



## **biOpen® 2** ( Mac OS X )

### *Modular Bioinformatics Software for Genetic Sequence Analysis & Management*

**biOpen®** from Aborygen is an innovative and intuitive molecular biology software designed to simplify and improve the research work of life scientists worldwide. Features in biOpen® include dynamic and seamless integration of sequence analysis tools with unique and powerful display capabilities, and easy-to-use project management interface.

#### **Extensive modularity**

biOpen® gives you the freedom to pick the sequence analysis tools that meet your needs and budget. All selected tools work in a fully integrated environment with powerful display and project management capabilities.

#### **Easy evolution of your configuration**

You can get new sequence analysis tools and integrate them in your biOpen® configuration when needed.

#### **3D visualization**

The relationship between the sequence and its structure can be studied simply by selecting a part of the sequence and seeing it identified on the corresponding structure.

#### **Powerful display features**

Fully synchronized views with dynamic display of sequence analysis results. This includes automated extraction and display of annotations from GenBank sequence files.

#### **Project management**

Organize and save your sequences, structures and results very easily. Import most popular file formats, including DNA Strider. Projects can be exchanged with your work colleagues.

#### **Graphical export**

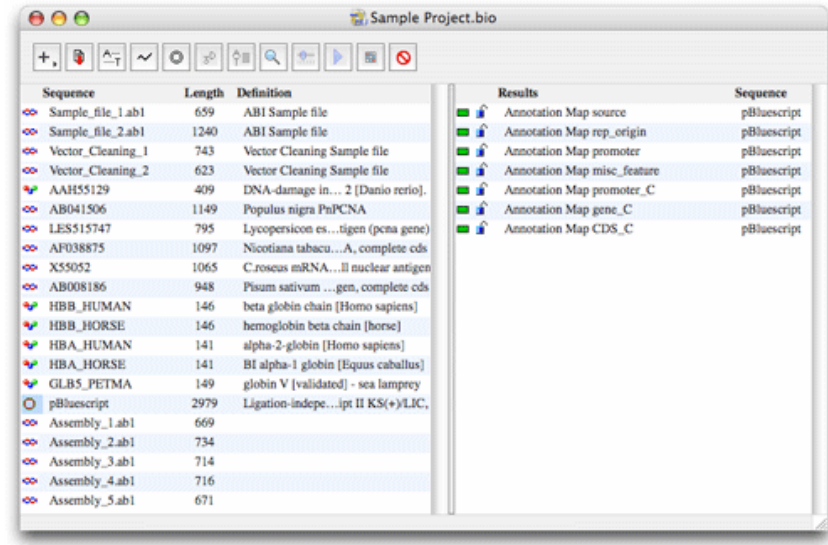
biOpen® views can be simply exported in your favorite word processor or presentation software. You just have to perform a selection and drag and drop it to your document. It can then form an integral part of your project report or presentation.

***FEATURES IN DETAIL.....***

**Project Management** In biOpen®, sequences are organized in projects. From the project window, you can import, open, export and organize sequences, structures and analysis results very easily. Projects including all your data can be exchanged with your work colleagues.

The left part of the Project window shows the sequences in the project. Sequence type, name, size (base pairs or amino acids), definition, accession number and organism are displayed.

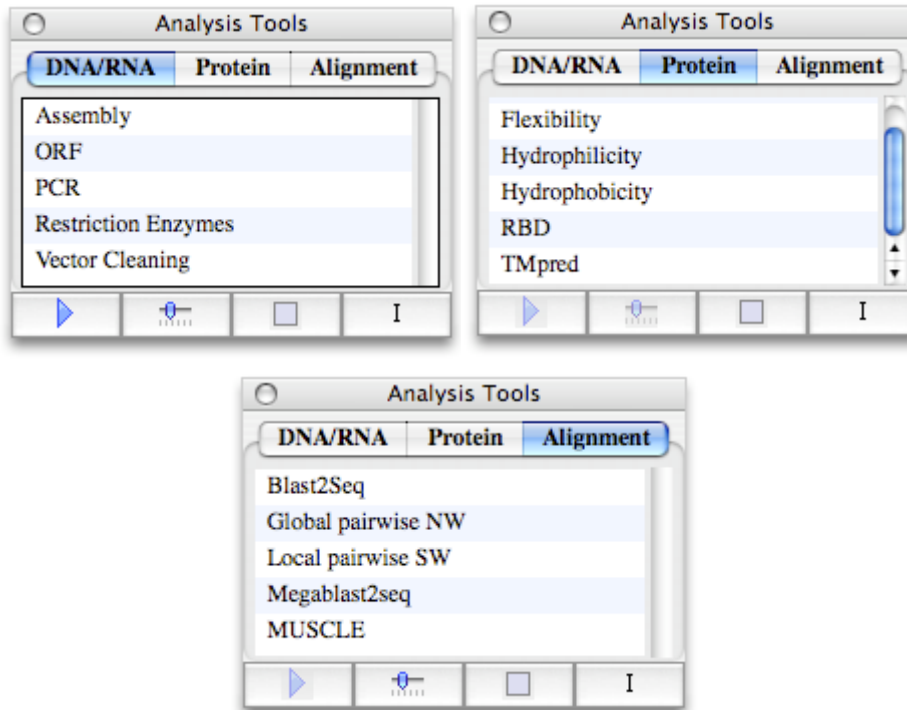
The right part of the Project window shows the results from sequence analysis in the project. Results available for a sequence are displayed by clicking on the sequence. If several sequences are selected, all results available for the selected sequences are displayed.



