



# CLC RNA Workbench

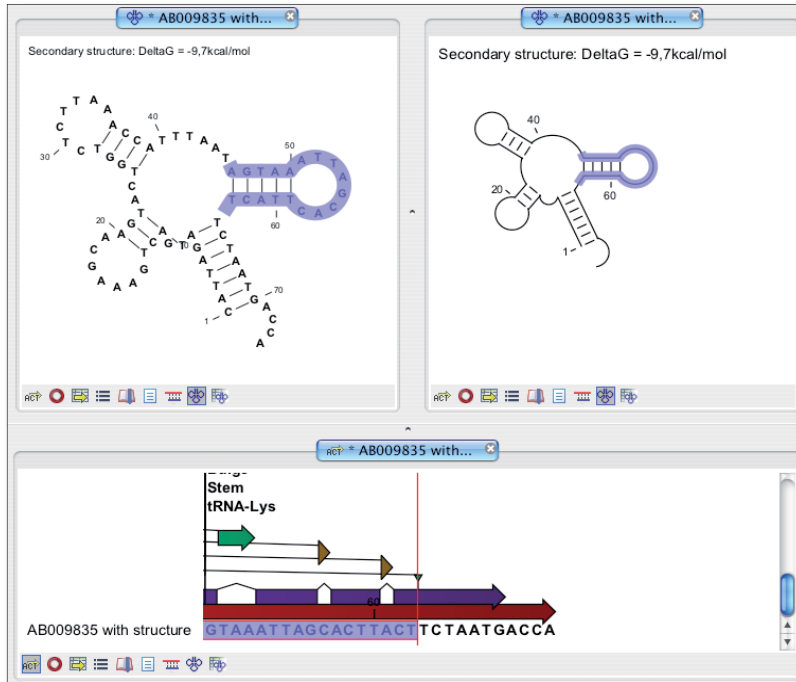
Version 1.0 for Windows, Mac OS X, and Linux



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## CLC RNA Workbench

With the all new CLC RNA Workbench, CLC bio brings you complex analysis of RNA molecules in a fully integrated, user-friendly and graphically advanced bioinformatics framework.



### Secondary structure editor

An optimal secondary structure has been predicted for a tRNA molecule. In the upper part of the figure, the structure is displayed at two different zoom levels. The lower part shows a linear view of the tRNA molecule where structural elements have been added as annotation. A stem region is selected in the linear view and this selection is also displayed in the two structural views.

### Advanced

The CLC RNA Workbench gives the user easy access to a range of complex algorithms and options. RNA secondary structures can be predicted using state-of-the-art free energy minimization algorithms and parameters, thermodynamic and statistical details are easily extracted and experimental information can be easily incorporated into the analysis.

### User-friendly

With the Workbench, RNA secondary structure information can be viewed and manipulated through a graphically and functionally advanced user interface. Through this, the user can simultaneously view linear, tabular, and 2D representations of RNA sequences and structures of choice. Thermodynamic and statistical properties of secondary structure elements can be easily accessed. And secondary structures can be edited to facilitate interpretation and publication.

### Easy

Advanced computer skills are not required. Due to a unique graphical user interface the CLC RNA Workbench is easy and intuitive to use, and the comprehensive user manual explains all the details. The full compatibility between all types of CLC workbenches provides strong support for efficient collaboration within research groups; allowing all researchers to easily share sequence data and research results.

