

Silviu-Alin Bacanu

List of Publications by Year in descending order

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Version: 2024-02-01

90
papers

7,428
citations

117625

34
h-index

64796

79
g-index

104
all docs

104
docs citations

104
times ranked

12356
citing authors

#	ARTICLE	IF	CITATIONS
1	Differences in genetic risk score profiles for drug use disorder, major depression, and ADHD as a function of sex, age at onset, recurrence, mode of ascertainment, and treatment. <i>Psychological Medicine</i> , 2023, 53, 3448-3460.	4.5	13
2	Optical genome mapping identifies rare structural variations as predisposition factors associated with severe COVID-19. <i>iScience</i> , 2022, 25, 103760.	4.1	15
3	Genome-wide analysis of schizophrenia and multiple sclerosis identifies shared genomic loci with mixed direction of effects. <i>Brain, Behavior, and Immunity</i> , 2022, 104, 183-190.	4.1	8
4	Shared genetic risk between eating disorder and substance use related phenotypes: Evidence from genome-wide association studies. <i>Addiction Biology</i> , 2021, 26, e12880.	2.6	28
5	Increasing the resolution and precision of psychiatric genome-wide association studies by re-imputing summary statistics using a large, diverse reference panel. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2021, 186, 16-27.	1.7	4
6	DECO: a framework for jointly analyzing <i>de novo</i> and rare case/control variants, and biological pathways. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	6
7	Genome-wide analyses of smoking behaviors in schizophrenia: Findings from the Psychiatric Genomics Consortium. <i>Journal of Psychiatric Research</i> , 2021, 137, 215-224.	3.1	10
8	Identifying a novel biological mechanism for alcohol addiction associated with circRNA networks acting as potential miRNA sponges. <i>Addiction Biology</i> , 2021, 26, e13071.	2.6	13
9	The Genetic Architecture of Depression in Individuals of East Asian Ancestry. <i>JAMA Psychiatry</i> , 2021, 78, 1258.	11.0	88
10	Pathway-based polygene risk for severe depression implicates drug metabolism in CONVERGE. <i>Psychological Medicine</i> , 2020, 50, 793-798.	4.5	3
11	The risk for drug abuse, alcohol use disorder, and psychosocial dysfunction in offspring from high-density pedigrees: its moderation by personal, family, and community factors. <i>Molecular Psychiatry</i> , 2020, 25, 1777-1786.	7.9	15
12	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. <i>Biological Psychiatry</i> , 2020, 87, 419-430.	1.3	27
13	The Genetics of the Mood Disorder Spectrum: Genome-wide Association Analyses of More Than 185,000 Cases and 439,000 Controls. <i>Biological Psychiatry</i> , 2020, 88, 169-184.	1.3	137
14	Genome-wide association study of shared liability to anxiety disorders in Army STARRS. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2020, 183, 197-207.	1.7	13
15	Genome-Wide Association Study of Suicide Death and Polygenic Prediction of Clinical Antecedents. <i>American Journal of Psychiatry</i> , 2020, 177, 917-927.	7.2	66
16	A large-scale genome-wide association study meta-analysis of cannabis use disorder. <i>Lancet Psychiatry</i> , 2020, 7, 1032-1045.	7.4	200
17	Analysis of Genetically Regulated Gene Expression Identifies a Prefrontal PTSD Gene, SNRNP35, Specific to Military Cohorts. <i>Cell Reports</i> , 2020, 31, 107716.	6.4	44
18	Assessing the Role of Long Noncoding RNA in Nucleus Accumbens in Subjects With Alcohol Dependence. <i>Alcoholism: Clinical and Experimental Research</i> , 2020, 44, 2468-2480.	2.4	12