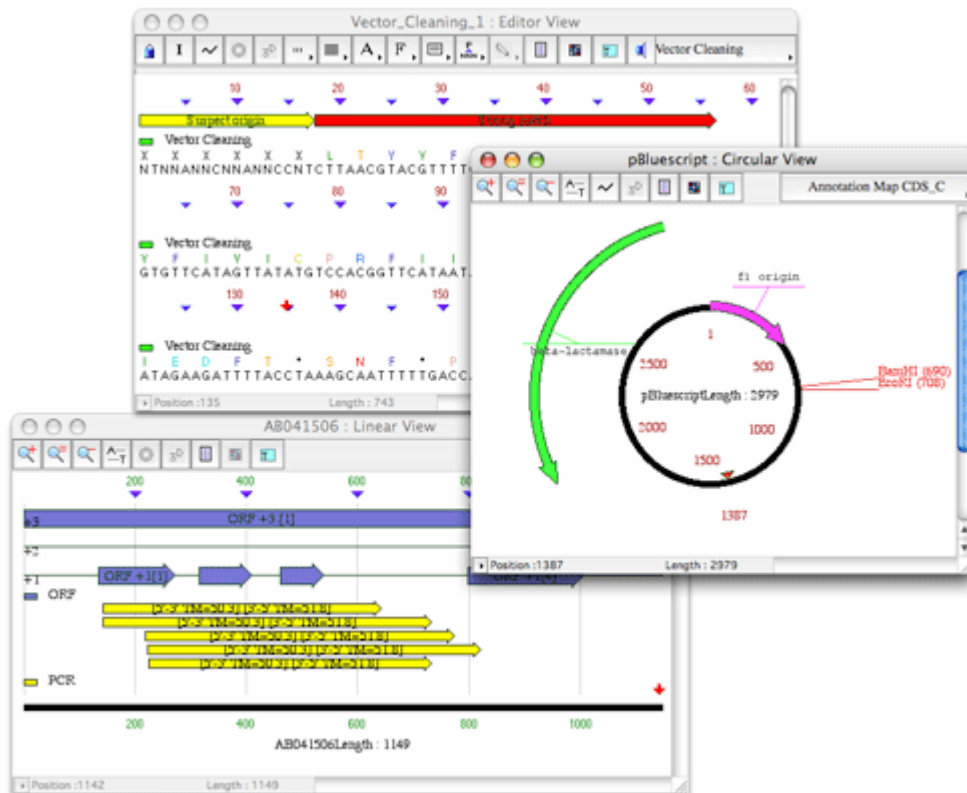
**biOpen® Interface** This is based around a series of views. Selections in one view are synchronized with other views showing related information. This allows different representations of sequences to be viewed simultaneously



