimental Medicine and Biology, 2020, 1194, 455-455.	0.8	0
41	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
42	Genetic Variation in Long-Range Enhancers. Current Topics in Behavioral Neurosciences, 2019, 42, 35-50.	0.8	2
43	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
44	Global landscape and genetic regulation of RNA editing in cortical samples from individuals with schizophrenia. Nature Neuroscience, 2019, 22, 1402-1412.	7.1	63
45	Integrative transcriptome imputation reveals tissue-specific and shared biological mechanisms mediating susceptibility to complex traits. Nature Communications, 2019, 10, 3834.	5.8	68
46	CommonMind Consortium provides transcriptomic and epigenomic data for Schizophrenia and Bipolar Disorder. Scientific Data, 2019, 6, 180.	2.4	149
47	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
48	Assessment of somatic single-nucleotide variation in brain tissue of cases with schizophrenia. Translational Psychiatry, 2019, 9, 21.	2.4	16
49	The expression of long noncoding RNA NEAT1 is reduced in schizophrenia and modulates oligodendrocytes transcription. NPJ Schizophrenia, 2019, 5, 3.	2.0	44
50	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	9.4	1,191
51	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
52	Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. Nature Genetics, 2019, 51, 659-674.	9.4	154
53	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
54	Identification of common genetic risk variants for autism spectrum disorder. Nature Genetics, 2019, 51, 431-444.	9.4	1,538

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55	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. Nature Genetics, 2019, 51, 63-75.	9.4	1,594
56	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
57	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
58	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. Science, 2018, 359, 693-697.	6.0	851
59	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
60	THC exposure of human iPSC neurons impacts genes associated with neuropsychiatric disorders. Translational Psychiatry, 2018, 8, 89.	2.4	35
61	A Bayesian framework for multiple trait colocalization from summary association statistics. Bioinformatics, 2018, 34, 2538-2545.	1.8	203
62	Stress-Dependent Association Between Polygenic Risk for Schizophrenia and Schizotypal Traits in Young Army Recruits. Schizophrenia Bulletin, 2018, 44, 338-347.	2.3	33
63	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
64	Winter birth, urbanicity and immigrant status predict psychometric schizotypy dimensions in adolescents. European Psychiatry, 2018, 47, 9-18.	0.1	8
65	Revealing the brain's molecular architecture. Science, 2018, 362, 1262-1263.	6.0	45
66	Neuron-specific signatures in the chromosomal connectome associated with schizophrenia risk. Science, 2018, 362, .	6.0	162
67	Transcriptome and epigenome landscape of human cortical development modeled in organoids. Science, 2018, 362, .	6.0	220
68	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. Science, 2018, 362, .	6.0	516
69	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. Science, 2018, 362, .	6.0	805
70	Comprehensive functional genomic resource and integrative model for the human brain. Science, 2018, 362, .	6.0	618
71	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. Nature Communications, 2018, 9, 5141.	5.8	119
72	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

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73	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
74	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	5.8	484
75	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
76	An atlas of chromatin accessibility in the adult human brain. Genome Research, 2018, 28, 1243-1252.	2.4	170
77	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
78	Evaluation of chromatin accessibility in prefrontal cortex of individuals with schizophrenia. Nature Communications, 2018, 9, 3121.	5.8	141
79	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
80	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085
81	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
82	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
83	Brain Cell Type Specific Gene Expression and Co-expression Network Architectures. Scientific Reports, 2018, 8, 8868.	1.6	335
84	The Mount Sinai cohort of large-scale genomic, transcriptomic and proteomic data in Alzheimer's disease. Scientific Data, 2018, 5, 180185.	2.4	320
85	Practical Guidelines for High-Resolution Epigenomic Profiling of Nucleosomal Histones in Postmortem Human Brain Tissue. Biological Psychiatry, 2017, 81, 162-170.	0.7	48
86	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
87	Evidence for genetic heterogeneity between clinical subtypes of bipolar disorder. Translational Psychiatry, 2017, 7, e993-e993.	2.4	162
88	minepath.org: a free interactive pathway analysis web server. Nucleic Acids Research, 2017, 45, W116-W121.	6.5	8
89	Large-Scale Identification of Common Trait and Disease Variants Affecting Gene Expression. American Journal of Human Genetics, 2017, 100, 885-894.	2.6	91
90	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

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91	Microvascular anomaly conditions in psychiatric disease. Schizophrenia â€“ angiogenesis connection. Neuroscience and Biobehavioral Reviews, 2017, 77, 327-339.	2.9	58
92	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
93	A functional genomics predictive network model identifies regulators of inflammatory bowel disease. Nature Genetics, 2017, 49, 1437-1449.	9.4	199
94	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
95	The methyltransferase SETDB1 regulates a large neuron-specific topological chromatin domain. Nature Genetics, 2017, 49, 1239-1250.	9.4	133
96	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
97	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
98	S4â€02â€03: Accelerating Medicines Partnership: Coâ€Expression Networks. Alzheimer's and Dementia, 2016, 12, P322.	0.4	0
99	Substantial DNA methylation differences between two major neuronal subtypes in human brain. Nucleic Acids Research, 2016, 44, 2593-2612.	6.5	97
100	Gene expression elucidates functional impact of polygenic risk for schizophrenia. Nature Neuroscience, 2016, 19, 1442-1453.	7.1	952
101	Associations of differential schizotypal dimensions with executive working memory: A moderated-mediation analysis. Comprehensive Psychiatry, 2016, 71, 39-48.	1.5	7
102	Activity-Dependent Changes in Gene Expression in Schizophrenia Human-Induced Pluripotent Stem Cell Neurons. JAMA Psychiatry, 2016, 73, 1180.	6.0	40
103	Cardiometabolic risk loci share downstream cis- and trans-gene regulation across tissues and diseases. Science, 2016, 353, 827-830.	6.0	241
104	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
105	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
106	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
107	Understanding the genetic liability to schizophrenia through the neuroepigenome. Schizophrenia Research, 2016, 177, 115-124.	1.1	22
108	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