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19	<sc>TWAS</sc> pathway method greatly enhances the number of leads for uncovering the molecular underpinnings of psychiatric disorders. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2020, 183, 454-463.	1.7	16
20	A method for estimating coherence of molecular mechanisms in major human disease and traits. BMC Bioinformatics, 2020, 21, 473.	2.6	1
21	Meta-Analysis of Associations Between Hypothalamic-Pituitary-Adrenal Axis Genes and Risk of Posttraumatic Stress Disorder. Journal of Traumatic Stress, 2020, 33, 688-698.	1.8	26
22	Leveraging genome-wide data to investigate differences between opioid use vs. opioid dependence in 41,176 individuals from the Psychiatric Genomics Consortium. Molecular Psychiatry, 2020, 25, 1673-1687.	7.9	82
23	The impact on estimations of genetic correlations by the use of super-normal, unscreened, and family-history screened controls in genome wide case-control studies. Genetic Epidemiology, 2020, 44, 283-289.	1.3	21
24	Network preservation reveals shared and unique biological processes associated with chronic alcohol abuse in NAc and PFC. PLoS ONE, 2020, 15, e0243857.	2.5	7
25	Title is missing!. , 2020, 15, e0243857.		0
26	Title is missing!. , 2020, 15, e0243857.		0
27	Title is missing!. , 2020, 15, e0243857.		0
28	Title is missing!. , 2020, 15, e0243857.		0
29	Title is missing!. , 2020, 15, e0243857.		0
30	Title is missing!. , 2020, 15, e0243857.		0
31	MOLECULAR GENETIC ANALYSIS SUBDIVIDED BY ADVERSITY EXPOSURE SUGGESTS ETIOLOGIC HETEROGENEITY IN MAJOR DEPRESSION. European Neuropsychopharmacology, 2019, 29, S792-S793.	0.7	0
32	Association of Whole-Genome and NETRIN1 Signaling Pathway-Derived Polygenic Risk Scores for Major Depressive Disorder and White Matter Microstructure in the UK Biobank. Biological Psychiatry: Cognitive Neuroscience and Neuroimaging, 2019, 4, 91-100.	1.5	16
33	The Coherence Problem: Finding Meaning in GWAS Complexity. Behavior Genetics, 2019, 49, 187-195.	2.1	8
34	GxE effects of FKBP5 and traumatic life events on PTSD: A meta-analysis. Journal of Affective Disorders, 2019, 243, 455-462.	4.1	44
35	Molecular Genetic Analysis Subdivided by Adversity Exposure Suggests Etiologic Heterogeneity in Major Depression. American Journal of Psychiatry, 2018, 175, 545-554.	7.2	69
36	JEPEGMIX2: improved gene-level joint analysis of eQTLs in cosmopolitan cohorts. Bioinformatics, 2018, 34, 286-288.	4.1	6

