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List of Publications by Year in descending order

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77 papers	6,053 citations	172457 29 h-index	76900 74 g-index
78 all docs	78 docs citations	78 times ranked	8936 citing authors

#	Article	IF	Citations
1	A polygenic approach to the association between smoking and schizophrenia. Addiction Biology, 2022, 27, e13104.	2.6	6
2	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	27.8	929
3	Association between psychiatric hospitalizations of patients with schizophrenia and polygenic risk scores based on genes with altered expression by antipsychotics. Acta Psychiatrica Scandinavica, 2022, 146, 139-150.	4.5	2
4	Colocalization of association signals at nicotinic acetylcholine receptor genes between schizophrenia and smoking traits. Drug and Alcohol Dependence, 2021, 220, 108517.	3.2	4
5	Genetic predisposition to alcohol dependence: The combined role of polygenic risk to general psychopathology and to high alcohol consumption. Drug and Alcohol Dependence, 2021, 221, 108556.	3.2	3
6	Interaction between the functional SNP rs2070951 in NR3C2 gene and high levels of plasma corticotropin-releasing hormone associates to postpartum depression. Archives of Women's Mental Health, 2020, 23, 413-420.	2.6	7
7	Identification of relevant hub genes for early intervention at gene coexpression modules with altered predicted expression in schizophrenia. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2020, 98, 109815.	4.8	12
8	The role of personality dimensions, depressive symptoms and other psychosocial variables in predicting postpartum suicidal ideation: a cohort study. Archives of Women's Mental Health, 2020, 23, 585-593.	2.6	8
9	Clock gene polygenic risk score and seasonality in major depressive disorder and bipolar disorder. Genes, Brain and Behavior, 2020, 19, e12683.	2.2	9
10	Relationships between substance abuse/dependence and psychiatric disorders based on polygenic scores. Genes, Brain and Behavior, 2019, 18, e12504.	2.2	26
11	Evidence of association of the DISC1 interactome gene set with schizophrenia from GWAS. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2019, 95, 109729.	4.8	16
12	BDNF genetic variants and methylation: effects on cognition in major depressive disorder. Translational Psychiatry, 2019, 9, 265.	4.8	42
13	Do polygenic risk and stressful life events predict pharmacological treatment response in obsessive compulsive disorder? A geneâ€“environment interaction approach. Translational Psychiatry, 2019, 9, 70.	4.8	19
14	Discoidin domain receptor 1 gene variants are associated with decreased white matter fractional anisotropy and decreased processing speed in schizophrenia. Journal of Psychiatric Research, 2019, 110, 74-82.	3.1	18
15	Enrichment of rare genetic variants in astrocyte gene enriched co-expression modules altered in postmortem brain samples of schizophrenia. Neurobiology of Disease, 2019, 121, 305-314.	4.4	12
16	Identification of putative second genetic hits in schizophrenia carriers of high-risk copy number variants and resequencing in additional samples. European Archives of Psychiatry and Clinical Neuroscience, 2018, 268, 585-592.	3.2	6
17	The highly pleiotropic gene SLC39A8 as an opportunity to gain insight into the molecular pathogenesis of schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2018, 177, 274-283.	1.7	52
18	Identification of genes carrying rare variants of moderate to large effect in schizophrenia: A replication study. Schizophrenia Research, 2018, 197, 577-578.	2.0	0