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109	Analyzing the Role of MicroRNAs in Schizophrenia in the Context of Common Genetic Risk Variants. JAMA Psychiatry, 2016, 73, 369.	6.0	78
110	Genome-wide autozygosity is associated with lower general cognitive ability. Molecular Psychiatry, 2016, 21, 837-843.	4.1	62
111	The Relationship of Common Risk Variants and Polygenic Risk for Schizophrenia to Sensorimotor Gating. Biological Psychiatry, 2016, 79, 988-996.	0.7	44
112	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
113	Disproportionate Contributions of Select Genomic Compartments and Cell Types to Genetic Risk for Coronary Artery Disease. PLoS Genetics, 2015, 11, e1005622.	1.5	70
114	Glutamate transporter splice variant expression in an enriched pyramidal cell population in schizophrenia. Translational Psychiatry, 2015, 5, e579-e579.	2.4	49
115	Genomic and Network Patterns of Schizophrenia Genetic Variation in Human Evolutionary Accelerated Regions. Molecular Biology and Evolution, 2015, 32, 1148-1160.	3.5	98
116	The effects of theCACNA1Crs1006737 A/G on affective startle modulation in healthy males. European Psychiatry, 2015, 30, 492-498.	0.1	13
117	Analysis of exome sequence in 604 trios for recessive genotypes in schizophrenia. Translational Psychiatry, 2015, 5, e607-e607.	2.4	35
118	The relationship between dopamine receptor D1 and cognitive performance. NPJ Schizophrenia, 2015, 1, 14002.	2.0	18
119	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
120	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
121	The PsychENCODE project. Nature Neuroscience, 2015, 18, 1707-1712.	7.1	371
122	The Role of H3K4me3 in Transcriptional Regulation Is Altered in Huntingtonâ€™s Disease. PLoS ONE, 2015, 10, e0144398.	1.1	47
123	Schizophrenia: susceptibility genes and oligodendroglial and myelin related abnormalities. Frontiers in Cellular Neuroscience, 2014, 8, 5.	1.8	78
124	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
125	A Role for Noncoding Variation in Schizophrenia. Cell Reports, 2014, 9, 1417-1429.	2.9	225
126	Conserved Higher-Order Chromatin Regulates NMDA Receptor Gene Expression and Cognition. Neuron, 2014, 84, 997-1008.	3.8	76

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127	The Future of Neuroepigenetics in the Human Brain. Progress in Molecular Biology and Translational Science, 2014, 128, 199-228.	0.9	14
128	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
129	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
130	De novo mutations in schizophrenia implicate synaptic networks. Nature, 2014, 506, 179-184.	13.7	1,510
131	A polygenic burden of rare disruptive mutations in schizophrenia. Nature, 2014, 506, 185-190.	13.7	1,305
132	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
133	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
134	Myelination, oligodendrocytes, and serious mental illness. Glia, 2014, 62, 1856-1877.	2.5	203
135	Cognitive and personality analysis of startle reactivity in a large cohort of healthy males. Biological Psychology, 2013, 94, 582-591.	1.1	7
136	CACNA1C as a risk factor for schizotypal personality disorder and schizotypy in healthy individuals. Psychiatry Research, 2013, 206, 122-123.	1.7	35
137	Molecular and Genetic Evidence for Abnormalities in the Nodes of Ranvier in Schizophrenia. Archives of General Psychiatry, 2012, 69, 7.	13.8	97
138	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
139	A System-Level Transcriptomic Analysis of Schizophrenia Using Postmortem Brain Tissue Samples. Archives of General Psychiatry, 2012, 69, 1205.	13.8	94
140	The Influence of Schizophrenia-Related Neuregulin-1 Polymorphisms on Sensorimotor Gating in Healthy Males. Biological Psychiatry, 2011, 69, 479-486.	0.7	58
141	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
142	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
143	Tolcapone, COMT polymorphisms and pharmacogenomic treatment of schizophrenia. Pharmacogenomics, 2011, 12, 559-566.	0.6	16
144	Sustained Attention and Working Memory Deficits Follow a Familial Pattern in Schizophrenia. Archives of Clinical Neuropsychology, 2011, 26, 687-695.	0.3	23

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145	Cognitive and emotional processing associated with the Season of Birth and dopamine D4 receptor gene. Neuropsychologia, 2010, 48, 3926-3933.	0.7	11
146	Cognitive and emotional processing in high novelty seeking associated with the L-DRD4 genotype. Neuropsychologia, 2009, 47, 1654-1659.	0.7	61
147	Azoles and antidepressants: a miniâ€review of the tolerability of coâ€administration. Mycoses, 2009, 52, 433-439.	1.8	4
148	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
149	A Risk PRODH Haplotype Affects Sensorimotor Gating, Memory, Schizotypy, and Anxiety in Healthy Male Subjects. Biological Psychiatry, 2009, 65, 1063-1070.	0.7	57
150	Planning, decision-making and the COMT rs4818 polymorphism in healthy males. Neuropsychologia, 2008, 46, 757-763.	0.7	72
151	The Dopamine D3 Receptor Ser9Gly Polymorphism Modulates Prepulse Inhibition of the Acoustic Startle Reflex. Biological Psychiatry, 2008, 64, 235-240.	0.7	53
152	Prepulse inhibition of the startle reflex depends on the catecholO-methyltransferase Val158Met gene polymorphism. Psychological Medicine, 2008, 38, 1651-1658.	2.7	77
153	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