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37	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018, 50, 668-681.	21.4	2,224
38	Does Childhood Trauma Moderate Polygenic Risk for Depression? A Meta-analysis of 5765 Subjects From the Psychiatric Genomics Consortium. <i>Biological Psychiatry</i> , 2018, 84, 138-147.	1.3	87
39	Transancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders. <i>Nature Neuroscience</i> , 2018, 21, 1656-1669.	14.8	490
40	Meta-Analysis of Genetic Influences on Initial Alcohol Sensitivity. <i>Alcoholism: Clinical and Experimental Research</i> , 2018, 42, 2349-2359.	2.4	21
41	Replication of the Interaction of PRKG1 and Trauma Exposure on Alcohol Misuse in an Independent African American Sample. <i>Journal of Traumatic Stress</i> , 2018, 31, 927-932.	1.8	9
42	Method to estimate the approximate samples size that yield a certain number of significant GWAS signals in polygenic traits. <i>Genetic Epidemiology</i> , 2018, 42, 488-496.	1.3	2
43	The Genetic Architecture of Major Depressive Disorder in Han Chinese Women. <i>JAMA Psychiatry</i> , 2017, 74, 162.	11.0	82
44	Association of Posttraumatic Stress Disorder With rs2267735 in the <i>ADCYAP1R1</i> Gene: A Meta-Analysis. <i>Journal of Traumatic Stress</i> , 2017, 30, 389-398.	1.8	33
45	The utility of empirically assigning ancestry groups in cross-population genetic studies of addiction. <i>American Journal on Addictions</i> , 2017, 26, 494-501.	1.4	46
46	The Effects of a <i>BDNF</i> Val66Met Polymorphism on Posttraumatic Stress Disorder: A Meta-Analysis. <i>Neuropsychobiology</i> , 2017, 76, 136-142.	1.9	18
47	Sharing extended summary data from contemporary genetics studies is unlikely to threaten subject privacy. <i>PLoS ONE</i> , 2017, 12, e0179504.	2.5	2
48	JEPEGMIX: gene-level joint analysis of functional SNPs in cosmopolitan cohorts. <i>Bioinformatics</i> , 2016, 32, 295-297.	4.1	8
49	CHRONICITY OF DEPRESSION AND MOLECULAR MARKERS IN A LARGE SAMPLE OF HAN CHINESE WOMEN. <i>Depression and Anxiety</i> , 2016, 33, 1048-1054.	4.1	18
50	Genetic Relationship between Schizophrenia and Nicotine Dependence. <i>Scientific Reports</i> , 2016, 6, 25671.	3.3	67
51	A simple yet accurate correction for winner's curse can predict signals discovered in much larger genome scans. <i>Bioinformatics</i> , 2016, 32, 2598-2603.	4.1	44
52	Evaluating the dopamine hypothesis of schizophrenia in a large-scale genome-wide association study. <i>Schizophrenia Research</i> , 2016, 176, 136-140.	2.0	30
53	Genome-wide association study reveals greater polygenic loading for schizophrenia in cases with a family history of illness. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2016, 171, 276-289.	1.7	28
54	Evidence for Genetic Overlap Between Schizophrenia and Age at First Birth in Women. <i>JAMA Psychiatry</i> , 2016, 73, 497.	11.0	51

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55	Meta-analysis of Positive and Negative Symptoms Reveals Schizophrenia Modifier Genes: Table 1.. Schizophrenia Bulletin, 2016, 42, 279-287.	4.3	40
56	DISTMIX: direct imputation of summary statistics for unmeasured SNPs from mixed ethnicity cohorts. Bioinformatics, 2015, 31, 3099-3104.	4.1	25
57	Transcriptome sequencing and genome-wide association analyses reveal lysosomal function and actin cytoskeleton remodeling in schizophrenia and bipolar disorder. Molecular Psychiatry, 2015, 20, 563-572.	7.9	124
58	Genome-wide gene pathway analysis of psychotic illness symptom dimensions based on a new schizophrenia-specific model of the OPCRIT. Schizophrenia Research, 2015, 164, 181-186.	2.0	19
59	JEPEG: a summary statistics based tool for gene-level joint testing of functional variants. Bioinformatics, 2015, 31, 1176-1182.	4.1	27
60	Integrating mRNA and miRNA Weighted Gene Co-Expression Networks with eQTLs in the Nucleus Accumbens of Subjects with Alcohol Dependence. PLoS ONE, 2015, 10, e0137671.	2.5	71
61	Testing for Measured Gene-Environment Interaction: Problems with the use of Cross-Product Terms and a Regression Model Reparameterization Solution. Behavior Genetics, 2014, 44, 165-181.	2.1	37
62	Molecular Validation of the Schizophrenia Spectrum. Schizophrenia Bulletin, 2014, 40, 60-65.	4.3	41
63	On schizophrenia as a "disease of humanity" Schizophrenia Research, 2013, 143, 223-224.	2.0	6
64	The genetic overlap between schizophrenia and height. Schizophrenia Research, 2013, 151, 226-228.	2.0	12
65	Extracting Actionable Information From Genome Scans. Genetic Epidemiology, 2013, 37, 48-59.	1.3	7
66	Testing for Modes of Inheritance Involving Compound Heterozygotes. Genetic Epidemiology, 2013, 37, 522-528.	1.3	3
67	Association Testing Strategy for Data from Dense Marker Panels. PLoS ONE, 2013, 8, e80540.	2.5	2
68	An Abundance of Rare Functional Variants in 202 Drug Target Genes Sequenced in 14,002 People. Science, 2012, 337, 100-104.	12.6	626
69	On Optimal Gene-Based Analysis of Genome Scans. Genetic Epidemiology, 2012, 36, 333-339.	1.3	13
70	Comparison of Statistical Tests for Association between Rare Variants and Binary Traits. PLoS ONE, 2012, 7, e42530.	2.5	11
71	Genome-Wide Gene-Environment Study Identifies Glutamate Receptor Gene GRIN2A as a Parkinson's Disease Modifier Gene via Interaction with Coffee. PLoS Genetics, 2011, 7, e1002237.	3.5	206
72	Comparison of methods and sampling designs to test for association between rare variants and quantitative traits. Genetic Epidemiology, 2011, 35, 226-235.	1.3	11

