

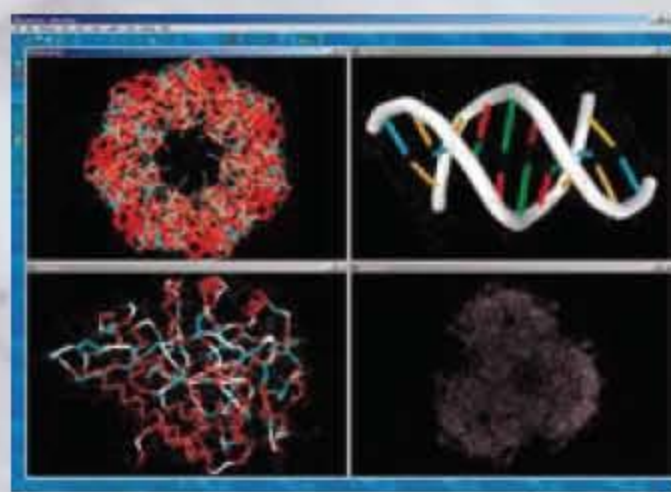
# BioAdviser

BioAdviser for Windows is a PC, Microsoft Windows software application that brings high-quality, super-fast molecular rendering. Targeting the display, analysis and manipulation of large biological molecules including proteins and nucleic acids, it also delivers superb tools for analysis of smaller molecules. The molecules can be viewed in Wire Frame, Ball & Stick, Cylinder and Space Filling modes. Protein specific features include representation by Lines, Wires, Flat and Solid Ribbons. Secondary structures can be viewed also using Tubes and Motifs. For Nucleic Acids the program offers Backbone, Rings and Ladder representations. BioAdviser Fast Mode offers simplified molecular rendering that has only pixel and ball representation. However, using this mode the user can open and manipulate structures that have hundreds of thousands of atoms using very moderate hardware.

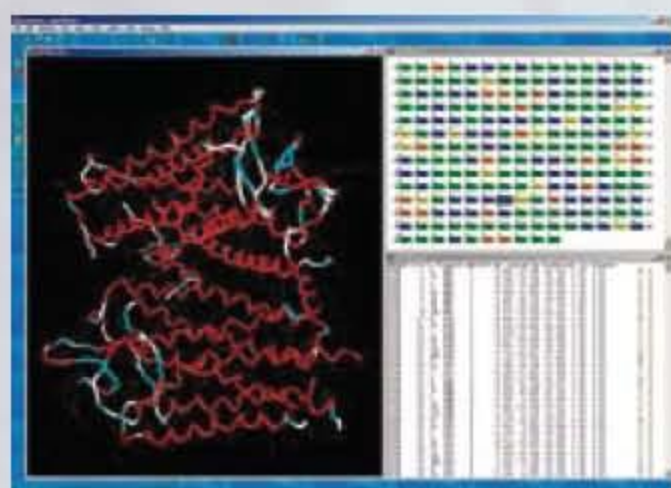
BioAdviser implements multiple molecular manipulation tools, including tools for hiding, showing and focusing on sub-structures. The selection tools allow the user to perform operations on specific, selected subsystems of the entire structure. The most important protein-specific molecular manipulation tools (like torsion or side-chain rotations) are also implemented. In addition to these tools, BioAdviser facilitates the initialization and analysis of the results of MOPAC 2002 jobs.

## Visualization capabilities

- Atom rendering styles: Wire Frame, Ball & Stick, Cylinder, and Space Filling.
- Protein display styles: Lines, Wires, Flat and Solid Ribbons, Tubes and Motifs.
- Nucleic acid representation: Backbone, Rings and Ladder.



- Fast Mode - simplified molecular rendering that facilitates the manipulation of structures that have hundreds of thousands of atoms.
- Stereo visualization.



## Analysis features

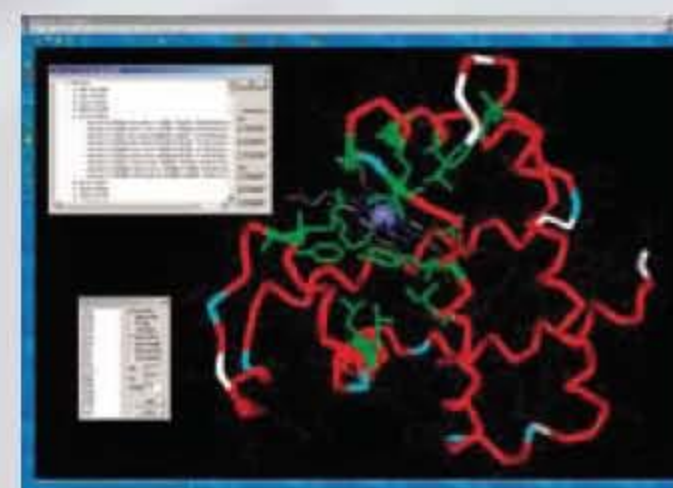
- Ramachandran plot.
- Protein properties plots: Hydrophobic index (Kyte & Doolittle; Hopp & Woods; Engelman, Steitz & Goldman, Charge), Scaled Hydrophobicity, and others.
- Aminoacid sequences.

## Structure building and editing

- Build and mutate protein.
- Edit PDB file in text mode.
- Automatic hydrogen atoms creation.
- Perform operations on specific, selected subsystems of the entire structure.
- Torsion or side-chain rotations.

## Other features

- Prepare and launch MOPAC 2002 jobs\*.
- Supports file formats: PDB, MOPAC DAT, MDL MOL, HyperChem HIN, and XYZ.



## System requirements

- Suggested hardware configuration for Windows version: Intel Pentium 1.0 GHz or higher; 512 MB RAM or more; 100MB HDD space or more.
- Operating Systems: Windows 95/98/2000/Me/XP

\* MOPAC 2002 is not included in the package.

