

## ABSTRACT

Gene expression regulation is crucial in all organisms with respect to all aspects of physiological processes and is carried out basically at the stage of transcription using a variety of transcription factors and non-coding RNA strands. Transcription factors are modulators of gene expression and act on all developmental stages of life and maintain cells in dynamically changing microenvironments. Transcription factors and non-coding RNAs are largest families of regulatory features of gene expression in different genomes. The mutual regulation between non-coding RNA and transcription factors has been emerged as an excellent regulatory network and help in understanding all the physiological and biochemical processes of cell. TF-ncRNA database is collection of information about the transcription factors related to different categories of non coding RNA in one way or the other. The database includes important model organisms from eukaryotes and prokaryotes. It presents transcription factor sequences, the structures and related ncRNA along with the relevant literature on one podium. The purpose of this database development is to serve as an informative biological database as well as a simple, user friendly interface.