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73	Comparison of association methods for dense marker data. <i>Genetic Epidemiology</i> , 2008, 32, 791-799.	1.3	12
74	Are exposure to cytomegalovirus and genetic variation on chromosome 6p joint risk factors for schizophrenia?. <i>Annals of Medicine</i> , 2007, 39, 145-153.	3.8	28
75	Analysis of single-locus tests to detect gene/disease associations. <i>Genetic Epidemiology</i> , 2005, 28, 207-219.	1.3	92
76	Characterization of multilocus linkage disequilibrium. <i>Genetic Epidemiology</i> , 2005, 28, 193-206.	1.3	101
77	Linkage analysis of a completely ascertained sample of familial schizophrenics and bipolars from Palau, Micronesia. <i>Human Genetics</i> , 2005, 117, 349-356.	3.8	22
78	Association of Multiple DRD2 Polymorphisms with Anorexia Nervosa. <i>Neuropsychopharmacology</i> , 2005, 30, 1703-1710.	5.4	127
79	Combined Analysis from Eleven Linkage Studies of Bipolar Disorder Provides Strong Evidence of Susceptibility Loci on Chromosomes 6q and 8q. <i>American Journal of Human Genetics</i> , 2005, 77, 582-595.	6.2	218
80	Heritability of Psychosis in Alzheimer Disease. <i>American Journal of Geriatric Psychiatry</i> , 2005, 13, 624-627.	1.2	47
81	Genomic Control to the extreme. <i>Nature Genetics</i> , 2004, 36, 1129-1130.	21.4	148
82	Genetic analysis of bulimia nervosa: Methods and sample description. <i>International Journal of Eating Disorders</i> , 2004, 35, 556-570.	4.0	50
83	Personality in men with eating disorders. <i>Journal of Psychosomatic Research</i> , 2004, 57, 273-278.	2.6	34
84	Heritability of fearful-anxious endophenotypes in infant rhesus macaques: a preliminary report. <i>Biological Psychiatry</i> , 2003, 53, 284-291.	1.3	96
85	Significant Linkage on Chromosome 10p in Families with Bulimia Nervosa. <i>American Journal of Human Genetics</i> , 2003, 72, 200-207.	6.2	125
86	Psychotic symptoms in Alzheimer disease: evidence for subtypes. <i>American Journal of Geriatric Psychiatry</i> , 2003, 11, 406-13.	1.2	12
87	Linkage analysis of anorexia nervosa incorporating behavioral covariates. <i>Human Molecular Genetics</i> , 2002, 11, 689-696.	2.9	144
88	Long-Term Comparison of Tacrolimus- and Cyclosporine-Induced Nephrotoxicity in Pediatric Heart-Transplant Recipients. <i>American Journal of Transplantation</i> , 2002, 2, 769-773.	4.7	64
89	The Power of Genomic Control. <i>American Journal of Human Genetics</i> , 2000, 66, 1933-1944.	6.2	338
90	Complications of endomyocardial biopsy in children. <i>Journal of the American College of Cardiology</i> , 1999, 34, 2105-2110.	2.8	179