



**Figure 23.** Instructive histone modifications mark functional genomic elements. Epigenomic mapping efforts identified instructive histone modifications and epigenetic factors that correlate with distinct genomic elements: H3K4me1, H3K27ac, and p300 (HAT) peak over enhancers (E), whereas CTCF (zinc-finger factor) accumulates at insulators (I). For active genes, there is an H3K4me3 peak at the promoter (P) and an extended tracking of H3K36me3, which reflects transcription of the elongating RNA Pol II across the gene body. Signatures for repressed chromatin regions are H3K27me3 (facultative heterochromatin, e.g., at Hox clusters) and H3K9me3 (constitutive heterochromatin, e.g., at repeats).