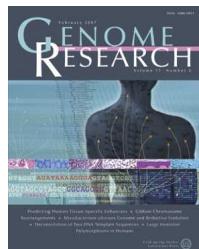


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Cover Deciphering of the genetic code of distant, tissue-specific enhancers in the human genome by the Enhancer Identification (EI) method. EI approach is based on the integration of multiple complementary computational approaches and genomic datasets that include (a) microarray multi-tissue gene expression data, (b) comparative genomics analysis of human and mouse genomes, and (c) analysis of patterns of transcription factor binding sites (TFBS). In summary, this advance in deciphering the so-called second code of the human genome promotes the ongoing foray into the mapping of human gene regulatory networks. (Cover illustration by Bang Wong, ClearScience, www.clearscience.info. [For details, see Pennacchio et al., pp. 201–211.])