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19	Grandmaternal Diethylstilbesterol and Attention-Deficit/Hyperactivity Disorder in Children. JAMA Pediatrics, 2018, 172, 1203.	6.2	1
20	Genome wide analysis of rare copy number variations in alcohol abuse or dependence. Journal of Psychiatric Research, 2018, 103, 212-218.	3.1	8
21	FKBP5 polymorphisms and hypothalamic-pituitary-adrenal axis negative feedback in major depression and obsessive-compulsive disorder. Journal of Psychiatric Research, 2018, 104, 227-234.	3.1	19
22	Exon-focused genome-wide association study of obsessive-compulsive disorder and shared polygenic risk with schizophrenia. Translational Psychiatry, 2016, 6, e768-e768.	4.8	41
23	Targeted resequencing of regulatory regions at schizophrenia risk loci: Role of rare functional variants at chromatin repressive states. Schizophrenia Research, 2016, 174, 10-16.	2.0	6
24	Coping strategies for postpartum depression: a multi-centric study of 1626 women. Archives of Women's Mental Health, 2016, 19, 455-461.	2.6	26
25	Cumulative role of rare and common putative functional genetic variants at NPAS3 in schizophrenia susceptibility. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2015, 168, 528-535.	1.7	5
26	Resequencing and association analysis of coding regions at twenty candidate genes suggest a role for rare risk variation at AKAP9 and protective variation at NRXN1 in schizophrenia susceptibility. Journal of Psychiatric Research, 2015, 66-67, 38-44.	3.1	18
27	An efficient screening method for simultaneous detection of recurrent copy number variants associated with psychiatric disorders. Clinica Chimica Acta, 2015, 445, 34-40.	1.1	7
28	The role of SHANK2 rare variants in schizophrenia susceptibility. Molecular Psychiatry, 2015, 20, 1486-1486.	7.9	16
29	Coping Strategies and Postpartum Depressive Symptoms: a Structural Equation Modelling Approach. European Psychiatry, 2015, 30, 701-708.	0.2	31
30	Comment on â€œCurrent understanding of ZIP and ZnT zinc transporters in human health and diseasesâ€. Cellular and Molecular Life Sciences, 2015, 72, 197-198.	5.4	4
31	Common variant at 16p11.2 conferring risk of psychosis. Molecular Psychiatry, 2014, 19, 108-114.	7.9	85
32	Replication of previous genome-wide association studies of psychiatric diseases in a large schizophrenia caseâ€“control sample from Spain. Schizophrenia Research, 2014, 159, 107-113.	2.0	36
33	Mitochondrial DNA (mtDNA) variants in the European haplogroups HV, JT, and U do not have a major role in schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2014, 165, 607-617.	1.7	8
34	Absence of low frequency variants associated with schizophrenia at the ultraconserved non-coding region of TCF4. Psychiatry Research, 2014, 215, 255-257.	3.3	1
35	Role of DISC1 Interacting Proteins in Schizophrenia Risk from Genomeâ€Wide Analysis of Missense SNPs. Annals of Human Genetics, 2013, 77, 504-512.	0.8	22
36	Research Letter: Is neuroticism a risk factor for postpartum depression?. Psychological Medicine, 2012, 42, 1559-1565.	4.5	37

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37	Association Study of Nonsynonymous Single Nucleotide Polymorphisms in Schizophrenia. Biological Psychiatry, 2012, 71, 169-177.	1.3	78
38	Genetic epistasis in female suicide attempters. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2012, 38, 294-301.	4.8	9
39	No evidence that major mtDNA European haplogroups confer risk to schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2012, 159B, 414-421.	1.7	25
40	The Discoidin domain receptor 1 gene has a functional A2RE sequence. Journal of Neurochemistry, 2012, 120, 408-418.	3.9	20
41	GDF: Dealing with High-throughput Genotyping Multiplatform Data for Medical and Population Genetic Applications. Journal of Proteomics and Bioinformatics, 2012, 05, .	0.4	2
42	Common variants at VRK2 and TCF4 conferring risk of schizophrenia. Human Molecular Genetics, 2011, 20, 4076-4081.	2.9	193
43	Interaction between COMT haplotypes and cannabis in schizophrenia: A case-only study in two samples from Spain. Schizophrenia Research, 2011, 127, 22-27.	2.0	57
44	Potential involvement of serotonin receptor genes with age of onset and gender in schizophrenia: A preliminary study in a Spanish sample. Psychiatry Research, 2011, 186, 153-154.	3.3	4
45	Heterozygosity at catechol-O-methyltransferase Val158Met and schizophrenia: New data and meta-analysis. Journal of Psychiatric Research, 2011, 45, 7-14.	3.1	61
46	Evolutionary Dynamics of the Ty3/Gypsy LTR Retrotransposons in the Genome of Anopheles gambiae. PLoS ONE, 2011, 6, e16328.	2.5	15
47	Nucleotide variation in central nervous system genes among male suicide attempters. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2010, 153B, 208-213.	1.7	13
48	Sequencing of Culex quinquefasciatus Establishes a Platform for Mosquito Comparative Genomics. Science, 2010, 330, 86-88.	12.6	424
49	Association study of 44 candidate genes with depressive and anxiety symptoms in post-partum women. Journal of Psychiatric Research, 2010, 44, 717-724.	3.1	69
50	Testing the antagonistic pleiotropy model of schizophrenia susceptibility by analysis of DAOA, PPP1R1B, and APOL1 genes. Psychiatry Research, 2010, 179, 126-129.	3.3	9
51	Recent adaptive selection at MAOB and ancestral susceptibility to schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2009, 150B, 369-374.	1.7	30
52	Identification of new putative susceptibility genes for several psychiatric disorders by association analysis of regulatory and nonâ€synonymous SNPs of 306 genes involved in neurotransmission and neurodevelopment. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2009, 150B, 808-816.	1.7	98
53	A common haplotype of DRD3 affected by recent positive selection is associated with protection from schizophrenia. Human Genetics, 2009, 124, 607-613.	3.8	15
54	Common variants conferring risk of schizophrenia. Nature, 2009, 460, 744-747.	27.8	1,572

