

Lasergene[®]

GeneQuest

GENE DISCOVERY AND SEQUENCE ANNOTATION

GeneQuest is a fully integrated module of Lasergene that assists users to locate genes, regulatory elements, patterns and structure in your primary DNA sequence. GeneQuest's comprehensive set of analytical methods can be easily applied and manipulated for projects of any size – small, BAC-sized or even larger. Users can easily compare sequences with existing genome and Expressed Sequence Tags (EST) data using the integrated BLAST feature and find out more about related sequences using the integrated Entrez search tool. GeneQuest also provides annotation and visualization tools so you can document your discoveries for your own use or for publication or submission to public databases.

MAIN GeneQuest WINDOW

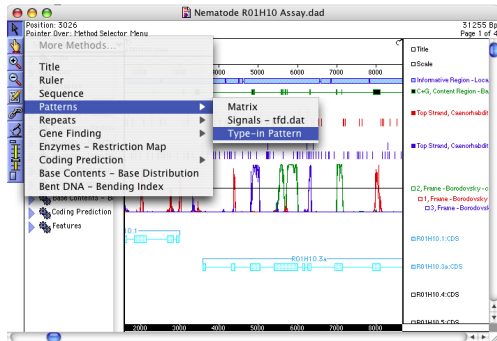
The image displays the GeneQuest software interface. The main window shows a DNA sequence analysis for 'C. Elegans.dnd'. It features a sequence viewer with a scale from 9000 to 12000, a method curtain on the left, and an assay surface showing multiple analytical applications. A dialog box titled 'K01G5.3' is open, showing a list of segments and options for adding, deleting, and setting ends.

Method curtain containing "drag and drop" options

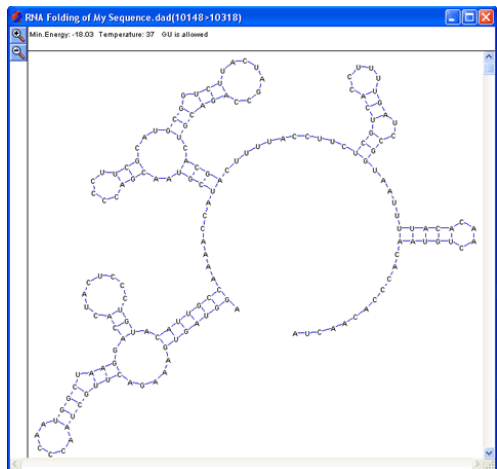
Assay surface shows multiple analytical applications

Easy integration between modules

GeneQuest FEATURES



Apply a variety of methods to the assay surface



Predict RNA folding

Sequence Entry

- Import data from many popular file formats
- Read sequences and features from other Lasergene project files
- Edit template sequence and share newly created feature through integration with SeqBuilder and other Lasergene modules
- Download sequences directly from NCBI or other BLAST servers using accession numbers, BLAST or text searches.

Gene Finding

- Predict coding regions using Borodovsky's Markov method
- Predict intron/exon boundaries using species-specific pattern files for splice sites
- Align known genes, ESTs or proteins with your sequence
- Predict where genes start using species-specific pattern files for start sites and transcription factor binding sites
- Locate ORFs, stops and starts
- Submit any selected feature, segment or all of your sequence as a BLAST query
- Investigate related sequences using keywords with the integrated Entrez search tool

Graphical Displays

- Juxtapose or superimpose related analysis methods or displays
- View project at base level and at full overview magnification simultaneously
- Display data as graphs or boxes indicating a range
- Customize line colors, fill patterns and fill colors for all display objects
- Display features in a variety of shapes
- Name individual segments for identification ease

Structure and Composition

- Display restriction sites
- Locate direct, dyad and inverted repeats
- Generate codon usage summaries
- View simulations of agarose gel separations of restriction digests
- Generate and graph base distribution summaries
- Plot base frequency and base skew
- Predict RNA folding
- Plot localized DNA bending