



CLC Free Workbench

Version 2.5 for Windows, Mac OS X and Linux

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CLC Free Workbench from CLC bio is a user-friendly bioinformatics tool to support your daily lab work. Download the latest release from our website. This release, as well as future releases, are free of charge and available for both Windows, MacOS X, and Linux platforms.

CLC Free Workbenches are fully integrated across IT platforms and fully integrated with other bioinformatics programs from CLC bio.

The screenshot displays the CLC Free Workbench interface. The top window, titled 'HUMHBB', shows a table of annotations with columns for Annotation, Name, Position, Start, and End. The bottom window shows a graphical representation of the HUMHBB sequence with various features highlighted.

Annotation	Name	Position	Start	End
CDS	HBB thalassaemia	join(62187..62...	62186	62408
CDS	HBE1	join(19541..19...	19540	20961
CDS	HBG2	join(34531..34...	34530	35982
CDS	HBG1	join(39467..39...	39466	40898
CDS	CDS	join(45710..45...	45709	47124
CDS	HBD	join(54790..54...	54789	56259
CDS	HBB	join(62187..62...	62186	63610
Conflict	Conflict	37486	37485	37486
Exon	Exon 1	<45710..45800	45709	45800
Exon	Exon 1	<62187..62278	62186	62278
Exon	Exon 2	62390..<62408	62389	62408
Exon	Exon 1	34478..34622	34477	34622
Exon	Exon 1	39414..39558	39413	39558
Exon	Exon 3	46997..<47124	46996	47124
Exon	Exon 1	54740..54881	54739	54881
Exon	Exon 1	62137..62278	62136	62278

Screenshot Sequence view

Two views of the HUMHBB sequence. The upper view shows the coding sequences (CDS), and the bottom view shows a selection corresponding to the CDS chosen in the upper view.

(Windows platform)

CLC Free Workbench provides

- Easy access to web based protein and nucleotide searches in GenBank, including download facilities and full graphical overview of sequence annotations of your choice
- User-friendly graphical tools used for finding and working with relevant regions of DNA, RNA, and protein sequences
- A number of basic bioinformatics algorithms
- Full integration of data input, data management, calculation results, and data export. This eliminates time spent on manual data transfers between different programs and databases
- Output functionalities, including printing, generation of reports, and generation of graphics output in various file formats
- Option of viewing and graphical manipulation of bioinformatics analyses performed in commercial software from CLC bio

Data management

Sequence data may be typed, copied, imported or downloaded into the workbench. These data, as well as calculations, search results, and files in external file formats are arranged in projects and saved locally on your desktop. The split-screen option allows easy comparison of different types of analyses made on the same dataset.

Handling of sequences

The interactive sequence viewer provides a zoomable overview of your data, whether they are multi-million base DNA sequences or small scale peptides. The viewer contains a large number of graphical and interactive user options, making it possible to set up the viewer exactly as needed. Both linear and circular sequence menus are available.

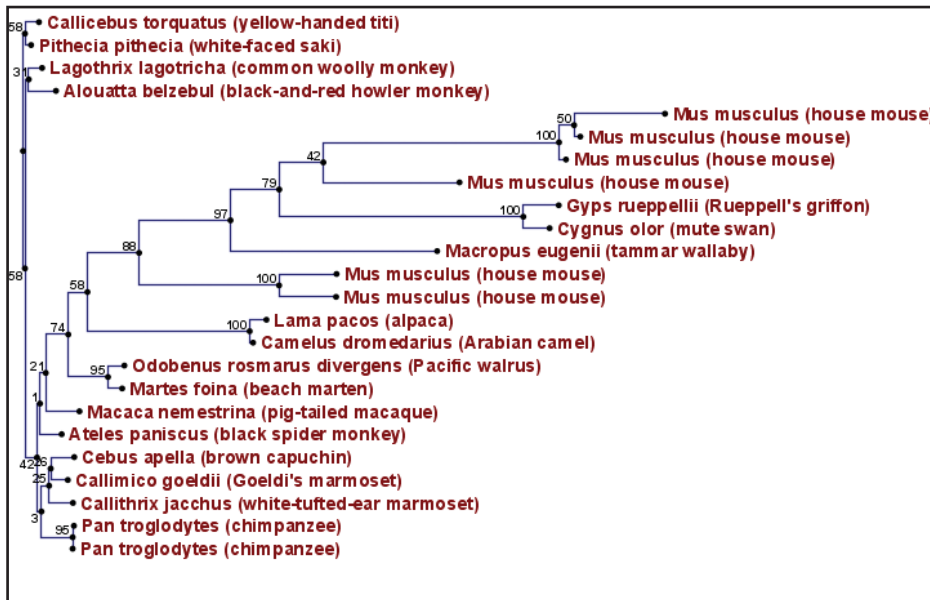
To get CLC Free Workbench, please visit www.clcbio.com for an easy download!



CLC Free Workbench

Phylogenetic trees

CLC Free Workbench offers basic phylogenetic analyses and viewing options. Trees may be made from DNA, RNA, and protein sequences. As is the case with all analyses in CLC Free Workbenches, phylogenetic trees may be both saved on your harddisk and exported to other CLC Free Workbench users.



Screenshot

A phylogenetic tree

The navigation area and the analyze area are present on the left.

(Windows platform)

Main features of CLC Free Workbench

- Fast multiple alignment of DNA, RNA, and proteins including consensus sequence and conservation information
- Open reading frame determination
- Restriction site analysis (based on REBASE data)
- Translation from DNA to proteins (all genetic translation tables)
- Reports with residue composition, molecular weight and isoelectric point (for proteins)
- Neighbor-joining and UPGMA phylogenies
- Integrated GenBank search and download
- Import/export of in from GenBank, Fasta, Phylip, Newick, Swiss-Prot, PIR, and EMBL format
- Full integration of data input, data management, calculations results, and data export
- High-quality printing of reports and graphics
- User defined export to various graphics file formats
- Option of working with different files, and in different file projects at the same time
- Option of having several active workspaces at a time, enabling simultaneous work on multiple projects

System requirements

- Windows 2000 or Windows XP
- MacOS X 10.3 or newer
- Linux: Redhat or SuSE
- 256 MB RAM required
- 512 MB RAM recommended
- 1024 x 768 display recommended