

Rapid and Pervasive Changes in Genome-wide Enhance Development

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Variation in Vertebrate Cis-Regulatory Elements in Evolution and Disease. <i>Transcription</i> , 2014, 5, e28848.	1.7	16
3	Chromatin remodeler mutations in human cancers: epigenetic implications. <i>Epigenomics</i> , 2014, 6, 397-414.	1.0	35
4	Tissue-Specific RNA Expression Marks Distant-Acting Developmental Enhancers. <i>PLoS Genetics</i> , 2014, 10, e1004610.	1.5	105
5	Integrating Diverse Datasets Improves Developmental Enhancer Prediction. <i>PLoS Computational Biology</i> , 2014, 10, e1003677.	1.5	149
6	High-resolution mapping of transcriptional dynamics across tissue development reveals a stable mRNA-tRNA interface. <i>Genome Research</i> , 2014, 24, 1797-1807.	2.4	89
7	Tissue-Resident Macrophage Enhancer Landscapes Are Shaped by the Local Microenvironment. <i>Cell</i> , 2014, 159, 1312-1326.	13.5	1,705
8	A dynamic CTCF chromatin binding landscape promotes DNA hydroxymethylation and transcriptional induction of adipocyte differentiation. <i>Nucleic Acids Research</i> , 2014, 42, 10943-10959.	6.5	71
9	Transcriptional Regulation of Enhancers Active in Protodomains of the Developing Cerebral Cortex. <i>Neuron</i> , 2014, 82, 989-1003.	3.8	99
10	Tissue-specific SMARCA4 binding at active and repressed regulatory elements during embryogenesis. <i>Genome Research</i> , 2014, 24, 920-929.	2.4	63
11	Axons hooked to Schwann cell metabolism. <i>Nature Neuroscience</i> , 2014, 17, 1293-1295.	7.1	7
12	Promoting FOS to an enhanced position. <i>Nature Neuroscience</i> , 2014, 17, 1291-1293.	7.1	1
13	Otx2 and Oct4 Drive Early Enhancer Activation during Embryonic Stem Cell Transition from Naive Pluripotency. <i>Cell Reports</i> , 2014, 7, 1968-1981.	2.9	117
14	The role of chromatin dynamics in immune cell development. <i>Immunological Reviews</i> , 2014, 261, 9-22.	2.8	57
15	Transcriptional and epigenetic networks of helper T and innate lymphoid cells. <i>Immunological Reviews</i> , 2014, 261, 23-49.	2.8	76
16	Enhancer Function: Mechanistic and Genome-Wide Insights Come Together. <i>Molecular Cell</i> , 2014, 55, 5-14.	4.5	199
17	Quantitation of interactions between two DNA loops demonstrates loop domain insulation in <i>E. coli</i> cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4449-57.	3.3	25
18	Genome-wide identification and characterization of functional neuronal activity-dependent enhancers. <i>Nature Neuroscience</i> , 2014, 17, 1330-1339.	7.1	244
19	Global transcriptome analysis and enhancer landscape of human primary T follicular helper and T effector lymphocytes. <i>Blood</i> , 2014, 124, 3719-3729.	0.6	55

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20	DNase I hypersensitivity analysis of the mouse brain and retina identifies region-specific regulatory elements. <i>Epigenetics and Chromatin</i> , 2015, 8, 8.	1.8	60
22	Discrete domains of gene expression in germinal layers distinguish the development of gyrencephaly. <i>EMBO Journal</i> , 2015, 34, 1859-1874.	3.5	146
23	Occupancy by key transcription factors is a more accurate predictor of enhancer activity than histone modifications or chromatin accessibility. <i>Epigenetics and Chromatin</i> , 2015, 8, 16.	1.8	100
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25	Transcriptional Enhancers: Bridging the Genome and Phenome. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2015, 80, 17-26.	2.0	28
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