**Analysis Tools Window** This displays all analytical tools available as plug-ins in your software configuration.

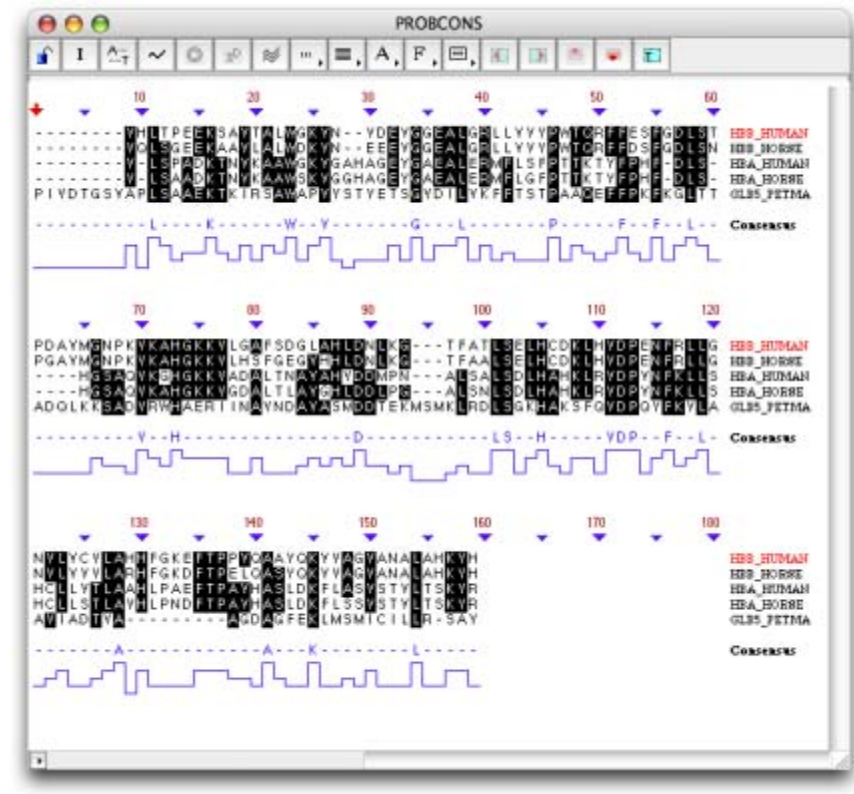


**Results Display Window** A major feature of the sequence editor and graphical views is that it allows the display of available results. The results can be dynamically displayed or hidden from view.



**Multiple Sequence Alignment Editor** The multiple sequence alignment window can be opened by double-clicking on the multiple sequence alignment result in the project window or by selecting the result from the sequence editor or graphical window. The multiple sequence alignment view shows the alignment of the sequences, with the consensus sequence and graph displayed at the bottom.

The 'use black shading' option allows you to color background in black and residues in white.



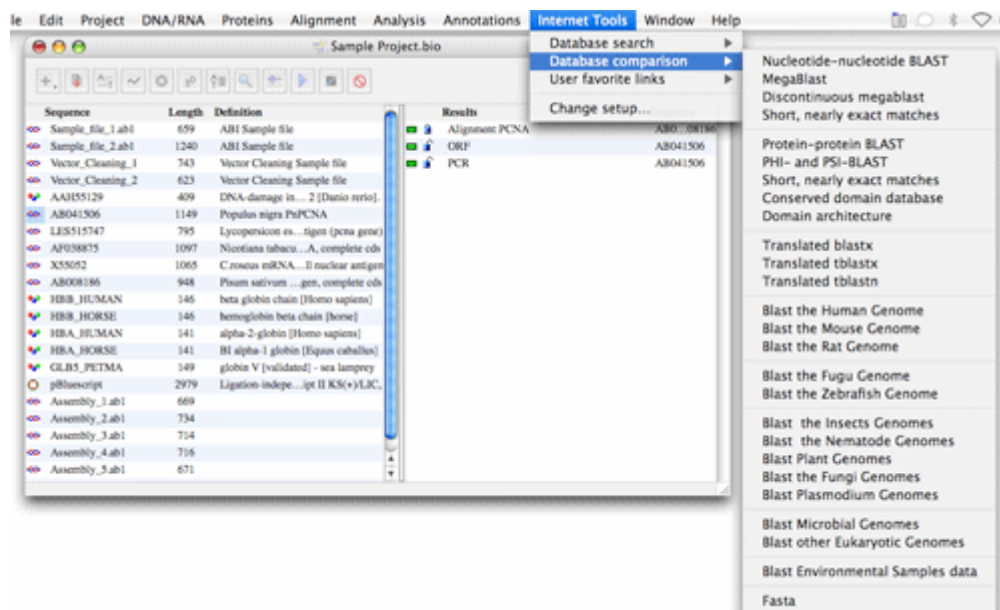
**Documentation Window** The documentation window is used to store notes and internet links and to perform some specific actions on your sequences.

