Andrey A Shabalin

List of Publications by Year
in descending order

59	17,607	201674 27	144013 57
papers	citations	h-index	g-index

65	65	65	37748
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	General v. specific vulnerabilities: polygenic risk scores and higher-order psychopathology dimensions in the Adolescent Brain Cognitive Development (ABCD) Study. Psychological Medicine, 2023, 53, 1937-1946.	4.5	17
2	Polygenic prediction of PTSD trajectories in 9/11 responders. Psychological Medicine, 2022, 52, 1981-1989.	4.5	18
3	Dissecting the Shared Genetic Architecture of Suicide Attempt, Psychiatric Disorders, and Known Risk Factors. Biological Psychiatry, 2022, 91, 313-327.	1.3	114
4	Suicide and Psychosis: Results From a Population-Based Cohort of Suicide Death (N = 4380). Schizophrenia Bulletin, 2022, 48, 457-462.	4.3	4
5	The benefit of diagnostic whole genome sequencing in schizophrenia and other psychotic disorders. Molecular Psychiatry, 2022, 27, 1435-1447.	7.9	12
6	Extended familial risk of suicide death is associated with younger age at death and elevated polygenic risk of suicide. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2022, 189, 60-73.	1.7	4
7	Genome-wide Association Meta-analysis of Childhood and Adolescent Internalizing Symptoms. Journal of the American Academy of Child and Adolescent Psychiatry, 2022, 61, 934-945.	0.5	26
8	Unique and joint associations of polygenic risk for major depression and opioid use disorder with endogenous opioid system function. Neuropsychopharmacology, 2022, 47, 1784-1790.	5.4	2
9	TwinEQTL: ultrafast and powerful association analysis for eQTL and GWAS in twin studies. Genetics, 2022, 221, .	2.9	0
10	Rare proteinâ€coding variants implicate genes involved in risk of suicide death. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2021, 186, 508-520.	1.7	14
11	Assessment of suicide attempt and death in bipolar affective disorder: a combined clinical and genetic approach. Translational Psychiatry, 2021, 11, 379.	4.8	8
12	Genetic association study of childhood aggression across raters, instruments, and age. Translational Psychiatry, 2021, 11, 413.	4.8	31
13	Exploring the genetic overlap of suicideâ€related behaviors and substance use disorders. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2021, 186, 445-455.	1.7	18
14	Independent Methylome-Wide Association Studies of Schizophrenia Detect Consistent Caseâ€“Control Differences. Schizophrenia Bulletin, 2020, 46, 319-327.	4.3	15
15	Methylome-wide association findings for major depressive disorder overlap in blood and brain and replicate in independent brain samples. Molecular Psychiatry, 2020, 25, 1344-1354.	7.9	61
16	Genome-wide significant regions in 43 Utah high-risk families implicate multiple genes involved in risk for completed suicide. Molecular Psychiatry, 2020, 25, 3077-3090.	7.9	40
17	A methylation study of long-term depression risk. Molecular Psychiatry, 2020, 25, 1334-1343.	7.9	56
18	Cell Typeâ€“Specific Methylome-wide Association Studies Implicate Neurotrophin and Innate Immune Signaling in Major Depressive Disorder. Biological Psychiatry, 2020, 87, 431-442.	1.3	35

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19	Genome-Wide Association Study of Suicide Death and Polygenic Prediction of Clinical Antecedents. American Journal of Psychiatry, 2020, 177, 917-927.	7.2	66
20	Test-statistic inflation in methylome-wide association studies. Epigenetics, 2020, 15, 1163-1166.	2.7	20
21	Molecular Genetic Risk for Psychosis Is Associated With Psychosis Risk Symptoms in a Population-Based UK Cohort: Findings From Generation Scotland. Schizophrenia Bulletin, 2020, 46, 1045-1052.	4.3	12
22	SA91A GENOME-WIDE ASSOCIATION STUDY OF COMPLETED SUICIDE IN UTAH. European Neuropsychopharmacology, 2019, 29, S1238.	0.7	0
23	PREDICTING THE FUTURE DISEASE STATUS OF DEPRESSED PATIENTS FROM DNA METHYLATION PATTERNS IN BLOOD. European Neuropsychopharmacology, 2019, 29, S793-S794.	0.7	0
24	66ANALYSES OF DISEASE-ASSOCIATED AND LIKELY FUNCTIONAL VARIANTS FROM PSYCHARRAY IMPLICATE GENES INVOLVED IN RISK FOR COMPLETED SUICIDE. European Neuropsychopharmacology, 2019, 29, S1105.	0.7	0
25	Polygenic risk scoring and prediction of mental health outcomes. Current Opinion in Psychology, 2019, 27, 77-81.	4.9	25
26	Epigenetic Aging in Major Depressive Disorder. American Journal of Psychiatry, 2018, 175, 774-782.	7.2	172
27	RaMWAS: fast methylome-wide association study pipeline for enrichment platforms. Bioinformatics, 2018, 34, 2283-2285.	4.1	42
28	Methyl-CpG-Binding Domain Sequencing: MBD-seq. Methods in Molecular Biology, 2018, 1708, 171-189.	0.9	21
29	Estimation of cis-eQTL Effect Sizes Using a Log of Linear Model. Biometrics, 2018, 74, 616-625.	1.4	10
30	A Whole Methylome Study of Ethanol Exposure in Brain and Blood: An Exploration of the Utility of Peripheral Blood as Proxy Tissue for Brain in Alcohol Methylation Studies. Alcoholism: Clinical and Experimental Research, 2018, 42, 2360-2368.	2.4	12
31	Enhancing Psychosis-Spectrum Nosology Through an International Data Sharing Initiative. Schizophrenia Bulletin, 2018, 44, S460-S467.	4.3	15
32	An empirical Bayes approach for multiple tissue eQTL analysis. Biostatistics, 2018, 19, 391-406.	1.5	37
33	Convergence of evidence from a methylome-wide CpG-SNP association study and GWAS of major depressive disorder. Translational Psychiatry, 2018, 8, 162.	4.8	16
34	Building a schizophrenia genetic network: transcription factor 4 regulates genes involved in neuronal development and schizophrenia risk. Human Molecular Genetics, 2018, 27, 3246-3256.	2.9	33
35	Correcting for cell-type effects in DNA methylation studies: reference-based method outperforms latent variable approaches in empirical studies. Genome Biology, 2017, 18, 24.	8.8	25
36	Deep Sequencing of 71 Candidate Genes to Characterize Variation Associated with Alcohol Dependence. Alcoholism: Clinical and Experimental Research, 2017, 41, 711-718.	2.4	13

