

# 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	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
2	An Abundance of Rare Functional Variants in 202 Drug Target Genes Sequenced in 14,002 People. <i>Science</i> , 2012, 337, 100-104.	12.6	626
3	Transancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders. <i>Nature Neuroscience</i> , 2018, 21, 1656-1669.	14.8	490
4	The Power of Genomic Control. <i>American Journal of Human Genetics</i> , 2000, 66, 1933-1944.	6.2	338
5	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
6	Genome-Wide Gene-Environment Study Identifies Glutamate Receptor Gene GRIN2A as a Parkinson's Disease Modifier Gene via Interaction with Coffee. <i>PLoS Genetics</i> , 2011, 7, e1002237.	3.5	206
7	A large-scale genome-wide association study meta-analysis of cannabis use disorder. <i>Lancet Psychiatry</i> , 2020, 7, 1032-1045.	7.4	200
8	Complications of endomyocardial biopsy in children. <i>Journal of the American College of Cardiology</i> , 1999, 34, 2105-2110.	2.8	179
9	Genomic Control to the extreme. <i>Nature Genetics</i> , 2004, 36, 1129-1130.	21.4	148
10	Linkage analysis of anorexia nervosa incorporating behavioral covariates. <i>Human Molecular Genetics</i> , 2002, 11, 689-696.	2.9	144
11	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
12	Association of Multiple DRD2 Polymorphisms with Anorexia Nervosa. <i>Neuropsychopharmacology</i> , 2005, 30, 1703-1710.	5.4	127
13	Significant Linkage on Chromosome 10p in Families with Bulimia Nervosa. <i>American Journal of Human Genetics</i> , 2003, 72, 200-207.	6.2	125
14	Transcriptome sequencing and genome-wide association analyses reveal lysosomal function and actin cytoskeleton remodeling in schizophrenia and bipolar disorder. <i>Molecular Psychiatry</i> , 2015, 20, 563-572.	7.9	124
15	Characterization of multilocus linkage disequilibrium. <i>Genetic Epidemiology</i> , 2005, 28, 193-206.	1.3	101
16	Heritability of fearful-anxious endophenotypes in infant rhesus macaques: a preliminary report. <i>Biological Psychiatry</i> , 2003, 53, 284-291.	1.3	96
17	Analysis of single-locus tests to detect gene/disease associations. <i>Genetic Epidemiology</i> , 2005, 28, 207-219.	1.3	92
18	The Genetic Architecture of Depression in Individuals of East Asian Ancestry. <i>JAMA Psychiatry</i> , 2021, 78, 1258.	11.0	88

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19	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
20	The Genetic Architecture of Major Depressive Disorder in Han Chinese Women. <i>JAMA Psychiatry</i> , 2017, 74, 162.	11.0	82
21	Leveraging genome-wide data to investigate differences between opioid use vs. opioid dependence in 41,176 individuals from the Psychiatric Genomics Consortium. <i>Molecular Psychiatry</i> , 2020, 25, 1673-1687.	7.9	82
22	Integrating mRNA and miRNA Weighted Gene Co-Expression Networks with eQTLs in the Nucleus Accumbens of Subjects with Alcohol Dependence. <i>PLoS ONE</i> , 2015, 10, e0137671.	2.5	71
23	Molecular Genetic Analysis Subdivided by Adversity Exposure Suggests Etiologic Heterogeneity in Major Depression. <i>American Journal of Psychiatry</i> , 2018, 175, 545-554.	7.2	69
24	Genetic Relationship between Schizophrenia and Nicotine Dependence. <i>Scientific Reports</i> , 2016, 6, 25671.	3.3	67
25	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
26	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
27	Evidence for Genetic Overlap Between Schizophrenia and Age at First Birth in Women. <i>JAMA Psychiatry</i> , 2016, 73, 497.	11.0	51
28	Genetic analysis of bulimia nervosa: Methods and sample description. <i>International Journal of Eating Disorders</i> , 2004, 35, 556-570.	4.0	50
29	Heritability of Psychosis in Alzheimer Disease. <i>American Journal of Geriatric Psychiatry</i> , 2005, 13, 624-627.	1.2	47
30	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
31	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
32	GxE effects of FKBP5 and traumatic life events on PTSD: A meta-analysis. <i>Journal of Affective Disorders</i> , 2019, 243, 455-462.	4.1	44
33	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
34	Molecular Validation of the Schizophrenia Spectrum. <i>Schizophrenia Bulletin</i> , 2014, 40, 60-65.	4.3	41
35	Meta-analysis of Positive and Negative Symptoms Reveals Schizophrenia Modifier Genes: Table 1.. <i>Schizophrenia Bulletin</i> , 2016, 42, 279-287.	4.3	40
36	Testing for Measured Gene-Environment Interaction: Problems with the use of Cross-Product Terms and a Regression Model Reparameterization Solution. <i>Behavior Genetics</i> , 2014, 44, 165-181.	2.1	37

