

The GENSCAN Web Server at MIT

Identification of complete gene structures in genomic DNA



[For information about Genscan, click here](#)

Server update, November, 2009: We've been recently upgrading the GENSCAN webserver hardware, which resulted in some problems in the output of GENSCAN. We apologize for the inconvenience. These output errors were resolved.

This server provides access to the program Genscan for predicting the locations and exon-intron structures of genes in genomic sequences from a variety of organisms.

This server can accept sequences up to 1 million base pairs (1 Mbp) in length. If you have trouble with the web server or if you have a large number of sequences to process, request a local copy of the program (see instructions at the bottom of this page).

Organism: Suboptimal exon cutoff (optional):

Sequence name (optional):

Print options:

Upload your DNA sequence file (upper or lower case, spaces/numbers ignored):

Or paste your DNA sequence here (upper or lower case, spaces/numbers ignored):

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GENSCAN was developed by Chris Burge in the research group of Samuel Karlin, Department of Mathematics, Stanford University. The program and the model that underlies it are described in:

Burge, C. and Karlin, S. (1997) Prediction of complete gene structures in human genomic DNA. *J. Mol. Biol.* **268**, 78-94.

The splice site models used are described in more detail in:

Burge, C. B. (1998) Modeling dependencies in pre-mRNA splicing signals. In Salzberg, S., Searls, D. and Kasif, S., eds. [Computational Methods in Molecular Biology](#), Elsevier Science, Amsterdam, pp. 127-163.

See also:

Burge, C. B. and Karlin, S. (1998) Finding the genes in genomic DNA. *Curr. Opin. Struct. Biol.* **8**, 346-354.

This web server is located in the Burge laboratory at the MIT Department of Biology.

Address any comments/questions/suggestions to: [Chris Burge \(cburge@mit.edu\)](mailto:cburge@mit.edu)

Please notify me by email (cburge@mit.edu) if: 1) the web/email server is not working; 2) you find a bug in GENSCAN; or 3) you have a suggestion for how to make the program more "user friendly". In your email, please specify which Genscan server you had trouble with (e.g., new MIT web server, MIT email server) and the nature of the problem.

NOTE. This server is for the program "GENSCAN", developed by Chris Burge at Stanford University, not to be confused with the Applied Biosystems sequencing software called "GENESCAN".

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GENSCAN is freely available for academic use. Executables are currently available for the following Unix platforms: Intel/Linux, Sun/Solaris, Intel/Solaris, SGI/Irix, DEC/Tru64, and IBM/AIX. Platforms not listed are not currently supported. To obtain a copy of GENSCAN for academic use, go to the [academic license agreement web site](#) and download the executable after completing the form.

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