



CLC Main Workbench

A comprehensive workbench for advanced DNA, RNA, & protein analyses

Advanced computer skills are not required. Due to a unique graphical user interface CLC Main 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.

Sample to Insight

Primer design

The primer design functionality in the workbench offers the user an unprecedented level of graphical interaction during the primer selection process. Primers can be designed for various experimental settings. In the primer editor the user can easily select regions to define primer sets and immediately view the properties of all primers using various levels of detail. When primer selection criteria, such as melting temperature and self-annealing values are adjusted, the effect can be immediately evaluated.

Alignment

Contrary to most other alignment programs, CLC Main Workbench allows you to show the annotations of the individual sequences in a multiple sequence alignment. This can easily identify whether certain domains are conserved throughout an alignment.

Cloning

CLC Main Workbench offers graphically advanced in silico cloning and design of vectors for various purposes. Our approach to visual cloning is based on another philosophy than most other software tools, as the users are in total in control of the cloning process - contrary to the more or less automatic and noncontrollable cloning processes in other applications.

BLAST/DB search

CLC Main Workbench offers to conduct BLAST searches on protein and DNA sequences or a combination of these using NCBI or it can run local if proprietary sequences are used. BLAST results are presented in a graphical overview together with a detailed tabular representation of the results. Sequence hits can easily be downloaded and analyzed further.

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Assembly

CLC Main Workbench allows you to import, view, edit, and analyze results from automated sequencing machines.

Phylogeny

CLC Main Workbench allows for creation and visualization of phylogenetic trees and associated metadata. It is easy, for example, to find the optimal statistical approach by model testing, and to visualize imported metadata on tree topology at high quality, ready for publication.

Workflow

Workflows can be built in the workbench to combine various tools from the toolbox into one analysis. It can be run in batch, making it a powerful tool for analysing a high number of samples using the same pipeline.

Molecular structure visualization

It is fast and intuitive to customize the visualization of molecules using CLC Main Workbench. The molecules are automatically sorted in categories; proteins, nucleic acids, ligands, cofactors, and water molecules.

Plug-ins

CLC bio's flexible IT architecture facilitates easy development of plug-ins for all of our bioinformatics workbenches, through our open API. When one or more plug-ins is installed on your computer, it is fully integrated with your CLC workbench – it runs as if it were one single (expanded) application. You can develop your own plug-ins using our Developer Kit, or you can choose to use plug-ins developed by us or by third parties.



CLC Main Workbench is available for Windows, Mac OS X, and Linux (Red Hat 5 or later, SUSE 10.2 or later). For detailed system requirements, please refer to clcbio.com/support/system-requirements.