

| PublisherInfo | | |
|----------------------|---|----------------|
| PublisherName | : | BioMed Central |
| PublisherLocation | : | London |
| PublisherImprintName | : | BioMed Central |

Identification of complete gene structures in genomic DNA

| ArticleInfo | | |
|-----------------------|---|--|
| ArticleID | : | 3596 |
| ArticleDOI | : | 10.1186/gb-2000-1-1-reports222 |
| ArticleCitationID | : | reports222 |
| ArticleSequenceNumber | : | 87 |
| ArticleCategory | : | Web report |
| ArticleFirstPage | : | 1 |
| ArticleLastPage | : | 4 |
| ArticleHistory | : | RegistrationDate : 1999-11-18 Received : 1999-11-18 OnlineDate : 2000-3-17 |
| ArticleCopyright | : | BioMed Central Ltd2000 |
| ArticleGrants | : | |
| ArticleContext | : | 130591111 |

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Abstract

The GENSCAN program is designed to predict complete gene structures, including exons, introns, promoter and polyadenylation signals, in genomic sequences.

Mirror sites

[GENSCAN web server at Pasteur Institute, Paris](#) and [GENSCAN web server at DKFZ/EMBnet, Heidelberg, Germany](#). Both of these mirror servers have a less cluttered and visually more appealing interface than the original MIT server.

Content

The GENSCAN program is designed to predict complete gene structures, including exons, introns, promoter and polyadenylation signals, in genomic sequences. The program was designed primarily to predict genes in human or vertebrate genomic sequences, although it works fairly well on *Drosophila* sequences and there are special versions for maize and *Arabidopsis* sequences. The server returns a table with the predicted exons, including position, length, reading frame, and some confidence scores. In addition, it returns the final predicted protein sequence, and the corresponding spliced DNA sequence (if desired). There is a graphical representation of the predicted coding regions, available in GIF or Postscript format.

Navigation

Although the submission form is easy to use, it is a bit difficult to find. You have to scroll down past some FAQ links, a list of GENSCAN-related websites and a cautionary note, before you get to the actual form. The form is followed up by a list of references and contact information.

Reporter's comments

Timeliness

There is no indication of when the site was last updated. There are a number of dead or incorrect links on the FAQ pages, none of which affects the functionality of the server.

Best feature

The best feature of GENSCAN is the output of the final spliced-together protein. Often, prediction programs stop short and just give a list of potential exons, requiring the researcher to splice them together manually. Using the GENSCAN protein sequence output and a program like NCBI's [Sequin](#), a researcher can quickly map the protein onto the genomic sequence and automatically annotate the predicted exon regions. Then one can start the manual 'tweaking' that is necessary with even the best prediction programs.

Worst feature

The blue background and white lettering on all of the pages makes them hard to read. Plain black and white would be preferable.

Wish list

Two things. Change the color scheme, and reorganize the site so that the submission form is the very first thing on the page, and the rest of the information (related web sites, FAQs, references, and so on) is available as links. This would speed loading time and allow repeat users to avoid all the information they have seen before.

Related websites

There are a number of gene prediction websites, including [PROCRUSTES](#), [Grail](#), [GeneMark](#) and [Genie](#).

Table of links

[GENSCAN web server](#)

[GENSCAN web server at Pasteur Institute, Paris](#)

[GENSCAN web server at DKFZ/EMBNET, Heidelberg, Germany](#)

[Sequin](#)

[PROCRUSTES](#)

[Grail](#)

[GeneMark](#)

[Genie](#)

References

1. [GENSCAN web server.](#)