

# Genome-Wide Quantitative Enhancer Activity Maps Ide

Science

339, 1074-1077

DOI: [10.1126/science.1232542](https://doi.org/10.1126/science.1232542)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Enhanced dissection of the regulatory genome. <i>Nature Methods</i> , 2013, 10, 710-712.	9.0	2
2	A Common Set of DNA Regulatory Elements Shapes <i>Drosophila</i> Appendages. <i>Developmental Cell</i> , 2013, 27, 306-318.	3.1	133
3	Topology of mammalian developmental enhancers and their regulatory landscapes. <i>Nature</i> , 2013, 502, 499-506.	13.7	463
5	Highly parallel assays of tissue-specific enhancers in whole <i>Drosophila</i> embryos. <i>Nature Methods</i> , 2013, 10, 774-780.	9.0	55
6	The role of <i>Dichaete</i> in transcriptional regulation during <i>Drosophila</i> embryonic development. <i>BMC Genomics</i> , 2013, 14, 861.	1.2	31
7	Pathogenic variants in non-coding sequences. <i>Clinical Genetics</i> , 2013, 84, 422-428.	1.0	31
8	Enhancing the hunt for enhancers. <i>Nature Reviews Genetics</i> , 2013, 14, 151-151.	7.7	2
9	Modification of Enhancer Chromatin: What, How, and Why?. <i>Molecular Cell</i> , 2013, 49, 825-837.	4.5	1,200
10	Low-affinity transcription factor binding sites shape morphogen responses and enhancer evolution. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20130018.	1.8	96
11	Many human accelerated regions are developmental enhancers. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20130025.	1.8	188
12	Massively parallel synthetic promoter assays reveal the in vivo effects of binding site variants. <i>Genome Research</i> , 2013, 23, 1908-1915.	2.4	99
13	Patient Individual Parameterization of Cardiac Ventricular Tachycardia Termination Algorithm. <i>Biomedizinische Technik</i> , 2013, 58 Suppl 1, .	0.9	0
14	Systematic dissection of regulatory motifs in 2000 predicted human enhancers using a massively parallel reporter assay. <i>Genome Research</i> , 2013, 23, 800-811.	2.4	298
15	Chromatin and epigenetic features of long-range gene regulation. <i>Nucleic Acids Research</i> , 2013, 41, 7185-7199.	6.5	96
16	Regulatory Genomics – Decoding <i>Drosophila</i> Regulatory Sequences. <i>Biomedizinische Technik</i> , 2013, 58 Suppl 1, .	0.9	0
17	DNA sequencing methods in human genetics and disease research. <i>F1000prime Reports</i> , 2013, 5, 34.	5.9	6
18	A Set of Structural Features Defines the Cis-Regulatory Modules of Antenna-Expressed Genes in <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2014, 9, e104342.	1.1	2
19	A Functional Insulator Screen Identifies NURF and dREAM Components to Be Required for Enhancer-Blocking. <i>PLoS ONE</i> , 2014, 9, e107765.	1.1	39

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20	High-throughput engineering of a mammalian genome reveals building principles of methylation states at CG rich regions. <i>ELife</i> , 2014, 3, e04094.	2.8	66
21	Dissection of thousands of cell type-specific enhancers identifies dinucleotide repeat motifs as general enhancer features. <i>Genome Research</i> , 2014, 24, 1147-1156.	2.4	129
22	Variation in Vertebrate Cis-Regulatory Elements in Evolution and Disease. <i>Transcription</i> , 2014, 5, e28848.	1.7	16
23	Evidence for Deep Regulatory Similarities in Early Developmental Programs across Highly Diverged Insects. <i>Genome Biology and Evolution</i> , 2014, 6, 2301-2320.	1.1	37
24	Activation of Muscle Enhancers by MyoD and epigenetic modifiers. <i>Journal of Cellular Biochemistry</i> , 2014, 115, n/a-n/a.	1.2	15
25	Chromatin Properties of Regulatory DNA Probed by Manipulation of Transcription Factors. <i>Journal of Computational Biology</i> , 2014, 21, 569-577.	0.8	4
26	Diverse patterns of genomic targeting by transcriptional regulators in <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2014, 24, 1224-1235.	2.4	31
27	An improved predictive recognition model for Cys2-His2 zinc finger proteins. <i>Nucleic Acids Research</i> , 2014, 42, 4800-4812.	6.5	66
28	Insulator function and topological domain border strength scale with architectural protein occupancy. <i>Genome Biology</i> , 2014, 15, R82.	13.9	275
29	Transcriptional enhancers: from properties to genome-wide predictions. <i>Nature Reviews Genetics</i> , 2014, 15, 272-286.	7.7	1,136
30	FIREWACH: high-throughput functional detection of transcriptional regulatory modules in mammalian cells. <i>Nature Methods</i> , 2014, 11, 559-565.	9.0	95
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34	Enhancer Malfunction in Cancer. <i>Molecular Cell</i> , 2014, 53, 859-866.	4.5	156
35	Dissecting the Causal Genetic Mechanisms of Coronary Heart Disease. <i>Current Atherosclerosis Reports</i> , 2014, 16, 406.	2.0	11
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39	Enhancer biology and enhanceropathies. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 210-219.	3.6	259
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91	Identification of active transcriptional regulatory elements from GRO-seq data. <i>Nature Methods</i> , 2015, 12, 433-438.	9.0	198

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130	Epigenetics, Enhancers, and Cancer. Energy Balance and Cancer, 2016, , 29-53.	0.2	1
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