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The aberrant chromatin interactions observed at the EPHA4 locus in the present study exemplify how the disruption of TAD structure by eliminating or interfering with boundary elements can lead to the functional rewiring of gene-enhancer interactions (schematically shown in Figure 7). This model also illustrates how different types of large ...

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Chromatin remodeling is the dynamic modification of chromatin architecture to allow access of condensed genomic DNA to the regulatory transcription machinery proteins, and thereby control gene expression. Such remodeling is principally carried out by 1) covalent histone modifications by specific enzymes, e.g., histone acetyltransferases (HATs), deacetylases, methyltransferases, and kinases, and ...

[Nucleosome - Wikipedia](#)

History of ATAC-Seq. The ATAC-Seq method was first published in 2013 in the journal Nature Methods by lead researcher Jason Buenro in the labs of Howard Chang and William Greenleaf at Stanford University.. At that time, they were looking for an alternative to current methods that were used to study open chromatin, nucleosome positioning, and transcription factor occupancy.

[A human cell atlas of fetal chromatin accessibility | Science](#)

In cancer, lncRNAs work through multiple mechanisms such as chromatin remodeling, chromatin interactions, ceRNAs, and natural antisense transcripts (NATs) (). lncRNAs can interface with chromatin remodeling machinery in several ways, including acting as signal lncRNAs or scaffold lncRNAs. Recently, another mechanism of action by which lncRNAs function to regulate transcription has been posited.

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Nonpolar (Hydrophobic) Amino Acids. The nonpolar amino acids can largely be subdivided into two more specific classes, the aliphatic amino acids and the aromatic amino acids. The aliphatic amino acids (glycine, alanine, valine, leucine, isoleucine, and proline) typically contain branched hydrocarbon chains with the simplest being glycine to the more complicated structures of leucine and valine.

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Accurate inference of gene interactions and causality is required for pathway reconstruction, which remains a major goal for many studies. Here, we take advantage of 2 recent technological developments, single-cell RNA sequencing and deep learning to propose an encoding scheme for gene expression data. We use this encoding in a supervised framework to perform several different types of ...

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This gene encodes a protein that belongs to the High Mobility Group-box superfamily. The encoded non-histone, nuclear DNA-binding protein regulates transcription, and is involved in organization of DNA. This protein plays a role in several cellular processes, including inflammation, cell differentiation and tumor cell migration. Multiple pseudogenes of this gene have been identified.

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The human alpha globin gene cluster located on chromosome 16 spans about 30 kb and includes seven loci: 5'- zeta - pseudozeta - mu - pseudoalpha-1 - alpha-2 - alpha-1 - theta - 3'. The alpha-2 (HBA2) and alpha-1 (HBA1) coding sequences are identical. These genes differ slightly over the 5' untranslated regions and the introns, but they differ significantly over the 3' untranslated regions.

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BIRD - [C++/R] - BIRD is a tool for predicting chromatin accessibility and inferring regulatory element activities in single cells using scRNA-seq. Global prediction of chromatin accessibility using small-cell-number and single-cell RNA-seq; ChromA - [C++/Fortran] - Chromatin Accessibility Annotation Tool.