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37	Enrichment methods provide a feasible approach to comprehensive and adequately powered investigations of the brain methylome. Nucleic Acids Research, 2017, 45, e97-e97.	14.5	32
38	A MBD-seq protocol for large-scale methylome-wide studies with (very) low amounts of DNA. Epigenetics, 2017, 12, 743-750.	2.7	42
39	A Whole Methylome CpG-SNP Association Study of Psychosis in Blood and Brain Tissue. Schizophrenia Bulletin, 2016, 42, 1018-1026.	4.3	41
40	Deep Sequencing of Three Loci Implicated in Large-Scale Genome-Wide Association Study Smoking Meta-Analyses. Nicotine and Tobacco Research, 2016, 18, 626-631.	2.6	10
41	Combined Whole Methylome and Genomewide Association Study ImplicatesCNTN4in Alcohol Use. Alcoholism: Clinical and Experimental Research, 2015, 39, 1396-1405.	2.4	15
42	High density methylation QTL analysis in human blood via next-generation sequencing of the methylated genomic DNA fraction. Genome Biology, 2015, 16, 291.	8.8	112
43	Refinement of schizophrenia GWAS loci using methylome-wide association data. Human Genetics, 2015, 134, 77-87.	3.8	25
44	Candidate gene methylation studies are at high risk of erroneous conclusions. Epigenomics, 2015, 7, 13-15.	2.1	14
45	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660.	12.6	4,659
46	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	27.8	1,994
47	Heritability and genomics of gene expression in peripheral blood. Nature Genetics, 2014, 46, 430-437.	21.4	370
48	Reconstruction of a low-rank matrix in the presence of Gaussian noise. Journal of Multivariate Analysis, 2013, 118, 67-76.	1.0	98
49	Resolving the polymorphism-in-probe problem is critical for correct interpretation of expression QTL studies. Nucleic Acids Research, 2013, 41, e88-e88.	14.5	39
50	The Genotype-Tissue Expression (GTEx) project. Nature Genetics, 2013, 45, 580-585.	21.4	6,815
51	seeQTL: a searchable database for human eQTLs. Bioinformatics, 2012, 28, 451-452.	4.1	313
52	Matrix eQTL: ultra fast eQTL analysis via large matrix operations. Bioinformatics, 2012, 28, 1353-1358.	4.1	1,465
53	Computational tools for discovery and interpretation of expression quantitative trait loci. Pharmacogenomics, 2012, 13, 343-352.	1.3	17
54	Basal-like Breast cancer DNA copy number losses identify genes involved in genomic instability, response to therapy, and patient survival. Breast Cancer Research and Treatment, 2012, 133, 865-880.	2.5	107

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55	Sex-specific gene expression in the BXD mouse liver. Physiological Genomics, 2010, 42, 456-468.	2.3	30
56	FastMap: Fast eQTL mapping in homozygous populations. Bioinformatics, 2009, 25, 482-489.	4.1	35
57	Finding large average submatrices in high dimensional data. Annals of Applied Statistics, 2009, 3, .	1.1	111
58	The Set2/Rpd3S Pathway Suppresses Cryptic Transcription without Regard to Gene Length or Transcription Frequency. PLoS ONE, 2009, 4, e4886.	2.5	57
59	Merging two gene-expression studies via cross-platform normalization. Bioinformatics, 2008, 24, 1154-1160.	4.1	198