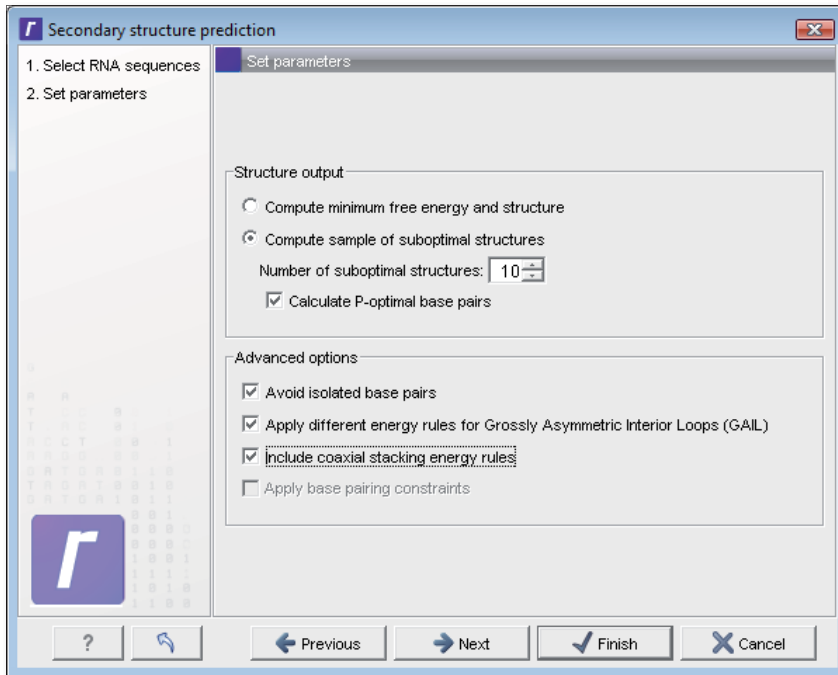
### CLC RNA Workbench provides

- State of the art algorithms for free energy minimization-based prediction of RNA secondary structure, including advanced options to include e.g. coaxial stacking, suboptimal structures and experimental constraints.
- Advanced tabular and fully integrated graphical editors for linear and 2D viewing and editing of RNA secondary structures and sequences.
- A range of RNA analyses, including motif finding and state-of-the-art graphical viewing and editing options.
- Detailed history log enabling tracking and documentation of all analyses and all modifying actions performed on a given piece of data (e.g. on a RNA sequence or on an alignment).
- Option of importing and working with external files such as PDF files, word processing files, and spreadsheet files directly from the program's data repository. All types of files related to a research project can thus be managed from a single application on your computer.
- Full integration of data management, bioinformatics analyses, reporting, and documentation of results. This eliminates the time spent on manual data transfers between different programs and databases.



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- A number of output functionalities, including printing and generation of graphics output in various file formats.
- Option of developing your own bioinformatics solutions using CLC Developer Kit.
- Full integration with CLC Bioinformatics Cube and Cell, providing hardware-accelerated database searches of high precision and high speed - up to 200 times faster than a laptop computer.



## Secondary structure prediction

A user-friendly interface gives the user easy access to a range of complex algorithms and options. This includes advanced options to include coaxial stacking energy rules, suboptimal structures and experimental constraints.

## Main Bioinformatics features of CLC RNA Workbench

- All features of CLC Free Workbench.
- State-of-the-art algorithms for free energy minimization-based prediction of RNA secondary structure, including advanced options.
- Advanced and fully integrated graphical editors for linear and 2D viewing and editing of RNA secondary structures and sequences.
- Advanced tabular editor with full, integrated access to thermodynamic details.
- Search and discovery of RNA patterns.
- Local complexity region analyses.
- Local and web-based BLAST integrated with advanced viewing of search results.
- RNA, DNA and protein sequence editor displaying both linear and circular molecules.
- RNA, DNA, and protein alignment editor.
- Interactive logos along both RNA, DNA and Protein alignments.
- Manual annotation of sequences, including advanced editing and copying options.
- Reverse translation from protein to gene, based on translation tables from a number of species.
- Advanced restriction enzyme analysis and management.
- Dot plot based analyses.
- Simulation of restriction maps.
- NCBI sequence data search.
- Access to web info from Google and PubMed.

Download a fully functional demo of CLC RNA Workbench on [www.clcbio.com](http://www.clcbio.com)