Signal peptide cleavage site prediction

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Abstract

SignalP provides a resource for the prediction of signal peptide cleavage sites in proteins.

Content

SignalP provides a resource for the prediction of signal peptide cleavage sites in proteins. The signal peptide is often used to localize proteins to specific regions within the cell, so knowledge of a specific signal peptide for a protein can provide a clue to its likely location. At present, there are three 'organism groups' for which predictions can be made - Gram-negative bacteria, Gram-positive bacteria, and eukaryotes. A new version of this software, SignalP v2.0.b2, is currently being tested from the website, and this version has several new features, including graphics integrated into the output.

Navigation

The site is quite easy to use. The amino-acid sequence to be analyzed can be pasted into a window on the opening web page, and the results are processed within a few seconds (depending on the size of the protein and the internet connection). There are links to background information as well as links to PDF files of the original articles for a detailed description of the methods used for signal peptide identification.

Reporter's comments

Timeliness

Overall, the site appears to be regularly updated, every few months. The main page was updated in October, 1999 (about 7 months ago), but some of the web pages date back to 1996.

Best feature

The V.2 beta version currently being tested is preferable to the original. This version incorporates a new signal peptide prediction method based on hidden Markov models which allows improved discrimination between signal peptides and uncleaved signal anchors for eukaryotic data. Prediction of cleavage site position is based on a newer dataset than the earlier version. I ran several sequences through the program, and printed the resulting output - including graphs - with ease. I also like the link to the Hot paper in bioinformatics interview with SignalP's designer Henrik Nielsen.

Related websites

There are several other CBS prediction servers that predict structural, biochemical and molecular features of DNA and protein sequences. For example, TargetP can give a predicted subcellular location of a protein on the basis of its amino-terminal sequence.

Table of links

SignalP

Hot paper in bioinformatics

CBS prediction servers

TargetP

References

1. SignalP.

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