Xiaojian Shao

List of Publications by Year
in descending order

38 papers	2,219 citations	393982 19 h-index	360668 35 g-index
42 all docs	42 docs citations	42 times ranked	5094 citing authors

#	ARTICLE	IF	CITATIONS
1	Blood DNA methylation at TXNIP and glycemic changes in response to weight-loss diet interventions: the POUNDS lost trial. International Journal of Obesity, 2022, 46, 1122-1127.	1.6	13
2	Differentially methylated CpGs in response to growth hormone administration in children with idiopathic short stature. Clinical Epigenetics, 2022, 14, 65.	1.8	1
3	Whole-genome sequencing of H3K4me3 and DNA methylation in human sperm reveals regions of overlap linked to fertility and development. Cell Reports, 2021, 36, 109418.	2.9	25
4	Thousands of CpGs Show DNA Methylation Differences in ACPA-Positive Individuals. Genes, 2021, 12, 1349.	1.0	2
5	The impact of lockdown timing on COVID-19 transmission across US counties. EClinicalMedicine, 2021, 38, 101035.	3.2	36
6	High-resolution analyses of human sperm dynamic methylome reveal thousands of novel age-related epigenetic alterations. Clinical Epigenetics, 2020, 12, 192.	1.8	29
7	Customized MethylC-Capture Sequencing to Evaluate Variation in the Human Sperm DNA Methylome Representative of Altered Folate Metabolism. Environmental Health Perspectives, 2019, 127, 87002.	2.8	20
8	Rheumatoid arthritis-relevant DNA methylation changes identified in ACPA-positive asymptomatic individuals using methylome capture sequencing. Clinical Epigenetics, 2019, 11, 110.	1.8	14
9	GenPipes: an open-source framework for distributed and scalable genomic analyses. GigaScience, 2019, 8, .	3.3	121
10	Human age prediction based on DNA methylation of non-blood tissues. Computer Methods and Programs in Biomedicine, 2019, 171, 11-18.	2.6	12
11	Dissecting features of epigenetic variants underlying cardiometabolic risk using full-resolution epigenome profiling in regulatory elements. Nature Communications, 2019, 10, 1209.	5.8	16
12	The heterogeneity of plasma miRNA profiles in hepatocellular carcinoma patients and the exploration of diagnostic circulating miRNAs for hepatocellular carcinoma. PLoS ONE, 2019, 14, e0211581.	1.1	15
13	Aging-like Spontaneous Epigenetic Silencing Facilitates Wnt Activation, Stemness, and BrafV600E-Induced Tumorigenesis. Cancer Cell, 2019, 35, 315-328.e6.	7.7	107
14	Predicting Gene Expression Noise from Gene Expression Variations. Methods in Molecular Biology, 2018, 1751, 183-198.	0.4	0
15	Microarray Data Analysis for Transcriptome Profiling. Methods in Molecular Biology, 2018, 1751, 17-33.	0.4	6
16	Optimizing ChIP-seq peak detectors using visual labels and supervised machine learning. Bioinformatics, 2017, 33, 491-499.	1.8	28
17	Functional variation in allelic methylomes underscores a strong genetic contribution and reveals novel epigenetic alterations in the human epigenome. Genome Biology, 2017, 18, 50.	3.8	71
18	DNA methylation and lung function: an epigenome-wide association study. , 2017, , .		0

#	Article	IF	Citations
19	Comparative DNA methylation analysis to decipher common and cell type-specific patterns among multiple cell types. Briefings in Functional Genomics, 2016, 15, elw013.	1.3	10
20	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. Cell, 2016, 167, 1398-1414.e24.	13.5	573
21	Inferring the determinants of protein evolutionary rates in mammals. Gene, 2016, 584, 161-166.	1.0	0
22	Population whole-genome bisulfite sequencing across two tissues highlights the environment as the principal source of human methylome variation. Genome Biology, 2015, 16, 290.	3.8	90
23	Systematic DNA methylation analysis of multiple cell lines reveals common and specific patterns within and across tissues of origin. Human Molecular Genetics, 2015, 24, 4374-4384.	1.4	39
24	Characterization of functional methylomes by next-generation capture sequencing identifies novel disease-associated variants. Nature Communications, 2015, 6, 7211.	5.8	84
25	Deciphering the heterogeneity in DNA methylation patterns during stem cell differentiation and reprogramming. BMC Genomics, 2014, 15, 978.	1.2	17
26	iHyd-PseAAC: Predicting Hydroxyproline and Hydroxylysine in Proteins by Incorporating Dipeptide Position-Specific Propensity into Pseudo Amino Acid Composition. International Journal of Molecular Sciences, 2014, 15, 7594-7610.	1.8	190
27	Prediction of posttranslational modification sites from amino acid sequences with kernel methods. Journal of Theoretical Biology, 2014, 344, 78-87.	0.8	42
28	The dynamics of DNA methylation fidelity during mouse embryonic stem cell self-renewal and differentiation. Genome Research, 2014, 24, 1296-1307.	2.4	72
29	Knowledge-based Support Vector Classification Based on C-SVC. Procedia Computer Science, 2013, 17, 1083-1090.	1.2	14
30	DMEAS: DNA methylation entropy analysis software. Bioinformatics, 2013, 29, 2044-2045.	1.8	19
31	iSNO-AAPair: incorporating amino acid pairwise coupling into PseAAC for predicting cysteine S-nitrosylation sites in proteins. PeerJ, 2013, 1, e171.	0.9	259
32	A regression framework incorporating quantitative and negative interaction data improves quantitative prediction of PDZ domain–peptide interaction from primary sequence. Bioinformatics, 2011, 27, 383-390.	1.8	114
33	Gene expression variations are predictive for stochastic noise. Nucleic Acids Research, 2011, 39, 403-413.	6.5	32
34	Differential effects of chromatin regulators and transcription factors on gene regulation: a nucleosomal perspective. Bioinformatics, 2011, 27, 147-152.	1.8	1
35	An incremental learning algorithm for Lagrangian support vector machines. Pattern Recognition Letters, 2009, 30, 1384-1391.	2.6	28
36	Predicting DNA- and RNA-binding proteins from sequences with kernel methods. Journal of Theoretical Biology, 2009, 258, 289-293.	0.8	67

#	ARTICLE	IF	CITATIONS
37	The Study on a Real-time Forecasting Model for Short-Term Traffic Flow Based on Online Incremental LSVR. , 2008, , .		0
38	Short-Term Traffic Flow Prediction Based on Lagrange Support Vector Regression. , 2007, , 1249.		7