

# A high-resolution map of human evolutionary constraints

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Combinatorial Patterning of Chromatin Regulators Uncovered by Genome-wide Location Analysis in Human Cells. <i>Cell</i> , 2011, 147, 1628-1639.	13.5	303
2	Mammalian alignments reveal human functional elements. <i>Nature Reviews Genetics</i> , 2011, 12, 807-807.	7.7	4
3	Locating protein-coding sequences under selection for additional, overlapping functions in 29 mammalian genomes. <i>Genome Research</i> , 2011, 21, 1916-1928.	2.4	83
4	New families of human regulatory RNA structures identified by comparative analysis of vertebrate genomes. <i>Genome Research</i> , 2011, 21, 1929-1943.	2.4	100
5	What fraction of the human genome is functional?. <i>Genome Research</i> , 2011, 21, 1769-1776.	2.4	134
6	Evidence of abundant stop codon readthrough in <i>Drosophila</i> and other metazoa. <i>Genome Research</i> , 2011, 21, 2096-2113.	2.4	196
7	Coevolution within and between Regulatory Loci Can Preserve Promoter Function Despite Evolutionary Rate Acceleration. <i>PLoS Genetics</i> , 2012, 8, e1002961.	1.5	47
8	Hundreds of conserved non-coding genomic regions are independently lost in mammals. <i>Nucleic Acids Research</i> , 2012, 40, 11463-11476.	6.5	48
9	A Resolution of the Mutation Load Paradox in Humans. <i>Genetics</i> , 2012, 191, 1321-1330.	1.2	50
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11	Regulation of Cell Adhesion and Migration by Kindlin-3 Cleavage by Calpain. <i>Journal of Biological Chemistry</i> , 2012, 287, 40012-40020.	1.6	30
12	Nuclear Gene Variation in Wild Brown Rats. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 1661-1664.	0.8	21
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20	The expanding scope of DNA sequencing. <i>Nature Biotechnology</i> , 2012, 30, 1084-1094.	9.4	280
21	A Novel Evolutionarily Conserved Element Is a General Transcriptional Repressor of p21WAF1/CIP1. <i>Cancer Research</i> , 2012, 72, 6236-6246.	0.4	5
22	Evolutionary Dynamics of Gene and Isoform Regulation in Mammalian Tissues. <i>Science</i> , 2012, 338, 1593-1599.	6.0	853
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54	Characterization of Enhancer Function from Genome-Wide Analyses. <i>Annual Review of Genomics and Human Genetics</i> , 2012, 13, 29-57.	2.5	86

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