

deepTools: a flexible platform for exploring deep-seque

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Citation Report

#	ARTICLE	IF	CITATIONS
1	metaseq: a Python package for integrative genome-wide analysis reveals relationships between chromatin insulators and associated nuclear mRNA. <i>Nucleic Acids Research</i> , 2014, 42, 9158-9170.	6.5	26
2	Insights into the epigenomic landscape of the human malaria vector <i>Anopheles gambiae</i> . <i>Frontiers in Genetics</i> , 2014, 5, 277.	1.1	22
3	Dynamic DNA methylation orchestrates cardiomyocyte development, maturation and disease. <i>Nature Communications</i> , 2014, 5, 5288.	5.8	272
4	Application of histone modification-specific interaction domains as an alternative to antibodies. <i>Genome Research</i> , 2014, 24, 1842-1853.	2.4	52
5	Suv39h-Dependent H3K9me3 Marks Intact Retrotransposons and Silences LINE Elements in Mouse Embryonic Stem Cells. <i>Molecular Cell</i> , 2014, 55, 277-290.	4.5	278
6	Global regulation of heterochromatin spreading by Leo1. <i>Open Biology</i> , 2015, 5, 150045.	1.5	43
7	A general concept for consistent documentation of computational analyses. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav050.	1.4	9
8	Alternative splicing detection workflow needs a careful combination of sample prep and bioinformatics analysis. <i>BMC Bioinformatics</i> , 2015, 16, S2.	1.2	16
9	cChIP-seq: a robust small-scale method for investigation of histone modifications. <i>BMC Genomics</i> , 2015, 16, 1083.	1.2	14
10	Liver ChIP-seq analysis in FGF19-treated mice reveals SHP as a global transcriptional partner of SREBP-2. <i>Genome Biology</i> , 2015, 16, 268.	3.8	33
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15	Epigenomic analysis of the HOX gene loci reveals mechanisms that may control canonical expression patterns in AML and normal hematopoietic cells. <i>Leukemia</i> , 2015, 29, 1279-1289.	3.3	96
16	Genome-wide comparison of PU.1 and Spi-B binding sites in a mouse B lymphoma cell line. <i>BMC Genomics</i> , 2015, 16, 76.	1.2	39
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18	Deciphering the Epigenetic Code of Cardiac Myocyte Transcription. <i>Circulation Research</i> , 2015, 117, 413-423.	2.0	71

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21	High-Affinity Sites Form an Interaction Network to Facilitate Spreading of the MSL Complex across the X Chromosome in Drosophila. <i>Molecular Cell</i> , 2015, 60, 146-162.	4.5	70
22	Adrenergic Repression of the Epigenetic Reader MeCP2 Facilitates Cardiac Adaptation in Chronic Heart Failure. <i>Circulation Research</i> , 2015, 117, 622-633.	2.0	57
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38	Reprogramming cell fate with a genome-scale library of artificial transcription factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E8257-E8266.	3.3	23
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146	EIN2 mediates direct regulation of histone acetylation in the ethylene response. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 10274-10279.	3.3	129
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