



CLC Protein Workbench

Version 1.5 for Windows, Mac OS X and Linux

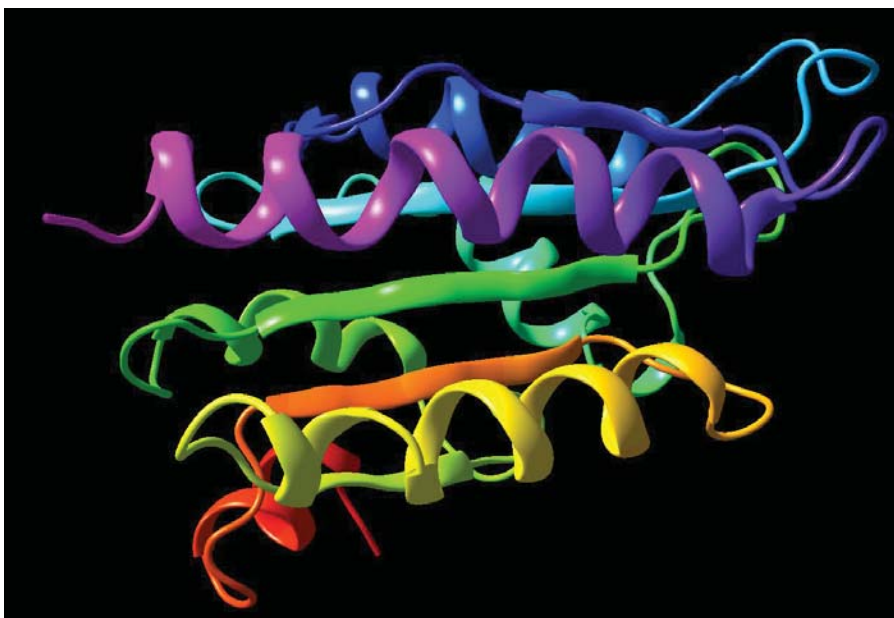
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CLC Protein Workbench from CLC bio is a user-friendly desktop program featuring a number of unique and innovative bioinformatics tools for supporting advanced biochemistry lab research.

CLC Protein Workbench is available for Windows, Mac OS X, and Linux platforms. Protein Workbench is fully integrated across these platforms and fully integrated with all other programs from CLC bio.

CLC Protein Workbench provides

- A wide range of protein 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
- Option of compiling a comprehensive report including all the protein analyses of the program at the user's choice into one single document. The report can be exported to PDF, printed or manipulated on the screen
- A number of output functionalities, including printing, generation of short-form reports, and generation of graphics output in various file formats



3D view

CLC Protein 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.

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 data formats are arranged in projects and saved locally on your desktop computer. The split-screen option allows easy comparison of different types of analyses made on the same data.

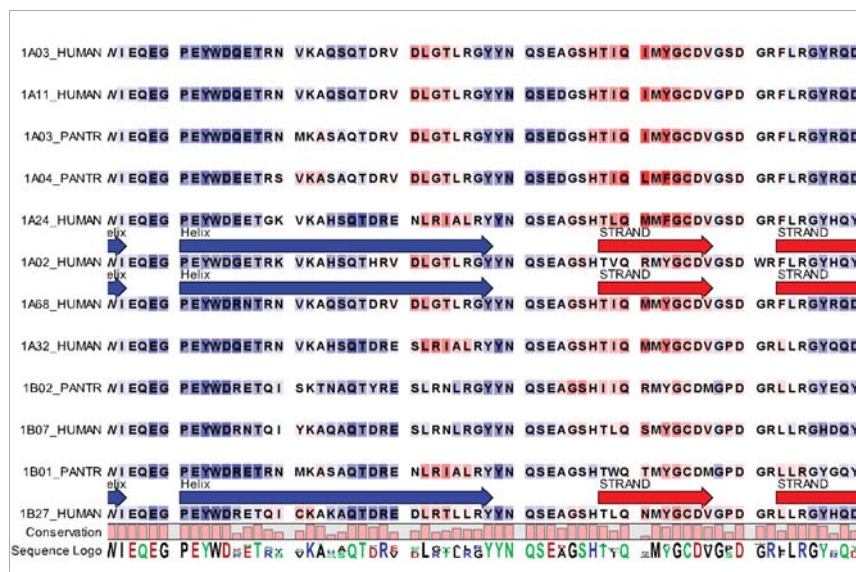


CLC Protein Workbench

Efficient collaboration support

The full integration between all CLC workbenches provides strong support for efficient collaboration within research groups: Advanced analyses and data searches can be performed on a CLC Protein Workbench, while more basic work tasks may be performed by other researchers equipped with CLC Free Workbenches.

Throughout the project, all researchers can be given easy access to knowledge obtained through sharing of sequence data and sharing of research results. Examples could be figures showing annotated sequences, alignments and their underlying sequences, reports on protein characteristics, phylogenetic trees, graphical views of BLAST results etc.



Alignment

Contrary to most other alignment programs, CLC Protein 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. Moreover the information content of the individual columns in the alignment can be shown in form of a sequence logo, which can show information on highly conserved regions. The conservation of the individual residues in the alignments is shown as a histogram below the alignment.

Some features of CLC Protein Workbench

- All features of CLC Free Workbench
- Integrated 3D structure viewer
- Secondary protein structure prediction
- Local complexity region analyses
- Prediction of signal peptides and their cleavage sites (SignalP)
- Transmembrane helix prediction (TMHMM)
- Pfam domain search
- Motif search (known patterns)
- Pattern discovery (unknown patterns)
- Integrated UniProt searches (both Swiss-Prot and TrEMBL)
- Web based BLAST integrated with advanced viewing of search results
- Integrated PubMed search
- DNA, RNA, and protein alignment editor
- Sequence logo graphs along DNA, RNA and Protein alignments
- Dot plot based analyses
- Manual annotation of sequences, including advanced editing and multi-copying options
- A number of hydrophobicity based analyses
- Reverse translation from protein to gene, based on translation tables from a number of species
- Proteolytic cleavage site detection
- Comprehensive protein report including one or more of the above analyses of the user's choice

You are welcome to download a fully functional demo of CLC Protein Workbench on www.clcbio.com