

Worksheet - 1

1. Activated JAKs catalyze the tyrosine phosphorylation of cytokine-receptor cytoplasmic domains, facilitating the creation of binding sites for the Src-homology-2 domain of the STAT proteins.
2. We exposed yeast to 20 minutes of amino acid deprivation and conducted measurements of ribosome footprints and mRNA abundance.
3. The assumptions regarding the uniformity of evolutionary rates across the genome, the independent evolution of sites based on their conservation status, and the equivalence of phylogenetic models for conserved and nonconserved regions oversimplify the complex process of sequence evolution in eukaryotic genomes.
4. The clarity regarding both the variety of mechanisms that cells may employ to interpret morphogens and the significance of design features such as feedback or local cell-cell communication remains uncertain.
5. Furthermore, applying new technologies to further understand the biology of the adipocyte, such as location analysis, global DNase hypersensitivity, high-throughput RNA-interference screens, and computational strategies, holds promise for enhancing our knowledge of this once-neglected cell.
6. In the mouse, the sequences of large noncoding RNAs, likely lacking a 3' polyA tail, were reconstructed from truncated cDNA fragments.
7. Localized fluctuations in substitution rate are commonly utilized to infer the phenotypic significance of genomic sequences.
8. Several promoters showed significant positive correlations between the estimated distribution of K from footprinting and the nucleosome score estimated from T-cells.
9. In this study, we conducted a comparative analysis of the radial distribution pattern of human chromosome 18- and 19-homologous chromatin across seven different primate species using three-dimensional fluorescence in situ hybridization.