

Shaunna L Clark

List of Publications by Year in descending order

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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	Understanding the Longitudinal Impact of School-Based Health Centers on Student Attendance. <i>Child and Youth Care Forum</i> , 2023, 52, 331-350.	1.6	1
2	Dual methylation and hydroxymethylation study of alcohol use disorder. <i>Addiction Biology</i> , 2022, 27, e13114.	2.6	12
3	Transcriptome-wide association study for postpartum depression implicates altered B-cell activation and insulin resistance. <i>Molecular Psychiatry</i> , 2022, 27, 2858-2867.	7.9	9
4	Methylomic Investigation of Problematic Adolescent Cannabis Use and Its Negative Mental Health Consequences. <i>Journal of the American Academy of Child and Adolescent Psychiatry</i> , 2021, 60, 1524-1532.	0.5	12
5	GW-SEM 2.0: Efficient, Flexible, and Accessible Multivariate GWAS. <i>Behavior Genetics</i> , 2021, 51, 343-357.	2.1	13
6	Clarifying the Genetic Influences on Nicotine Dependence and Quantity of Use in Cigarette Smokers. <i>Behavior Genetics</i> , 2021, 51, 375-384.	2.1	4
7	Methylome-wide association findings for major depressive disorder overlap in blood and brain and replicate in independent brain samples. <i>Molecular Psychiatry</i> , 2020, 25, 1344-1354.	7.9	61
8	A methylation study of long-term depression risk. <i>Molecular Psychiatry</i> , 2020, 25, 1334-1343.	7.9	56
9	A multi-method investigation of the personality correlates of digital aggression. <i>Journal of Research in Personality</i> , 2020, 85, 103923.	1.7	6
10	Epigenetic Aging in Major Depressive Disorder. <i>American Journal of Psychiatry</i> , 2018, 175, 774-782.	7.2	172
11	RaMWAS: fast methylome-wide association study pipeline for enrichment platforms. <i>Bioinformatics</i> , 2018, 34, 2283-2285.	4.1	42
12	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. <i>Alcoholism: Clinical and Experimental Research</i> , 2018, 42, 2360-2368.	2.4	12
13	Convergence of evidence from a methylome-wide CpG-SNP association study and GWAS of major depressive disorder. <i>Translational Psychiatry</i> , 2018, 8, 162.	4.8	16
14	Correcting for cell-type effects in DNA methylation studies: reference-based method outperforms latent variable approaches in empirical studies. <i>Genome Biology</i> , 2017, 18, 24.	8.8	25
15	Deep Sequencing of 71 Candidate Genes to Characterize Variation Associated with Alcohol Dependence. <i>Alcoholism: Clinical and Experimental Research</i> , 2017, 41, 711-718.	2.4	13
16	Enrichment methods provide a feasible approach to comprehensive and adequately powered investigations of the brain methylome. <i>Nucleic Acids Research</i> , 2017, 45, e97-e97.	14.5	32
17	Using Patterns of Genetic Association to Elucidate Shared Genetic Etiologies Across Psychiatric Disorders. <i>Behavior Genetics</i> , 2017, 47, 405-415.	2.1	3
18	Predicting Tobacco Use across the First Year of College. <i>American Journal of Health Behavior</i> , 2016, 40, 484-495.	1.4	9

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19	Regime Switching Modeling of Substance Use: Time-Varying and Second-Order Markov Models and Individual Probability Plots. <i>Structural Equation Modeling</i> , 2016, 23, 221-233.	3.8	2
20	A Whole Methylome CpG-SNP Association Study of Psychosis in Blood and Brain Tissue. <i>Schizophrenia Bulletin</i> , 2016, 42, 1018-1026.	4.3	41
21	Psychometric modeling of abuse and dependence symptoms across six illicit substances indicates novel dimensions of misuse. <i>Addictive Behaviors</i> , 2016, 53, 132-140.	3.0	14
22	Deep Sequencing of Three Loci Implicated in Large-Scale Genome-Wide Association Study Smoking Meta-Analyses. <i>Nicotine and Tobacco Research</i> , 2016, 18, 626-631.	2.6	10
23	Genome-Wide Meta-Analysis of Longitudinal Alcohol Consumption Across Youth and Early Adulthood. <i>Twin Research and Human Genetics</i> , 2015, 18, 335-347.	0.6	26
24	Combined Whole Methylome and Genomewide Association Study Implicates <i>CNTN4</i> in Alcohol Use. <i>Alcoholism: Clinical and Experimental Research</i> , 2015, 39, 1396-1405.	2.4	15
25	Patterns of Substance Use Across the First Year of College and Associated Risk Factors. <i>Frontiers in Psychiatry</i> , 2015, 6, 152.	2.6	41
26	High density methylation QTL analysis in human blood via next-generation sequencing of the methylated genomic DNA fraction. <i>Genome Biology</i> , 2015, 16, 291.	8.8	112
27	Refinement of schizophrenia GWAS loci using methylome-wide association data. <i>Human Genetics</i> , 2015, 134, 77-87.	3.8	25
28	Testing the Temporal Relationship Between Maternal and Adolescent Depressive and Anxiety Symptoms in a Community Sample. <i>Journal of Clinical Child and Adolescent Psychology</i> , 2015, 44, 566-579.	3.4	11
29	Evaluation of Methyl-Binding Domain Based Enrichment Approaches Revisited. <i>PLoS ONE</i> , 2015, 10, e0132205.	2.5	26
30	Comparing Factor, Class, and Mixture Models of Cannabis Initiation and DSM Cannabis Use Disorder Criteria, Including Craving, in the Brisbane Longitudinal Twin Study. <i>Twin Research and Human Genetics</i> , 2014, 17, 89-98.	0.6	10
31	A methylome-wide study of aging using massively parallel sequencing of the methyl-CpG-enriched genomic fraction from blood in over 700 subjects. <i>Human Molecular Genetics</i> , 2014, 23, 1175-1185.	2.9	147
32	Longitudinal Interactions of Pain and Posttraumatic Stress Disorder Symptoms in U.S. Military Service Members Following Blast Exposure. <i>Journal of Pain</i> , 2014, 15, 1023-1032.	1.4	35
33	Sample Size Requirements for Structural Equation Models. <i>Educational and Psychological Measurement</i> , 2013, 73, 913-934.	2.4	1,885
34	Genome-wide association study of patient-rated and clinician-rated global impression of severity during antipsychotic treatment. <i>Pharmacogenetics and Genomics</i> , 2013, 23, 69-77.	1.5	43
35	Genotype-Based Ancestral Background Consistently Predicts Efficacy and Side Effects across Treatments in CATIE and STAR*D. <i>PLoS ONE</i> , 2013, 8, e55239.	2.5	6
36	MBD-seq as a cost-effective approach for methylome-wide association studies: demonstration in 1500 case-control samples. <i>Epigenomics</i> , 2012, 4, 605-621.	2.1	86

#	ARTICLE	IF	CITATIONS
37	School Attendance Problems and Youth Psychopathology: Structural Cross-Lagged Regression Models in Three Longitudinal Data Sets. <i>Child Development</i> , 2012, 83, 351-366.	3.0	79
38	Analysis of efficacy and side effects in CATIE demonstrates drug response subgroups and potential for personalized medicine. <i>Schizophrenia Research</i> , 2011, 132, 114-120.	2.0	18
39	Family and social risk, and parental investments during the early childhood years as predictors of low-income children's school readiness outcomes. <i>Early Childhood Research Quarterly</i> , 2010, 25, 432-449.	2.7	194