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	The Genotype-Tissue Expression (GTEx) project. Nature Genetics, 2013, 45, 580-585.	21.4	6,815
2	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660.	12.6	4,659
3	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	27.8	1,994
4	Matrix eQTL: ultra fast eQTL analysis via large matrix operations. Bioinformatics, 2012, 28, 1353-1358.	4.1	1,465
5	Heritability and genomics of gene expression in peripheral blood. Nature Genetics, 2014, 46, 430-437.	21.4	370
6	seeQTL: a searchable database for human eQTLs. Bioinformatics, 2012, 28, 451-452.	4.1	313
7	Merging two gene-expression studies via cross-platform normalization. Bioinformatics, 2008, 24, 1154-1160.	4.1	198
8	Epigenetic Aging in Major Depressive Disorder. American Journal of Psychiatry, 2018, 175, 774-782.	7.2	172
9	Dissecting the Shared Genetic Architecture of Suicide Attempt, Psychiatric Disorders, and Known Risk Factors. Biological Psychiatry, 2022, 91, 313-327.	1.3	114
10	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
11	Finding large average submatrices in high dimensional data. Annals of Applied Statistics, 2009, 3, .	1.1	111
12	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
13	Reconstruction of a low-rank matrix in the presence of Gaussian noise. Journal of Multivariate Analysis, 2013, 118, 67-76.	1.0	98
14	Genome-Wide Association Study of Suicide Death and Polygenic Prediction of Clinical Antecedents. American Journal of Psychiatry, 2020, 177, 917-927.	7.2	66
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	The Set2/Rpd3S Pathway Suppresses Cryptic Transcription without Regard to Gene Length or Transcription Frequency. PLoS ONE, 2009, 4, e4886.	2.5	57
17	A methylation study of long-term depression risk. Molecular Psychiatry, 2020, 25, 1334-1343.	7.9	56
18	A MBD-seq protocol for large-scale methylome-wide studies with (very) low amounts of DNA. Epigenetics, 2017, 12, 743-750.	2.7	42

#	Article	IF	Citations
19	RaMWAS: fast methylome-wide association study pipeline for enrichment platforms. Bioinformatics, 2018, 34, 2283-2285.	4.1	42
20	A Whole Methylome CpG-SNP Association Study of Psychosis in Blood and Brain Tissue. Schizophrenia Bulletin, 2016, 42, 1018-1026.	4.3	41
21	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
22	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
23	An empirical Bayes approach for multiple tissue eQTL analysis. Biostatistics, 2018, 19, 391-406.	1.5	37
24	FastMap: Fast eQTL mapping in homozygous populations. Bioinformatics, 2009, 25, 482-489.	4.1	35
25	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
26	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
27	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
28	Genetic association study of childhood aggression across raters, instruments, and age. Translational Psychiatry, 2021, 11, 413.	4.8	31
29	Sex-specific gene expression in the BXD mouse liver. Physiological Genomics, 2010, 42, 456-468.	2.3	30
30	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
31	Refinement of schizophrenia GWAS loci using methylome-wide association data. Human Genetics, 2015, 134, 77-87.	3.8	25
32	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
33	Polygenic risk scoring and prediction of mental health outcomes. Current Opinion in Psychology, 2019, 27, 77-81.	4.9	25
34	Methyl-CpG-Binding Domain Sequencing: MBD-seq. Methods in Molecular Biology, 2018, 1708, 171-189.	0.9	21
35	Test-statistic inflation in methylome-wide association studies. Epigenetics, 2020, 15, 1163-1166.	2.7	20
36	Polygenic prediction of PTSD trajectories in 9/11 responders. Psychological Medicine, 2022, 52, 1981-1989.	4.5	18

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37	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
38	Computational tools for discovery and interpretation of expression quantitative trait loci. Pharmacogenomics, 2012, 13, 343-352.	1.3	17
39	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
40	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
41	Combined Whole Methylome and Genomewide Association Study ImplicatesCNTN4in Alcohol Use. Alcoholism: Clinical and Experimental Research, 2015, 39, 1396-1405.	2.4	15
42	Enhancing Psychosis-Spectrum Nosology Through an International Data Sharing Initiative. Schizophrenia Bulletin, 2018, 44, S460-S467.	4.3	15
43	Independent Methylome-Wide Association Studies of Schizophrenia Detect Consistent Caseâ€“Control Differences. Schizophrenia Bulletin, 2020, 46, 319-327.	4.3	15
44	Candidate gene methylation studies are at high risk of erroneous conclusions. Epigenomics, 2015, 7, 13-15.	2.1	14
45	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
46	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
47	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
48	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
49	The benefit of diagnostic whole genome sequencing in schizophrenia and other psychotic disorders. Molecular Psychiatry, 2022, 27, 1435-1447.	7.9	12
50	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
51	Estimation of cis-eQTL Effect Sizes Using a Log of Linear Model. Biometrics, 2018, 74, 616-625.	1.4	10
52	Assessment of suicide attempt and death in bipolar affective disorder: a combined clinical and genetic approach. Translational Psychiatry, 2021, 11, 379.	4.8	8
53	Suicide and Psychosis: Results From a Population-Based Cohort of Suicide Death (N= 4380). Schizophrenia Bulletin, 2022, 48, 457-462.	4.3	4
54	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

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55	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
56	SA91A GENOME-WIDE ASSOCIATION STUDY OF COMPLETED SUICIDE IN UTAH. European Neuropsychopharmacology, 2019, 29, S1238.	0.7	0
57	PREDICTING THE FUTURE DISEASE STATUS OF DEPRESSED PATIENTS FROM DNA METHYLATION PATTERNS IN BLOOD. European Neuropsychopharmacology, 2019, 29, S793-S794.	0.7	0
58	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
59	TwinEQTL: ultrafast and powerful association analysis for eQTL and GWAS in twin studies. Genetics, 2022, 221, .	2.9	0