You can paste any text in the documentation window. Internet links are opened by double-clicking. Specific actions can be performed from the documentation window. For example, you can open the editor view for the sequence by using the action editor\_view(), then display a result by using the action result(result\_name), then select a region by using the action selection(start,stop). Specific actions are performed by double-clicking.

You can access the documentation window for any sequence by selecting Project | Show Documentation or by using Cmd-U from the Project window.

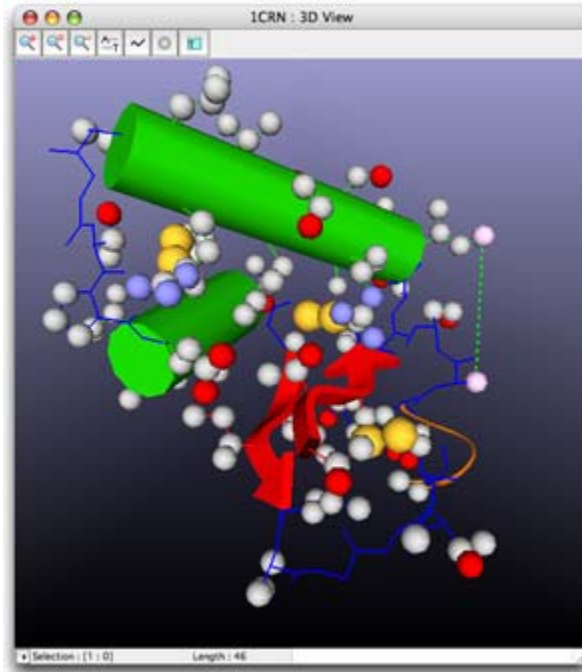


**Connecting to Internet Data Bases** The Internet Tools menu offers links to useful databases and analysis tools. Selecting a page from the menu will open it with your default Internet browser.

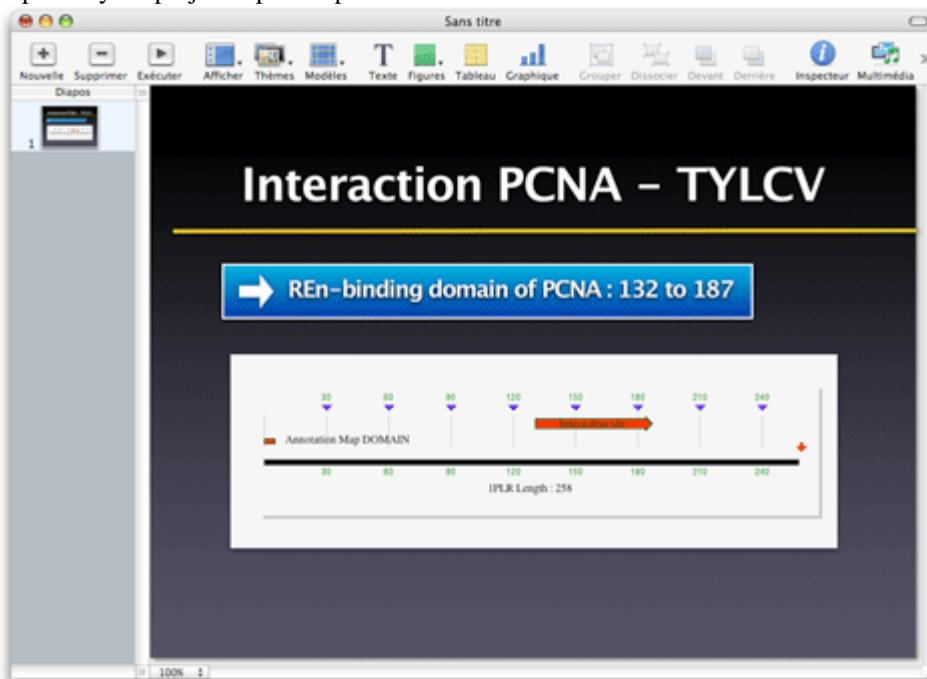


When required, sequences can be dragged and dropped from biOpen to the appropriate forms in the Internet pages. To download a sequence or structure file, hyperlinks can be dragged and dropped from the browser to the project window.

**3D Structure Visualisation** The 3D window is used to visualize the 3D structure, to rotate the molecule, to make residue and atom selections and to calculate distance and angle between atoms.



**Scientific Reports & Publications** All sequence views (editor, graphical or 3D) can be simply exported. You just have to perform a selection and to drag and drop it to your document. It can then form an integral part of your project report or presentation.



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