**提供哪些下载？格式？**

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**表格

描述已自动生成**

**放什么结果的visualization图？**

**Intro**

**Introduction**

TM-Map is a manually curated, open-access database of transcription factor (TF)-mediated chromatin interactions in humans, derived from HiChIP and ChIA-PET datasets. This resource allows users to find locations of chromatin loops mediated by specific TFs. The current version of TM-Map includes data from 300 HiChIP and ChIA-PET datasets, covering 33 articles, CTCF and 15 human TFs, and 61 cell lines.

TM-Map provides the following information:

* Metadata of samples
* Locations of TF binding sites
* Locations of TF-mediated loops
* Target genes of TF-mediated loops
* GWAS SNPs located in loops, with annotation and ranking of these SNPs
* eQTLs located in loops with corresponding target genes

All the samples can be searched and graphically visualized on the "Search" page. Additionally, statistics of these samples are presented and visualized on the "Statistics" page. Users can also download files of peaks, loops, and loop annotations, with detailed download guidance and file formats available on the "Tutorial" page.

This website has been tested on Chrome, Microsoft Edge, and Firefox browsers. Microsoft IE may not work well.

**Cite us:**

TM-Map: comprehensive TF-mediated chromatin interaction map reveals human disease loci. *Nature* 30 Oct, 2024

**HiChIP**

HiChIP (High-throughput Chromosome Conformation Capture combined with Chromatin ImmunoPrecipitation) is a technique that integrates the advantages of Hi-C and ChIP-seq. It maps 3D genome interactions mediated by specific proteins, offering insights into how protein-DNA interactions influence the spatial organization of the genome and gene regulation.

**ChIA-PET**

ChIA-PET (Chromatin Interaction Analysis by Paired-End Tag sequencing) is a technique` that intergrates ChIP with proximity ligation and paired-end tag sequencing to 3D chromatin interactions mediated by specific proteins. It reveals how different genome regions interact to regulate gene expression.

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**About**

**Xionglab**

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**Lab Web：**

The Xiong Lab at Zhejiang University Medical Center seeks to understand the regulatory circuits and mechanisms of genetic diseases, including brain and heart disorders, from multiple layers, including genetics, epigenomics, epitranscriptomics (i.e. RNA modification), and transcriptome. The ultimate goal of our research is to identify the "missing regulation" of disease genetics and help guide the development of new therapeutics for human disease from multiple molecular levels.

We integrate computational biology, AI (mainly deep learning) and statistical genetics, in combination with experimental approaches, to answer the questions and provide validations.

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