About yeast nucleosomes... Chromatin is composed of arrays of nucleosomes, with each nucleosome comprising an octamer formed by two copies each of the H2A-H2B and H3-H4 heterodimers. In Saccharomyces cerevisiae, each of the canonical histones is encoded by two genes: H2A by HTA1 and HTA2, H2B by HTB1 and HTB2, H3 by HHT1 and HHT2, and H4 by HHF1 and HHF2. The eight genes are organized into four pairs of divergently-transcribed loci: HTA1-HTB1 and HTA2-HTB2, each encoding histone proteins H2A and H2B; and HHT1-HHF1 and HHT2-HHF2, each encoding histone proteins H3 and H4. As a result of this redundancy, deletion of any one histone locus does not cause lethality. The H3-H4 protein dimers interact via a four-helix bundle at the H3 C-termini, and the H2A-H2B dimers bind to the resulting central H3-H4 tetramer via a similar four-helix bundle interaction between the H2B and H4 C-termini. Approximately 150 bp of duplex DNA is wound onto the histone octamer as two turns of a negative superhelix. A single copy of the linker histone H1binds between the superhelices at the site of DNA entry and exit. In some nucleosomes, the histone variant H2A.Zis substituted for the canonical H2A in a wide, but nonrandom, genomic distribution, enriched in promoter regions as compared to coding regions. The positioning of nucleosomes along chromatin has been implicated in the regulation of gene expression, since the packaging of DNA into nucleosomes affects sequence accessibility. Nucleosomes prevent many DNA-binding proteins from approaching their sites, whereas appropriately positioned nucleosomes can bring discontiguous DNA sequences into close proximity to promote transcription.About the H1 linker histone... Histone H1 is a linker histone that binds the outside of nucleosomes and modifies chromatin structure. Saccharomyces cerevisiae encodes a single H1 linker histone, Hho1p, which facilitates chromatin folding and contains two globular domains. The ability of Hho1p to facilitate chromatin folding is conferred by its lysine-rich C-terminal tail, and the globular domains appear to act as structure recognition modules, placing the lysine-rich C-terminal tail at a location on the nucleosome where it assumes a helical character when associated with the linker DNA. The C-terminal tail also effects partial charge neutralization of the DNA that connects adjacent nucleosomes, which is assumed to stabilize chromatin fibers. Hho1p inhibits transcriptional silencing and reinforces the action of several types of barrier elements, which are DNA sequences that protect transcriptionally active euchromatic regions from encroachment by neighboring transcriptionally repressed heterochromatin. The H1 histones form a large family of proteins, with eight isotypes identified in mammals, including five somatic isotypes, a testis-specific H1t, an oocyte-specific H1oo, and H1o, a replacement variant associated with terminally differentiated cell types and related to H5, which is found in nucleated avian erythrocytes. The canonical metazoan H1 contains a globular domain flanked by variable N-terminal and C-terminal regions. Some lower eukaryotes have atypical linker histones, such as Tetrahymena, in which H1 resembles an isolated C-terminal tail, or S. cerevisiae, where H1 contains the two globular domains mentioned above.