

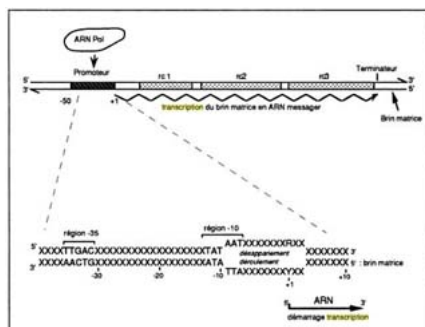


MUTUALISATION DES COMPÉTENCES ET DES ÉQUIPEMENTS FRANÇAIS
POUR L'ANALYSE GÉNOMIQUE ET LA BIO-INFORMATIQUE

[HOME](#)
[ABOUT FRANCE
GÉNOMIQUE](#)
[FRANCE
GÉNOMIQUE OFFER](#)
[AREAS OF
EXPERTISE ▾](#)
[BIOINFORMATIC
TOOLS AND
DATABASES ▾](#)
[LARGE SCALE
PROJECTS](#)
[TRAINING AND E-
LEARNING](#)
[PUBLICATIONS](#)

MAPPING OF TRANSCRIPTION START SITES – TSS

A transcription start site (TSS) is the location where the first DNA nucleotide is transcribed into RNA. It is difficult to determine the exact position of the TSS using bioinformatics, but experimental methods can be used to locate it, notably high throughput sequencing.



The Institut Pasteur platform is likely to be able to meet your needs for TSS mapping. The chosen protocol uses the TAP or « Tobacco Acid Pyrophosphatase » enzyme, which allows conversion of the 5'PPP ends of native RNAs to 5' ends, making them compatible for adapter ligation.

The study is performed by comparing the results of sequencing the 5' end of the RNA, in conditions where it is either treated or untreated with TAP. If untreated with TAP, the sequencing will provide access to all the RNAs (ribosomal RNA, tRNAs, RNA messengers in the process of degradation or maturation) except for native 5' ends. If treated with TAP, the same sequences will be obtained but in addition native RNA sequences will also be obtained.

Statistical methods that allow identification of differentially expressed genes cannot be applied for identification of TSS. The

TSS must therefore be identified by the experimenter with the aid of visualisation tools.

In practice, this can be done using a method adapted from Illumina protocols.

This type of study also allows identification of alternative start sites and new transcripts.

