

ZINBA integrates local covariates with DNA-seq data to
of enrichment, even within amplified genomic regions

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Citation Report

#	ARTICLE	IF	CITATIONS
1	ChIP-Seq: technical considerations for obtaining high-quality data. <i>Nature Immunology</i> , 2011, 12, 918-922.	7.0	199
2	An integrated strategy for identification of both sharp and broad peaks from next-generation sequencing data. <i>Genome Biology</i> , 2011, 12, 120.	13.9	3
3	Tumor-specific retargeting of an oncogenic transcription factor chimera results in dysregulation of chromatin and transcription. <i>Genome Research</i> , 2012, 22, 259-270.	2.4	96
4	Copy-number-aware differential analysis of quantitative DNA sequencing data. <i>Genome Research</i> , 2012, 22, 2489-2496.	2.4	28
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6	Using formaldehyde-assisted isolation of regulatory elements (FAIRE) to isolate active regulatory DNA. <i>Nature Protocols</i> , 2012, 7, 256-267.	5.5	274
7	Site identification in high-throughput RNA-protein interaction data. <i>Bioinformatics</i> , 2012, 28, 3013-3020.	1.8	272
8	Normalization of ChIP-seq data with control. <i>BMC Bioinformatics</i> , 2012, 13, 199.	1.2	100
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21	Improving detection of copy-number variation by simultaneous bias correction and read-depth segmentation. <i>Nucleic Acids Research</i> , 2013, 41, 1519-1532.	6.5	33
22	kmer-SVM: a web server for identifying predictive regulatory sequence features in genomic data sets. <i>Nucleic Acids Research</i> , 2013, 41, W544-W556.	6.5	118
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