

# An atlas of active enhancers across human cell types and

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Approaches for establishing the function of regulatory genetic variants involved in disease. <i>Genome Medicine</i> , 2014, 6, 92.	3.6	34
2	lncRNA and gene looping. <i>Transcription</i> , 2014, 5, e28658.	1.7	26
3	Enhancer variants: evaluating functions in common disease. <i>Genome Medicine</i> , 2014, 6, 85.	3.6	195
4	OncoCis: annotation of cis-regulatory mutations in cancer. <i>Genome Biology</i> , 2014, 15, 485.	3.8	22
5	Non-coding RNA derived from the region adjacent to the human HO-1 E2 enhancer selectively regulates HO-1 gene induction by modulating Pol II binding. <i>Nucleic Acids Research</i> , 2014, 42, 13599-13614.	6.5	50
6	De-repressing lncRNA-Targeted Genes to Upregulate Gene Expression: Focus on Small Molecule Therapeutics. <i>Molecular Therapy - Nucleic Acids</i> , 2014, 3, e196.	2.3	63
7	A Role for Noncoding Variation in Schizophrenia. <i>Cell Reports</i> , 2014, 9, 1417-1429.	2.9	225
8	UCbase 2.0: ultraconserved sequences database (2014 update). <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau062-bau062.	1.4	19
9	Tissue-Specific RNA Expression Marks Distant-Acting Developmental Enhancers. <i>PLoS Genetics</i> , 2014, 10, e1004610.	1.5	105
10	The Case for Junk DNA. <i>PLoS Genetics</i> , 2014, 10, e1004351.	1.5	202
11	Identification of TNF- $\alpha$ -Responsive Promoters and Enhancers in the Intestinal Epithelial Cell Model Caco-2. <i>DNA Research</i> , 2014, 21, 569-583.	1.5	12
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13	A PiggyBac-mediated approach for muscle gene transfer or cell therapy. <i>Stem Cell Research</i> , 2014, 13, 390-403.	0.3	12
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15	Transcription factor binding predicts histone modifications in human cell lines. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 13367-13372.	3.3	109
16	Convergent Transcription at Intragenic Super-Enhancers Targets AID-Initiated Genomic Instability. <i>Cell</i> , 2014, 159, 1538-1548.	13.5	221
17	Conserved Higher-Order Chromatin Regulates NMDA Receptor Gene Expression and Cognition. <i>Neuron</i> , 2014, 84, 997-1008.	3.8	76
18	Transcriptomic analysis of mononuclear phagocyte differentiation and activation. <i>Immunological Reviews</i> , 2014, 262, 74-84.	2.8	62

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19	A shared architecture for promoters and enhancers. <i>Nature Genetics</i> , 2014, 46, 1253-1254.	9.4	18
20	<i>Arabidopsis</i> DPB3-1, a DREB2A Interactor, Specifically Enhances Heat Stress-Induced Gene Expression by Forming a Heat Stress-Specific Transcriptional Complex with NF-Y Subunits. <i>Plant Cell</i> , 2014, 26, 4954-4973.	3.1	143
21	Enhancer RNAs. <i>Cell Cycle</i> , 2014, 13, 3151-3152.	1.3	16
22	Environment Drives Selection and Function of Enhancers Controlling Tissue-Specific Macrophage Identities. <i>Cell</i> , 2014, 159, 1327-1340.	13.5	1,078
23	TermGenie – a web-application for pattern-based ontology class generation. <i>Journal of Biomedical Semantics</i> , 2014, 5, 48.	0.9	30
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26	Genetic variation within transcriptional regulatory elements and its implications for human disease. <i>Biological Chemistry</i> , 2014, 395, 1453-1460.	1.2	7
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32	Analysis of nascent RNA identifies a unified architecture of initiation regions at mammalian promoters and enhancers. <i>Nature Genetics</i> , 2014, 46, 1311-1320.	9.4	572
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44	Intratumor DNA Methylation Heterogeneity Reflects Clonal Evolution in Aggressive Prostate Cancer. <i>Cell Reports</i> , 2014, 8, 798-806.	2.9	219
45	Transcriptional and epigenetic networks of helper T and innate lymphoid cells. <i>Immunological Reviews</i> , 2014, 261, 23-49.	2.8	76
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