**سیویلیکا - ناشر تخصصی مقالات کنفرانس ها و ژورنال ها**
گواهی ثبت مقاله در سیویلیکا
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## عنوان مقاله:
computational promoter analysis based on transcription factor binding sites and modules

## محل انتشار:
هشتمین همایش بیوانفورماتیک ایران (سال: 1397)

تعداد صفحات اصل مقاله: 1

## نویسندگان:
کبری عرب - *ابیوتکنولوژی*

کبری عرب - *۲دانشگاه شهرکرد-دانشکده کشارزی*

## خلاصه مقاله:
Genomatix site (https://www.genomatix.de/) in our study had used to find out where the transcription factors were found in MatInspecter. A new version of the MatInspecter was presented by Cartharius et al. (2005). Which identifies the location of the binding of the transcription factors using a large library of heavy matrices, matrix families in the nucleotide sequences. We imported the sequences of the S-like RNase promoter from rice (the Niponbare species) and displayed all the details in the matrix family and other characteristics, and the result presence of 260 matches on a sequence of 1278 base pair. And there were many modules on this promoter, of which the most important are OSPTBP, OSVTBP, OSXCPE &... PSOPAQ modules contains transcriptional activating proteins, including rice transcription activator (RITA) and basic leucine zipper proteins, which increase expression during seed development. in PSEPFF modules there are zinc fingers from EPF type, and there are two zinc fingers on Cyc2/His2 along with the motifs that are apart. In more than 70 percent of modules there are zinc finger, leucine zipper, MYBs, WRKYs that triggered resistance to salt and drought stress

## کلمات کلیدی:
Key words: promoter analysis, transcription factors, Genomatix

## لینک ثابت مقاله در پایگاه سیویلیکا:
https://civilica.com/doc/908691