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BIOINFORMATICS





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Gene prediction



Bioinformatics



OUTLINES



Prediction of non-coding tRNA genes (non-coding genes)



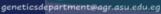
output format

















Bioinformatics



Prediction of non-coding tRNA genes (non-coding genes)

tRNA scan -SE is the most widely adopted tool for the prediction of tRNA gene transfer in genetic sequences over the past two decades.

The tRNAscan-SE interface consists of three main components:

- · Choose search mode
- Choose query sequence
- Configured search mode and results display options.









Gene prediction



Bioinformatics



Prediction of non-coding tRNA genes (non-coding genes)

Output Format:

The default output of tRNAscan -SE includes summary data that includes:

Enumerate the total number of tRNAs found Number of tRNA pseudogenes found Number of tRNAs with introns and any antigens detected

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Prediction of non-coding tRNA genes (non-coding genes)

The output shows the expected secondary structure for each selected sequence. With an additional click on the "View tRNA" button to the right of each tRNA, a 2D representation of the tRNA structure can be viewed, resulting in the familiar cloverleaf structure.

The output also displays the total length of the sequence, the location of the anticodon, and the overall score. tRNAscan-SE scores for known RNA sequences of different species are included on the website to facilitate the assessment of the significance of the result, which is measured as a percentage score from 0 to 100, where 100% means an exact and identical prediction of one of the tRNAs from the database.

Bioinformatics

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