Shaunna L Clark

List of Publications by Year
in descending order

39 papers	3,324 citations	394421 19 h-index	302126 39 g-index
40 all docs	40 docs citations	40 times ranked	6079 citing authors

#	Article	IF	Citations
1	Sample Size Requirements for Structural Equation Models. Educational and Psychological Measurement, 2013, 73, 913-934.	2.4	1,885
2	Family and social risk, and parental investments during the early childhood years as predictors of low-income children's school readiness outcomes. Early Childhood Research Quarterly, 2010, 25, 432-449.	2.7	194
3	Epigenetic Aging in Major Depressive Disorder. American Journal of Psychiatry, 2018, 175, 774-782.	7.2	172
4	A methylome-wide study of aging using massively parallel sequencing of the methyl-CpG-enriched genomic fraction from blood in over 700 subjects. Human Molecular Genetics, 2014, 23, 1175-1185.	2.9	147
5	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
6	MBD-seq as a cost-effective approach for methylome-wide association studies: demonstration in 1500 caseâ€“control samples. Epigenomics, 2012, 4, 605-621.	2.1	86
7	School Attendance Problems and Youth Psychopathology: Structural Crossâ€Lagged Regression Models in Three Longitudinal Data Sets. Child Development, 2012, 83, 351-366.	3.0	79
8	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
9	A methylation study of long-term depression risk. Molecular Psychiatry, 2020, 25, 1334-1343.	7.9	56
10	Genome-wide association study of patient-rated and clinician-rated global impression of severity during antipsychotic treatment. Pharmacogenetics and Genomics, 2013, 23, 69-77.	1.5	43
11	RaMWAS: fast methylome-wide association study pipeline for enrichment platforms. Bioinformatics, 2018, 34, 2283-2285.	4.1	42
12	Patterns of Substance Use Across the First Year of College and Associated Risk Factors. Frontiers in Psychiatry, 2015, 6, 152.	2.6	41
13	A Whole Methylome CpG-SNP Association Study of Psychosis in Blood and Brain Tissue. Schizophrenia Bulletin, 2016, 42, 1018-1026.	4.3	41
14	Longitudinal Interactions of Pain and Posttraumatic Stress Disorder Symptoms in U.S. Military Service Members Following Blast Exposure. Journal of Pain, 2014, 15, 1023-1032.	1.4	35
15	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
16	Genome-Wide Meta-Analysis of Longitudinal Alcohol Consumption Across Youth and Early Adulthood. Twin Research and Human Genetics, 2015, 18, 335-347.	0.6	26
17	Evaluation of Methyl-Binding Domain Based Enrichment Approaches Revisited. PLoS ONE, 2015, 10, e0132205.	2.5	26
18	Refinement of schizophrenia GWAS loci using methylome-wide association data. Human Genetics, 2015, 134, 77-87.	3.8	25

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19	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
20	Analysis of efficacy and side effects in CATIE demonstrates drug response subgroups and potential for personalized medicine. Schizophrenia Research, 2011, 132, 114-120.	2.0	18
21	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
22	Combined Whole Methylome and Genomewide Association Study ImplicatesCNTN4in Alcohol Use. Alcoholism: Clinical and Experimental Research, 2015, 39, 1396-1405.	2.4	15
23	Psychometric modeling of abuse and dependence symptoms across six illicit substances indicates novel dimensions of misuse. Addictive Behaviors, 2016, 53, 132-140.	3.0	14
24	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
25	GW-SEM 2.0: Efficient, Flexible, and Accessible Multivariate GWAS. Behavior Genetics, 2021, 51, 343-357.	2.1	13
26	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
27	Methylomic Investigation of Problematic Adolescent Cannabis Use and Its Negative Mental Health Consequences. Journal of the American Academy of Child and Adolescent Psychiatry, 2021, 60, 1524-1532.	0.5	12
28	Dual methylation and hydroxymethylation study of alcohol use disorder. Addiction Biology, 2022, 27, e13114.	2.6	12
29	Testing the Temporal Relationship Between Maternal and Adolescent Depressive and Anxiety Symptoms in a Community Sample. Journal of Clinical Child and Adolescent Psychology, 2015, 44, 566-579.	3.4	11
30	Comparing Factor, Class, and Mixture Models of Cannabis Initiation and DSM Cannabis Use Disorder Criteria, Including Craving, in the Brisbane Longitudinal Twin Study. Twin Research and Human Genetics, 2014, 17, 89-98.	0.6	10
31	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
32	Predicting Tobacco Use across the First Year of College. American Journal of Health Behavior, 2016, 40, 484-495.	1.4	9
33	Transcriptome-wide association study for postpartum depression implicates altered B-cell activation and insulin resistance. Molecular Psychiatry, 2022, 27, 2858-2867.	7.9	9
34	Genotype-Based Ancestral Background Consistently Predicts Efficacy and Side Effects across Treatments in CATIE and STAR*D. PLoS ONE, 2013, 8, e55239.	2.5	6
35	A multi-method investigation of the personality correlates of digital aggression. Journal of Research in Personality, 2020, 85, 103923.	1.7	6
36	Clarifying the Genetic Influences on Nicotine Dependence and Quantity of Use in Cigarette Smokers. Behavior Genetics, 2021, 51, 375-384.	2.1	4

#	Article	IF	Citations
37	Using Patterns of Genetic Association to Elucidate Shared Genetic Etiologies Across Psychiatric Disorders. Behavior Genetics, 2017, 47, 405-415.	2.1	3
38	Regime Switching Modeling of Substance Use: Time-Varying and Second-Order Markov Models and Individual Probability Plots. Structural Equation Modeling, 2016, 23, 221-233.	3.8	2
39	Understanding the Longitudinal Impact of School-Based Health Centers on Student Attendance. Child and Youth Care Forum, 2023, 52, 331-350.	1.6	1