

# Xiaojian Shao

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3853505/publications.pdf>

Version: 2024-02-01

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	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. <i>Cell</i> , 2016, 167, 1398-1414.e24.	13.5	573
2	iSNO-AAPair: incorporating amino acid pairwise coupling into PseAAC for predicting cysteine<i>S</i>-nitrosylation sites in proteins. <i>PeerJ</i> , 2013, 1, e171.	0.9	259
3	iHyd-PseAAC: Predicting Hydroxyproline and Hydroxylysine in Proteins by Incorporating Dipeptide Position-Specific Propensity into Pseudo Amino Acid Composition. <i>International Journal of Molecular Sciences</i> , 2014, 15, 7594-7610.	1.8	190
4	GenPipes: an open-source framework for distributed and scalable genomic analyses. <i>GigaScience</i> , 2019, 8, .	3.3	121
5	A regression framework incorporating quantitative and negative interaction data improves quantitative prediction of PDZ domainâ€œpeptide interaction from primary sequence. <i>Bioinformatics</i> , 2011, 27, 383-390.	1.8	114
6	Aging-like Spontaneous Epigenetic Silencing Facilitates Wnt Activation, Stemness, and BrafV600E-Induced Tumorigenesis. <i>Cancer Cell</i> , 2019, 35, 315-328.e6.	7.7	107
7	Population whole-genome bisulfite sequencing across two tissues highlights the environment as the principal source of human methylome variation. <i>Genome Biology</i> , 2015, 16, 290.	3.8	90
8	Characterization of functional methylomes by next-generation capture sequencing identifies novel disease-associated variants. <i>Nature Communications</i> , 2015, 6, 7211.	5.8	84
9	The dynamics of DNA methylation fidelity during mouse embryonic stem cell self-renewal and differentiation. <i>Genome Research</i> , 2014, 24, 1296-1307.	2.4	72
10	Functional variation in allelic methylomes underscores a strong genetic contribution and reveals novel epigenetic alterations in the human epigenome. <i>Genome Biology</i> , 2017, 18, 50.	3.8	71
11	Predicting DNA- and RNA-binding proteins from sequences with kernel methods. <i>Journal of Theoretical Biology</i> , 2009, 258, 289-293.	0.8	67
12	Prediction of posttranslational modification sites from amino acid sequences with kernel methods. <i>Journal of Theoretical Biology</i> , 2014, 344, 78-87.	0.8	42
13	Systematic DNA methylation analysis of multiple cell lines reveals common and specific patterns within and across tissues of origin. <i>Human Molecular Genetics</i> , 2015, 24, 4374-4384.	1.4	39
14	The impact of lockdown timing on COVID-19 transmission across US counties. <i>EClinicalMedicine</i> , 2021, 38, 101035.	3.2	36
15	Gene expression variations are predictive for stochastic noise. <i>Nucleic Acids Research</i> , 2011, 39, 403-413.	6.5	32
16	High-resolution analyses of human sperm dynamic methylome reveal thousands of novel age-related epigenetic alterations. <i>Clinical Epigenetics</i> , 2020, 12, 192.	1.8	29
17	An incremental learning algorithm for Lagrangian support vector machines. <i>Pattern Recognition Letters</i> , 2009, 30, 1384-1391.	2.6	28
18	Optimizing ChIP-seq peak detectors using visual labels and supervised machine learning. <i>Bioinformatics</i> , 2017, 33, 491-499.	1.8	28

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19	Whole-genome sequencing of H3K4me3 and DNA methylation in human sperm reveals regions of overlap linked to fertility and development. <i>Cell Reports</i> , 2021, 36, 109418.	2.9	25
20	Customized MethylC-Capture Sequencing to Evaluate Variation in the Human Sperm DNA Methylome Representative of Altered Folate Metabolism. <i>Environmental Health Perspectives</i> , 2019, 127, 87002.	2.8	20
21	DMEAS: DNA methylation entropy analysis software. <i>Bioinformatics</i> , 2013, 29, 2044-2045.	1.8	19
22	Deciphering the heterogeneity in DNA methylation patterns during stem cell differentiation and reprogramming. <i>BMC Genomics</i> , 2014, 15, 978.	1.2	17
23	Dissecting features of epigenetic variants underlying cardiometabolic risk using full-resolution epigenome profiling in regulatory elements. <i>Nature Communications</i> , 2019, 10, 1209.	5.8	16
24	The heterogeneity of plasma miRNA profiles in hepatocellular carcinoma patients and the exploration of diagnostic circulating miRNAs for hepatocellular carcinoma. <i>PLoS ONE</i> , 2019, 14, e0211581.	1.1	15
25	Knowledge-based Support Vector Classification Based on C-SVC. <i>Procedia Computer Science</i> , 2013, 17, 1083-1090.	1.2	14
26	Rheumatoid arthritis-relevant DNA methylation changes identified in ACPA-positive asymptomatic individuals using methylome capture sequencing. <i>Clinical Epigenetics</i> , 2019, 11, 110.	1.8	14
27	Blood DNA methylation at TXNIP and glycemic changes in response to weight-loss diet interventions: the POUNDS lost trial. <i>International Journal of Obesity</i> , 2022, 46, 1122-1127.	1.6	13
28	Human age prediction based on DNA methylation of non-blood tissues. <i>Computer Methods and Programs in Biomedicine</i> , 2019, 171, 11-18.	2.6	12
29	Comparative DNA methylation analysis to decipher common and cell type-specific patterns among multiple cell types. <i>Briefings in Functional Genomics</i> , 2016, 15, elw013.	1.3	10
30	Short-Term Traffic Flow Prediction Based on Lagrange Support Vector Regression. , 2007, , 1249.		7
31	Microarray Data Analysis for Transcriptome Profiling. <i>Methods in Molecular Biology</i> , 2018, 1751, 17-33.	0.4	6
32	Thousands of CpGs Show DNA Methylation Differences in ACPA-Positive Individuals. <i>Genes</i> , 2021, 12, 1349.	1.0	2
33	Differential effects of chromatin regulators and transcription factors on gene regulation: a nucleosomal perspective. <i>Bioinformatics</i> , 2011, 27, 147-152.	1.8	1
34	Differentially methylated CpGs in response to growth hormone administration in children with idiopathic short stature. <i>Clinical Epigenetics</i> , 2022, 14, 65.	1.8	1
35	The Study on a Real-time Forecasting Model for Short-Term Traffic Flow Based on Online Incremental LSVR. , 2008, , .		0
36	Inferring the determinants of protein evolutionary rates in mammals. <i>Gene</i> , 2016, 584, 161-166.	1.0	0

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37	Predicting Gene Expression Noise from Gene Expression Variations. <i>Methods in Molecular Biology</i> , 2018, 1751, 183-198.	0.4	0
38	DNA methylation and lung function: an epigenome-wide association study. , 2017, , .		0