Ribbons Software Information

The *ribbons* software distribution package (the software) for general molecular illustration and for error analysis in protein crystallography is copyrighted 1987−1997 by Mike Carson (the author) and licensed through the University of Alabama at Birmingham (UAB) Center for Macromolecular Crystallography (CMC).

Ribbons interactively displays molecular models, analyzes crystallographic results, and creates publication quality images.

The CMC's NASA grant encourages commercialization of our work. Thus we are selling the program. Old unsupported (free) versions also exist (see below), but they are not nearly as good as the licensed version.

License Options are:

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No support .    Don't get the source code and don't get to ask me
                 any    questions (read the manual).
              Cost (academic):  $100 (   $0 for ACA members )

Full support . Get the source code and e-mail support
                for all your questions.
              Cost (academic):  $300 ( $200 for ACA members )
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To receive *ribbons*, FAX or US−mail the author the signed *ribbons* license agreement, and make contact via E−mail. A password for an FTP account will be issued.Hopefully we can conduct all business on the internet.

Our licensed products:

- **Ribbons 2.6** (for SGI workstations running IRIX 5.2 or higher)
- **Ribbons 2.7** (for SGI workstations running IRIX 6.2 or higher)

This is the current version of the popular, easy to use and robust software package that has been distributed the last six years (See: "Ribbons 2.0" in J.Appl.Cryst. (1991) 24:958−961).*Ribbons* is designed to display molecular models as rendered images. The data required consist of atomic coordinates in Protein Data Bank format and optional files of color−coding information. The program is coded in ANSI C using OpenGL for graphics and X/Motif for the window interface.

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Features include:
 * Complete Online Manual in HTML format.
 * Display of multiple chains of proteins and/or nucleic acids;
    interactive control of style, size and texture of ribbon drawings.
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* Color coding by a wide variety of biological and geometrical
   properties, including our crystallographic error analysis,
   plus tools to add color coding from the output of "XPLOR" and "O".
* Display of spheres (atoms), cylinders (bonds), and text;
   interactive control of size, style, and color.
* Display of triangular and dot surfaces;
   interactive control of style, and color.
* Interactive control over the material colors and the light sources.
* Display of simple animation sequences.
* Output of primitives for several ray-tracer formats,
   and in Inventor (VRML) format.
* Full-screen antialiasing for very high quality output images.
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- **Ribbons for DEC Alpha** (UNIX)

Should work, if you have C/OpenGL/X/Motif. We pretty much had it going on a test machine here. Contact the author if interested.

- **Ribbons 3.0/Ribbons++** (in the works)

A version with all the capabilites of ribbons 2.6, plus lots of advanced graphics tricks and very high−quality PostScript output is partially ready. This is written in C++ and uses the object−oriented IRIS Open Inventor 3−D toolkit. Anticipated by '97. Full−support ribbons licensees will get the executable version at no charge.

- **Protein Crystallographic Error Analysis**

A suite of non−graphical programs for error analysis are available for a variety of machines, including VAXen. (see: "Error Detection in Crystallographic Models" in Acta Cryst.D (1994) 50:900−909). This package is supplied with *ribbons.* Questions/comments on this are welcome whether or not you purchased support.

Unlicensed Options are:

- No support whatsoever.
- Software supplied as−is.
- No questions answered.

Our free software:

- **Ribbons 2.4** (SGI version 2.4 compiled under IRIX 4.0.5)
- **Ribbons 2.45** (SGI version 2.4 compiled under IRIX 5.2)

These were the licensed versions until 1994. Should work fine on the right SGI machine. About 75% the capabilities of the present version. No online help, but a decent manual.

- **ESV Ribbons 2.2** (ESV ????)

Converted to PEX through heroic efforts of Lily Yang at the UAB/CMC . Not as robust and very picky as to your exact ESV configuration.

- **IBM Ribbons 2.4** (IBM RS/6000)

A conversion has been made by Mike Tung of NIST. I have never seen this one, but if you have this machine...

The past and the future:

The author first got involved with graphics trying to understand molecular dynamics simulations while working with Jan Hermans at UNC in the early '80s. Much of the organization and style is due to the historical baggage from working with E&S PS300s (ASCII files created and loaded on the PS300 for viewing or photography). The old BSribbon ('85) program was developed on a PS300. This software has evolved over a long time into its present state.

Much is planned for *Ribbons++*, primarily in the area of user interaction. However, I'm also trying to do some science, with four other projects currently going on in crystallography and structure–based drug design. All information is subject to change without notice and should not be construed as a commitment by the author or the UAB/CMC for further development and support. As long as I am here and healthy, I shall continue to incrementally develop *ribbons* and offer assistance to its users.

–ps, I'm well–meaning but somewhat absent–minded. If you don't get a response in a reasonable time, please get back to me. –mike

Mike Carson
UAB/CMC
July 12, 1997