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37	Personality in men with eating disorders. <i>Journal of Psychosomatic Research</i> , 2004, 57, 273-278.	2.6	34
38	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
39	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
40	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
41	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
42	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
43	JEPEG: a summary statistics based tool for gene-level joint testing of functional variants. <i>Bioinformatics</i> , 2015, 31, 1176-1182.	4.1	27
44	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
45	Meta-Analysis of Associations Between Hypothalamic-Pituitary-Adrenal Axis Genes and Risk of Posttraumatic Stress Disorder. <i>Journal of Traumatic Stress</i> , 2020, 33, 688-698.	1.8	26
46	DISTMIX: direct imputation of summary statistics for unmeasured SNPs from mixed ethnicity cohorts. <i>Bioinformatics</i> , 2015, 31, 3099-3104.	4.1	25
47	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
48	Meta-Analysis of Genetic Influences on Initial Alcohol Sensitivity. <i>Alcoholism: Clinical and Experimental Research</i> , 2018, 42, 2349-2359.	2.4	21
49	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. <i>Genetic Epidemiology</i> , 2020, 44, 283-289.	1.3	21
50	Genome-wide gene pathway analysis of psychotic illness symptom dimensions based on a new schizophrenia-specific model of the OPCRIT. <i>Schizophrenia Research</i> , 2015, 164, 181-186.	2.0	19
51	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
52	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
53	Association of Whole-Genome and <i>NETRIN1</i> Signaling Pathway-Derived Polygenic Risk Scores for Major Depressive Disorder and White Matter Microstructure in the UK Biobank. <i>Biological Psychiatry: Cognitive Neuroscience and Neuroimaging</i> , 2019, 4, 91-100.	1.5	16
54	<i>TWAS</i> pathway method greatly enhances the number of leads for uncovering the molecular underpinnings of psychiatric disorders. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2020, 183, 454-463.	1.7	16

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55	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
56	Optical genome mapping identifies rare structural variations as predisposition factors associated with severe COVID-19. <i>iScience</i> , 2022, 25, 103760.	4.1	15
57	On Optimal Gene-Based Analysis of Genome Scans. <i>Genetic Epidemiology</i> , 2012, 36, 333-339.	1.3	13
58	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
59	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
60	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
61	Comparison of association methods for dense marker data. <i>Genetic Epidemiology</i> , 2008, 32, 791-799.	1.3	12
62	The genetic overlap between schizophrenia and height. <i>Schizophrenia Research</i> , 2013, 151, 226-228.	2.0	12
63	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
64	Psychotic symptoms in Alzheimer disease: evidence for subtypes. <i>American Journal of Geriatric Psychiatry</i> , 2003, 11, 406-13.	1.2	12
65	Comparison of methods and sampling designs to test for association between rare variants and quantitative traits. <i>Genetic Epidemiology</i> , 2011, 35, 226-235.	1.3	11
66	Comparison of Statistical Tests for Association between Rare Variants and Binary Traits. <i>PLoS ONE</i> , 2012, 7, e42530.	2.5	11
67	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
68	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
69	JEPEGMIX: gene-level joint analysis of functional SNPs in cosmopolitan cohorts. <i>Bioinformatics</i> , 2016, 32, 295-297.	4.1	8
70	The Coherence Problem: Finding Meaning in GWAS Complexity. <i>Behavior Genetics</i> , 2019, 49, 187-195.	2.1	8
71	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
72	Extracting Actionable Information From Genome Scans. <i>Genetic Epidemiology</i> , 2013, 37, 48-59.	1.3	7

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73	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
74	On schizophrenia as a "disease of humanity" Schizophrenia Research, 2013, 143, 223-224.	2.0	6
75	JEPEG MIX2: improved gene-level joint analysis of eQTLs in cosmopolitan cohorts. Bioinformatics, 2018, 34, 286-288.	4.1	6
76	DECO: a framework for jointly analyzing <i>de novo</i> and rare case/control variants, and biological pathways. Briefings in Bioinformatics, 2021, 22, .	6.5	6
77	Increasing the resolution and precision of psychiatric genome-wide association studies by re-imputing summary statistics using a large, diverse reference panel. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2021, 186, 16-27.	1.7	4
78	Testing for Modes of Inheritance Involving Compound Heterozygotes. Genetic Epidemiology, 2013, 37, 522-528.	1.3	3
79	Pathway-based polygene risk for severe depression implicates drug metabolism in CONVERGE. Psychological Medicine, 2020, 50, 793-798.	4.5	3
80	Method to estimate the approximate samples size that yield a certain number of significant GWAS signals in polygenic traits. Genetic Epidemiology, 2018, 42, 488-496.	1.3	2
81	Association Testing Strategy for Data from Dense Marker Panels. PLoS ONE, 2013, 8, e80540.	2.5	2
82	Sharing extended summary data from contemporary genetics studies is unlikely to threaten subject privacy. PLoS ONE, 2017, 12, e0179504.	2.5	2
83	A method for estimating coherence of molecular mechanisms in major human disease and traits. BMC Bioinformatics, 2020, 21, 473.	2.6	1
84	MOLECULAR GENETIC ANALYSIS SUBDIVIDED BY ADVERSITY EXPOSURE SUGGESTS ETIOLOGIC HETEROGENEITY IN MAJOR DEPRESSION. European Neuropsychopharmacology, 2019, 29, S792-S793.	0.7	0
85	Title is missing!. , 2020, 15, e0243857.		0
86	Title is missing!. , 2020, 15, e0243857.		0
87	Title is missing!. , 2020, 15, e0243857.		0
88	Title is missing!. , 2020, 15, e0243857.		0
89	Title is missing!. , 2020, 15, e0243857.		0
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