Shuying Sun

List of Publications by Year
in descending order

27 papers	591 citations	623734 14 h-index	610901 24 g-index
30 all docs	30 docs citations	30 times ranked	1272 citing authors

#	Article	IF	Citations
1	Thorough statistical analyses of breast cancer co-methylation patterns. BMC Genomic Data, 2022, 23, 29.	1.7	3
2	Statistical and bioinformatic analysis of hemimethylation patterns in non-small cell lung cancer. BMC Cancer, 2021, 21, 268.	2.6	1
3	Hemimethylation Patterns in Breast Cancer Cell Lines. Cancer Informatics, 2019, 18, 117693511987295.	1.9	4
4	Preliminary Analysis of Within-Sample Co-methylation Patterns in Normal and Cancerous Breast Samples. Cancer Informatics, 2019, 18, 117693511988051.	1.9	3
5	Within-sample co-methylation patterns in normal tissues. BioData Mining, 2019, 12, 9.	4.0	8
6	Integrative analysis of gene expression and methylation data for breast cancer cell lines. BioData Mining, 2018, 11, 13.	4.0	8
7	Statistical Genetic Terminology. Methods in Molecular Biology, 2017, 1666, 1-9.	0.9	2
8	DNA Methylation Heterogeneity Patterns in Breast Cancer Cell Lines. Cancer Informatics, 2016, 15s4, CIN.S40300.	1.9	3
9	HMM-Fisher: identifying differential methylation using a hidden Markov model and Fisherâ€™s exact test. Statistical Applications in Genetics and Molecular Biology, 2016, 15, 55-67.	0.6	25
10	HMM-DM: identifying differentially methylated regions using a hidden Markov model. Statistical Applications in Genetics and Molecular Biology, 2016, 15, 69-81.	0.6	24
11	Comparing five statistical methods of differential methylation identification using bisulfite sequencing data. Statistical Applications in Genetics and Molecular Biology, 2016, 15, 173-91.	0.6	20
12	Epigenetic Loss of MLH1 Expression in Normal Human Hematopoietic Stem Cell Clones is Defined by the Promoter CpG Methylation Pattern Observed by High-Throughput Methylation Specific Sequencing. International Journal of Stem Cell Research and Therapy, 2016, 3, .	1.0	6
13	HMPL: A Pipeline for Identifying Hemimethylation Patterns by Comparing Two Samples. Cancer Informatics, 2015, 14s2, CIN.S17286.	1.9	6
14	Comparing a few SNP calling algorithms using low-coverage sequencing data. BMC Bioinformatics, 2013, 14, 274.	2.6	96
15	MethyQA: a pipeline for bisulfite-treated methylation sequencing quality assessment. BMC Bioinformatics, 2013, 14, 259.	2.6	21
16	Global mutational profiling of formalin-fixed human colon cancers from a pathology archive. Modern Pathology, 2012, 25, 1599-1608.	5.5	22
17	How do alignment programs perform on sequencing data with varying qualities and from repetitive regions?. BioData Mining, 2012, 5, 6.	4.0	33
18	Genetic Terminology. Methods in Molecular Biology, 2012, 850, 1-9.	0.9	16

#	Article	IF	Citations
19	Preprocessing differential methylation hybridization microarray data. BioData Mining, 2011, 4, 13.	4.0	16
20	Identifying hypermethylated CpG islands using a quantile regression model. BMC Bioinformatics, 2011, 12, 54.	2.6	7
21	How old is this mutation? - a study of three Ashkenazi Jewish founder mutations. BMC Genetics, 2010, 11, 39.	2.7	21
22	Genome-Wide DNA Methylation Profiling in 40 Breast Cancer Cell Lines. Lecture Notes in Computer Science, 2010, , 277-284.	1.3	1
23	Identifying differentially methylated genes using mixed effect and generalized least square models. BMC Bioinformatics, 2009, 10, 404.	2.6	7
24	Origins and Prevalence of the American Founder Mutation of MSH2. Cancer Research, 2008, 68, 2145-2153.	0.9	34
25	Breast Cancerâ€"Associated Fibroblasts Confer AKT1-Mediated Epigenetic Silencing of Cystatin M in Epithelial Cells. Cancer Research, 2008, 68, 10257-10266.	0.9	65
26	Haplotype inference using a Bayesian Hidden Markov model. Genetic Epidemiology, 2007, 31, 937-948.	1.3	25
27	Association between the interleukin-1 family gene cluster and psoriatic arthritis. Arthritis and Rheumatism, 2006, 54, 2321-2325.	6.7	114