



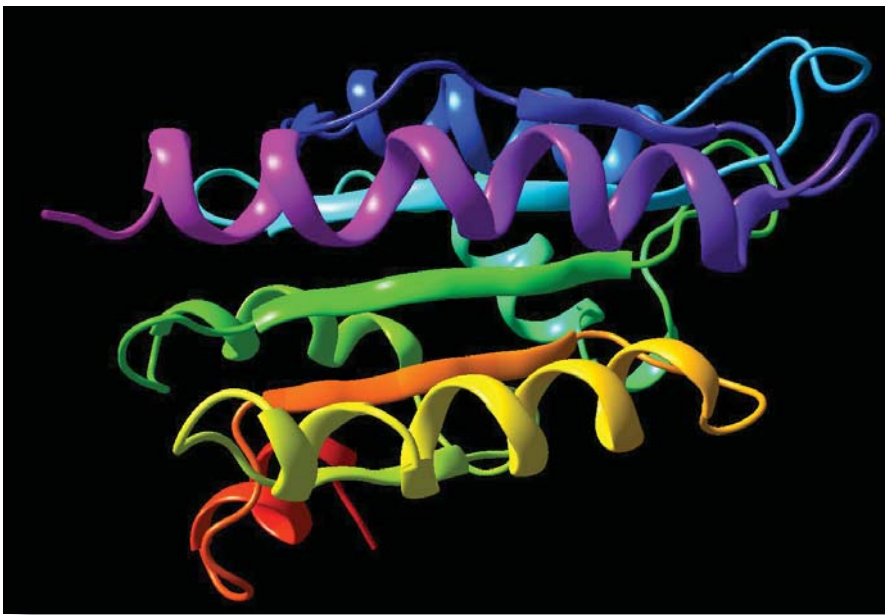
# CLC Combined Workbench

Version 1.0 for Windows, Mac OS X and Linux.

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CLC Combined Workbench includes all features and functions of CLC Free Workbench, CLC Protein Workbench, and CLC Gene Workbench.

The application sets new standards for bioinformatics software with its overall graphical display, usability driven and user-friendly interface, while featuring a number of unique and innovative bioinformatics tools for supporting advanced biochemistry and molecular biology lab research. CLC Combined Workbench is available for Windows, Mac OS X, and Linux platforms. CLC Combined is fully integrated across these platforms and fully integrated with all other programs from CLC bio.



## 3D view

CLC Combined Workbench has integrated viewing of three-dimensional structures in both PDB and mmCIF formats. Furthermore the 3D structures can be retrieved directly from the Protein DataBank via integrated BLAST homology searches. Structures can be visualized in a range of ways, creating stunning graphics which can be used for presentations and reports.

## CLC bio Combined Workbench features

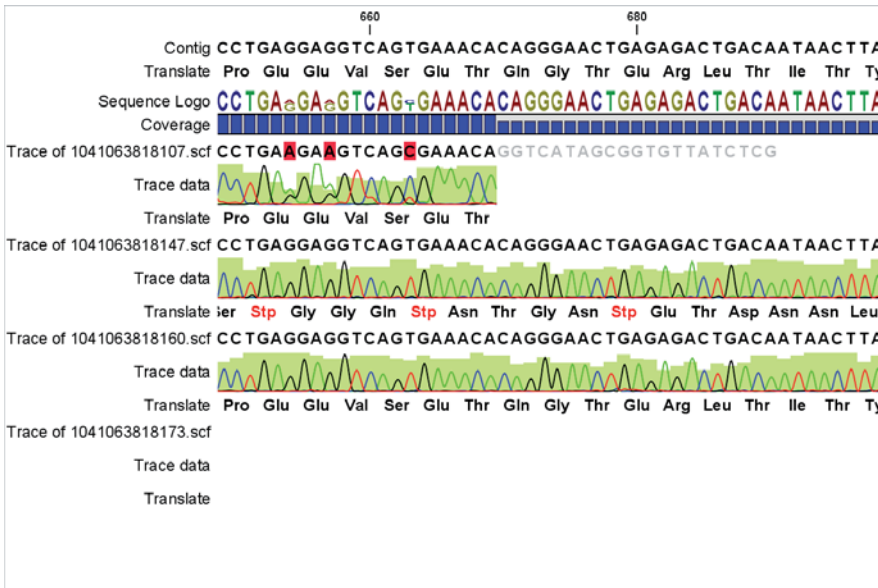
- Graphically and methodologically advanced bioinformatical tools to perform primer design, contig assembly and cloning vector design
- A wide range of additional Protein and DNA sequence analyses, including state-of-the-art graphical viewing and editing options
- Detailed history log enabling tracking and documentation of all analyses and all modifying actions performed on a given object (e.g. on a protein 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 may thus be managed from one single application on your computer
- Full integration of data management, bioinformatics analyses, reporting, and documentation of results. This eliminates time spent on manual data transfers between different programs and databases
- A number of output functionalities, including printing and generation of graphics output in various file formats



# CLC Combined Workbench

## Main bioinformatics features

- Editor for graphically and algorithmically advanced primer design
- Integrated 3D structure viewer
- Editor for graphically and algorithmically advanced primer design
- Contig assembly and editing from chromatogram trace-files
- Automatic SNP annotation of sequences
- Secondary protein structure prediction
- Signal peptide prediction and localization (SignalP)
- Transmembrane helix prediction (TMHMM)
- Local complexity region analyses and complexity plots
- Local Pfam domain search
- Hydrophobicity analyses and graphs
- Antigenicity analysis and graphs
- Proteolytic cleavage site detection
- Web based BLAST, integrated with advanced viewing of search results
- Discovery of protein patterns and DNA patterns
- Motif search
- DNA, RNA and protein sequence editor displaying both linear and circular molecules
- DNA, RNA, and protein alignment editor
- 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
- Integrated PubMed searches
- Sequence logo graphs along DNA, RNA, and protein alignments



## Assembly

CLC Gene Workbench allows you to import, view, edit and analyze results from automated sequencing machines. Here, four sequencing reads have been automatically assembled into a contig sequence. The color intensity of each of the four nucleotides is shown as a trace-graph under the called sequence of each sequencing read, and the associated quality values are shown as shaded green boxes in the background of the graph, allowing the user to easily interpret and edit the contig based on the full experimental data. Automated algorithms for "trimming" the trace data prior to assembly are also included. Furthermore, the integrated framework of the workbench allows the user to perform various analyses on the contig and trace sequences, such as the open reading frame prediction, the coverage graph, and the logo shown below the sequences. These again aid in the interpretation of the experimental data.