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55	Generalized lattice graphs for 2D-visualization of biological information. Journal of Theoretical Biology, 2009, 261, 136-147.	1.7	41
56	Genetic variation in the nuclear factor ÎºB pathway in relation to susceptibility to rheumatoid arthritis. Annals of the Rheumatic Diseases, 2009, 68, 579-583.	0.9	40
57	Association of schizophrenia with DTNBP1 but not with DAO, DAOA, NRG1 and RGS4 nor their genetic interaction. Journal of Psychiatric Research, 2008, 42, 278-288.	3.1	80
58	Rapid evolving RNA gene HAR1A and schizophrenia. Schizophrenia Research, 2008, 99, 370-372.	2.0	22
59	Analyses of variants located in estrogen metabolism genes (ESR1, ESR2, COMT and APOE) and schizophrenia. Schizophrenia Research, 2008, 100, 308-315.	2.0	23
60	Mood changes after delivery: role of the serotonin transporter gene. British Journal of Psychiatry, 2008, 193, 383-388.	2.8	95
61	Genome Sequence of Aedes aegypti, a Major Arbovirus Vector. Science, 2007, 316, 1718-1723.	12.6	1,025
62	Extensive linkage disequilibrium mapping at HTR2A and DRD3 for schizophrenia susceptibility genes in the Galician population. Schizophrenia Research, 2007, 90, 123-129.	2.0	36
63	The discoidin domain receptor 1 as a novel susceptibility gene for schizophrenia. Molecular Psychiatry, 2007, 12, 833-841.	7.9	50
64	High variability in CYP21A2 mutated alleles in Spanish 21-hydroxylase deficiency patients, six novel mutations and a founder effect. Clinical Endocrinology, 2006, 64, 330-336.	2.4	53
65	Structural and Evolutionary Analyses of the Ty3/gypsy Group of LTR Retrotransposons in the Genome of Anopheles gambiae. Molecular Biology and Evolution, 2005, 22, 29-39.	8.9	26
66	Human genome-wide screen of haplotype-like blocks of reduced diversity. Gene, 2005, 349, 219-225.	2.2	43
67	Relative efficiency of the linkage disequilibrium mapping approach in detecting candidate genes for schizophrenia in different European populations. Genomics, 2005, 86, 280-286.	2.9	9
68	Dynamics and function of intron sequences of the wingless gene during the evolution of the Drosophila genus. Evolution & Development, 2004, 6, 325-335.	2.0	7
69	Molecular Characterization of the Recent Intragenomic Spread of the Murine Endogenous Retrovirus MuERV-L. Journal of Molecular Evolution, 2003, 56, 181-186.	1.8	27
70	Genomic characterization of a repetitive motif strongly associated with developmental genes in Drosophila. BMC Genomics, 2003, 4, 52.	2.8	4
71	Turnover of binding sites for transcription factors involved in early Drosophila development. Gene, 2003, 310, 215-220.	2.2	55
72	Characterization of the Intragenomic Spread of the Human Endogenous Retrovirus Family HERV-W. Molecular Biology and Evolution, 2002, 19, 526-533.	8.9	73

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73	Amplification and Phylogenetic Relationships of a Subfamily of blood, a Retrotransposable Element of Drosophila. Journal of Molecular Evolution, 2001, 52, 342-350.	1.8	11
74	Structural Features of the mdg1 Lineage of the Ty3/gypsy Group of LTR Retrotransposons Inferred from the Phylogenetic Analyses of Its Open Reading Frames. Journal of Molecular Evolution, 2001, 53, 165-171.	1.8	8
75	Evolutionary Dynamics of the Human Endogenous Retrovirus Family HERV-K Inferred from Full-Length Proviral Genomes. Journal of Molecular Evolution, 2001, 53, 237-243.	1.8	43
76	Length variability and interspersion patterns of the HRAS1 minisatellite: a new approach for the reconstruction of human population relationships. Annals of Human Genetics, 2001, 65, 351-361.	0.8	2
77	Evolutionary History of the Human Endogenous Retrovirus Family ERV9. Molecular Biology and Evolution, 2000, 17, 320-330.	8.9	44