

# MEME-ChIP

The **MEME-ChIP** web service is a tool designed for **motif discovery and enrichment analysis** in **ChIP-seq** data. It processes **FASTA-formatted sequences** centered on **ChIP-seq tag peaks**, identifies **novel motifs**, and determines their **enrichment** using various algorithms:

- **Preprocessing:** Uploaded sequences are centered and trimmed to **100 bp** for motif discovery, but the full-length sequences are used for visualization.
- **Motif Discovery:**
  - **DREME:** Discovers short, statistically significant motifs in all trimmed sequences.
  - **MEME:** Identifies longer, more complex motifs, but is limited to **600 randomly selected sequences** due to computational constraints.
- **Motif Enrichment Analysis:**
  - **AME (Analysis of Motif Enrichment):** Measures the statistical enrichment of known motifs from the **JASPAR CORE database** in the input sequences.
  - **AMA (Average Motif Affinity):** Computes the average binding affinity of MEME-discovered motifs for each sequence.
- **Motif Visualization:**

– **MAST:** Maps discovered motifs to the **full-length** input sequences.

– **Comparison to JASPAR CORE:** Identifies **transcription factors (TFs)** that may bind to the discovered motifs.

